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<p>(54) Title: BIALLELIC MARKERS (57) Abstract  The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.</p>		

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## BIALLELIC MARKERS

## RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996, the entire teachings of which are incorporated herein by reference.

## BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution, generating variant forms of progenitor sequences (Gusella, *Ann: Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; W090/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., W0 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include  $\beta$ -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater

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frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

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## SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

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## DETAILED DESCRIPTION OF THE INVENTION

## DEFINITIONS

An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.

10 Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.

25 Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).

As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

30

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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 5 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with 15 the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same 20 chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site 25 is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include 30 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

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and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

#### I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,



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and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference  
5 in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being  
10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table  
15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the  
20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are  
25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

## II. Analysis of Polymorphisms

### A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid  
30 from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For  
5 example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.  
10  
15

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988),  
20 transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification  
25 methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

### 30 B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,

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sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

#### 20 1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

## 2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

### 3. Allele-Specific Primers

5 An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in  
10 conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows  
15 a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of  
20 the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

### 4. Direct-Sequencing

The direct analysis of the sequence of polymorphisms of  
25 the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,  
30 1988)).

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## 5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

## 10 6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

## 25 III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

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## A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See  
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in  
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population  
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic  
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of  
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime  
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by chance.

$p(\text{ID})$  is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies  $x$  and  $y$ , the probability of each genotype in a diploid organism is (see WO 95/12607):

- 10 Homozygote:  $p(\text{AA}) = x^2$   
 Homozygote:  $p(\text{BB}) = y^2 = (1-x)^2$   
 Single Heterozygote:  $p(\text{AB}) = p(\text{BA}) = xy = x(1-x)$   
 Both Heterozygotes:  $p(\text{AB}+\text{BA}) = 2xy = 2x(1-x)$

The probability of identity at one locus (i.e, the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(\text{ID}) = (x^2)^2 + (2xy)^2 + (y^2)^2.$$

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity  $p(\text{ID})$  for a 3-allele system where the alleles have the frequencies in the population of  $x$ ,  $y$  and  $z$ , respectively, is equal to the sum of the squares of the genotype frequencies:

25 
$$p(\text{ID}) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$$

In a locus of  $n$  alleles, the appropriate binomial expansion is used to calculate  $p(\text{ID})$  and  $p(\text{exc})$ .

The cumulative probability of identity ( $\text{cum } p(\text{ID})$ ) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

30 
$$\text{cum } p(\text{ID}) = p(\text{ID}_1)p(\text{ID}_2)p(\text{ID}_3) \dots p(\text{ID}_n)$$



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The cumulative probability of non-identity for  $n$  loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5        If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10        B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

- 15        Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20        If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child
- 25        attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- 30        The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site  $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$ ), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3}) \dots$$

$$p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

#### C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the

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circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of  
5 individuals who have been tested for the presence or  
absence of a phenotypic trait of interest and for  
polymorphic markers sets. To perform such analysis, the  
presence or absence of a set of polymorphisms (i.e. a  
polymorphic set) is determined for a set of the  
10 individuals, some of whom exhibit a particular trait, and  
some of which exhibit lack of the trait. The alleles of  
each polymorphism of the set are then reviewed to determine  
whether the presence or absence of a particular allele is  
associated with the trait of interest. Correlation can be  
15 performed by standard statistical methods such as a  $\chi^2$ -  
squared test and statistically significant correlations  
between polymorphic form(s) and phenotypic characteristics  
are noted. For example, it might be found that the  
presence of allele A1 at polymorphism A correlates with  
20 heart disease. As a further example, it might be found  
that the combined presence of allele A1 at polymorphism A  
and allele B1 at polymorphism B correlates with increased  
milk production of a farm animal.

Such correlations can be exploited in several ways. In  
25 the case of a strong correlation between a set of one or  
more polymorphic forms and a disease for which treatment is  
available, detection of the polymorphic form set in a human  
or animal patient may justify immediate administration of  
treatment, or at least the institution of regular  
30 monitoring of the patient. Detection of a polymorphic form  
correlated with serious disease in a couple contemplating a  
family may also be valuable to the couple in their  
reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where  $Y_{ijkpn}$  is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record;  $\mu$  is an overall mean;  $YS_i$  is the effect common to all cows calving in year-season;  $X_k$  is the effect common to cows in either the high or average selection line;  $\beta_1$  to  $\beta_{17}$  are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms;  $PE_n$  is permanent environmental effect common to all records of cow  $n$ ;  $a_n$  is effect of animal  $n$  and is composed of the additive genetic contribution of sire and dam breeding values and a  
5 Mendelian sampling effect; and  $e_p$  is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next  
10 generation of the herd.

#### D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present  
15 section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such  
20 analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84,  
25 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6  
30 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

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for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-

5 segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the  
10 odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction  $\theta$ , versus the situation in which the two are not linked, and thus segregating independently (Thompson &  
15 Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions ( $\theta$ ),  
20 ranging from  $\theta = 0.0$  (coincident loci) to  $\theta = 0.50$  (unlinked). Thus, the likelihood at a given value of  $\theta$  is: probability of data if loci linked at  $\theta$  to probability of data if loci unlinked. The computed likelihoods are usually expressed as the  $\log_{10}$  of this ratio (i.e., a lod  
25 score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod  
30 scores for differing values of  $\theta$  (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

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Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of  $\theta$  at which the lod score is the highest is considered to be the best estimate  
5 of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of  $\theta$ ) than the possibility that the two loci are unlinked. By convention, a combined lod  
10 score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared.  
15 Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

#### IV. Modified Polypeptides and Gene Sequences

20 The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some  
25 nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component)  
30 except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the



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corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or  
5 other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate  
10 promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host  
15 sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include  
20 fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as  
25 *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing  
30 includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby, *5 Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is  
10 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene  
15 and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating  
20 the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292  
25 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

30 In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate

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the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and  
5 antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to  
10 corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide-fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A*  
15 *Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of  
20 immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

#### V. Kits

25 The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific  
30 oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means  
5 used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

10 The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

#### 15 EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to  
20 microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference  
25 sequences of the fragments shown in the Table, column 1. The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154 (1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence.

5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three additional probe sets. Thus, there are four probes

10 corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in

15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different references sequences were included

20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or

25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For

30 example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by

5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined a priori, such

15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

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All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and  
5 individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
						TGTGAAACTCCACTTGAAGCCAAAGAAAGAACTCACACTTAAACACATGCCAGTTGGGAAGGTCT
						GAAAACTCAGTGCATAATAGGAACACTTGAGACTAATGAAAGAGAGAGTTGAGACCAATCTTTATTT
						GTACTGGCCAAATACTGAATAAACAGTTGAAGGAAAGACATTTGAAAAAGCTTTTGAGGATAATGT
WI-7070	226	C T	---		---	TACTAGACTTTATGCCATGGTGCTTTTC/TAGTTTAAATGCTGTCTCTGTCCAG
						AAGCCATTGACGTAAACATCTCAGAGGTTATTGTCATGGATTGACTCCTGGGACAAAAGGAC(G/C)AA
						AAACACTCTTCTGGGATATCTGCGAGATAGTACCCAAAGATCAGATGCTACCCAGATGTGTTT
						GATAATACATAAGCCCCCTAGGATTAGATACAATCTTGAAGAAACATGAGACAGATAATCTGAAIT
WI-10744	61	G C	---		---	AAATGAGGTAAAGTTTCAGGCACTCA
						GGGCAAAATACCAGAAAAAGTCAAAATACCAGCATCAAAGTCAGGTGCAAAGGAGGTAGAACA
						TTACAGTAACATATGTCATCTTTTGTATATTAGTATTATCTGCCCAATGCCTAGAATAC/TAGTG
						GGTCCCTAATAGTTATTAGTTCTTTTCTCCTCTTCTCACTCTGAAATTTATTTTATAGTTAA
WI-9975	126	C T	---		---	GGGATTAGTTACCACCAAAATGTGTATGATCAATTTGATTCITTAAGAA
						GCTAGGTTTGTCTGTGGTCTCTCACTAGACTGAGATGACTTGATTACAGTAATCCCTATGT
						GATGTAACATAGCTAGACCTCCCTCTCCGCAATCCAGCTCCAGGTTTCAGAAAAGTATGCCACAC
						TCAACCTTCTCTCCAGTTTATCTGTATTAATTTCTCCCAATTAATTCAAAAGGAGTGGACAGGT
WI-8010	247	G T	---		---	CCCTGGCTGAAAAGAAATAAGAGATCCCCAAAGTGGTGGGG(G/T)CTT
						GCCGGGCTATCTTTAAATTTAACTTGATCTTTGGTGTTCTCCATCCTAGGATCTGCCITTAAT
						CTTTGCTGCTGTGTA(G/C)ATTACCTGATCTACTTTTGATACACAAAGGCTGATGGCTCACAATGT
						AGTAGGCCAAATCTCAGGTCTCTTTGAAATTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA
WI-5222b	85	G C	---		---	TCTCGACTCTATAACAACCTCCAAACAGAA
						GCCCGGCTATCTTTAAATTTAACTTGATCTTTGGTGTTCTCCATCCTA(G/C)GATTCTGCCITAT
						AATCTTTGCTGCTGTGTAGATTACCTGATCTACTTTTGATACAAAGGCTGATGGCTCACAATGT
						AGTAGGCCAAATCTCAGGTCTCTTTGAAATTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA
WI-5222	52	G C	---		---	TCTCGACTCTATAACAACCTCCAAACAGAA
						TATGCACCTCCACAAAAGCGATATAATTTAAAGTTTTTTCATTAGAAATAAATGTATAAAAATAA
						ATATGTTATTATAGGCATTTATTACTAACTATAGTCTCTCTGGAAAGAACACCCCAACCAATACCTT
						ATAAAGTACATGTAATTTATAGTAACATATTTTACTATATACATATGAAAAAATCATATTTCTACA
WI-8007	242	C A	---		---	GAAGAGCTGAACAGACATTCACCGGATACGACTGTTGGAC(G/A)AGCTGCTG
						TCAGTTGCAAAAATGCTGCCATAAACATGCTTTGCTTATCTCTGTCATATGATGTGTTTGTAG
						TCTATATTCACACATATGAGTGAAATTT(C/T)GGGGCATGGGAAATACATCTTTATGAGACATTGA
						ACTGCTCACCACATCATAGTATCCATTTAAACAGACCCCAACAATGTATAAGAAATCCCTTTGTTTTAC
WI-9823	97	C T	---		---	ATGCTTCCCAATCTGATTTTGTATGACTATTGTATGCACAGTTGGATCACC



WI-9651b	105 A T ---	---	---	TCCTACATCTATGGACAACCTCCATGCCCTTGCACATGCTGATCCCTCCTCCCTGGAATTCCTTCCT ACTTGCTCCTCATGACAAATTTTCTGCTGCTCTCAJATGGGGCAGCTTGCAAGCCTCCCTTTAGAC ACCTACAGGTACAGCCGACCATGCCCTACCTCCATGCCATGCCAGGGACCCCTATAGGCCCTCTG TCCTTAACCTGTAATGGTATATTAATCCTTGGTGTTGMAATGTCICIC
WI-9651	139 T C ---	---	---	TCCTACATCTATGGACAACCTCCATGCCCTTGCACATGCTGATCCCTCCTCCCTGGAATTCCTTCCT ACTTGCTCCTCATGACAAATTTTCTGCTGCTCTCAAGGGCAGCTTGCAAGCCTCCCTTTAGACACCT CTCJACAGGTACAGCCGACCATGCCCTACCTCCATGCCATGCCAGGGACCCCTATAGGCCCTCTGT CTTTAAACCTGTAATGGTATATTAATCCTTGGTGTTGMAATGTCICIC
WI-7676b	309 A C ---	---	---	GTGACCTTCCTGCAGCGTGGAGATGGCACATCCTTGTGCTGGGGACTTGGCCCTGCTATTTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCCAAGGGTAGATGGGAGGGTCTGTGTGAAGGG GCCGGCTTCTCTGGTGCCTGCTGGGTTGCAGGGGCAGGAAGCGTGTGGACTGCAGCTTCTGCTGGTGC TCCCCCGTCTCCTGGAGGCAGTATAGGAGAGAGAGCAAGGATTGAGT
WI-7676	139 C T ---	---	---	GTGACCTTCCTGCAGCGTGGAGATGGCACATCCTTGTGCTGGGGACTTGGCCCTGCTATTTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCCAAGGGTAGATGGGAGGGTCTGTGTGAAGGG GCCTGGCTTCTCTGGTGCCTGCTGGGTTGCAGGGGCAGGAAGCGTGTGGACTGCAGCTTCTGCTG GTGCTCCCCCGTCTCCTGGAGGCAGTATAGGAGAGAGAGCAAGGATT
WI-10072	105 G A ---	---	---	CATTATCTGTCTGGTCTGTTCATTCACCTTCTCTCTCCCAATGAAGAGGATATTTAAGCATCAT CATCTGGCCCTTTTGGATTTTGAATATTTTGTGJAGTACCTCTATGCACATGATAAATTTGTTA TGCTGTCTCTATCTATCTTTTGTATAGGAGTTTGGCCATGACCCCTTATGAGGAGAAAAGGA TCACCCCTTTTGGCTCTACACCTTATAGATATTTAAATATCTTT
WI-9986	42 T C ---	---	---	TTGGTGTGAACCTCAGAATATAGGAAATAAGACAATTTGAATTA/CJGTACCCAGGAAACAAGAG CCCTGCACCTTGACTCCAAAGGAGTCTATTTCTGGCTGTTCCAGACTTTATGTATCTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTCATCATCTGTATCCAGGGTAGTACTCACAAGAACATGTCA ATATCAATAGCATGCATATGGGGTGTGGATTCTTAGAACTTATTGCAATT
WI-7041	174 C A ---	---	---	GTCTATTGCAGGAGAAACGTCCCTTGGCACTCCCACTCTCATCAGGCCCAAGTGGAGGACTGGCCAGA GGGCTGCACATGCAAACTCCAGTCCCTGCCTTCAGAGAGCTGAAAAGGGTCCCTCGGTCTTTATTT CAGGGCTTTCATGCGCTCTATCCCTCTGCTCTC/CJACACCTTCTTTGGAGCAAGGAGATGC AGCTGATTGTGTAAACAAGCTCATTTGTACAGTGTCTGTTCATGTAATAA
WI-7224	134 T C ---	---	---	ATAACCCCTTGTGTATGTATCACCACCACTCAATTTATCAACTTATGTGCTATCAGATATCCTCTCT ACCCCTCAGTTATTTTGAAGAAAATCCTAAACATCAAAATACTTTCATCCATAAAAATGTCAGCATTT /CJATTAATAAACAAATAACCTTTTAAAGAAACATAAGGACACATTTTCAAAATTAATAAAAATAAAG GCATTTTAAGGATGGCCTGTGATTATCTTGGGAAGCAGAGTGAATCATGCTAG

WI-10826	132 A C ---	---	TCCTATTGCAATTCACAGTAGCCCATGAAGTAGGTATAACACAGCCTCTATTTTAAACATGAGAAGAT GGAGGCCCTTTTCCAAATGGACTAAGTAATGTGTCTCAGGTTTTCTTAATAAGCAAGACCTGCAJVC JOCCTGGCTTCTGAGTCCAAAGCTTATCCCTTCTCATGTCTGTGTCAGCCAGGACCCCATGCGCA GAAAGCCAGCCTCTCCATCCCCAC .
TIGR- A004S25	145 G A ---	---	AGATCGCCATTAGTATTATTCCTTTGAAGATACTTTGGAGATTCAATTTCTTGAGTGGCACTGCAT GCTCATTGAGTGAAGAACTTTGGGGGTATAGAAATGGAATGGAGATTCAAACAGCTTTGCTGAAAC TGTACTTTGGG/GA/CTCCAGACTTCACTGCTCTTAGGCATTGAACCATCACCTGGTTTGCATTCTTC ATGACTGAGGTTAACTTAAATGACTGAGGTTAACTTAAAC
WI-1021	24 A T ---	---	AAACACAGAAATCATCAAGCAC/A/TATCTGTGTTTGAGATAAAATGATAGTCTGAGTCACCTATG TAAGAAGTAACCTCGAAATAGTAGGATAGTATTATCATTTCTGTAAATAGATTACCTCTCAGCAAT TGGTCTGTTTTCATTCTATGGAACCTCTCCGTACTGTAATTTTCATTCTATGGAACCTCCCATACTGT AATTGGACAGTTTGGTTCCAC
WI-4687	121 G T ---	---	TAGTATGTCACCTGCCATGGTAAGGACTTTGATCAGTAGGAAATAGAACACTTTGAATGGTCTTGTC TTTCAATAAAAGAGTGACATGATTGAACATGTTTTAGATAAAGGGCACCTT[G/T]GCAGGAGTGT TTAGGATGAAGAGAGAGAGATTAAAGGAAGATCAGGAAGAAAGTAGCAATGGGAATGAAATAAG GAGGCCCTGAGATCCACTGGATAATCTAAAAACCAGAGAAAGAACTTGAT
WI-4719b	107 T G ---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTGTCTTGGGTGAGCGGATT ATGCTGACGCCATGGGTGTTTCAATAGTGACTTGAGAGTTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTTCATTCACAAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCGCCACTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-4719	70 G A ---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTGTCTTGGGTGAGCGGATT AT[G/A]TCTGACGCCATGGGTGTTTCAATAGTGACTTGAGAGTTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTTCATTCACAAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCGCCACTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-9484b	216 G C ---	---	TCAACACGCTTTTATTGCCACTTCTGGCTCCCTCGTCCAGGAAGATTCTTACCTTACCCGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCACITCTCTCTGACACTGCCAAGT TAAAGAAACCCCTGCTTGTGAGAGGGAGGGCCAGACAGGGAGGAATTCAGGGCATGTATGGCTC AGTCCCACTTCT[G/C]ACTGCAGAGTATAGGGACCAGGGTTCCAACTTT
WI-9484	178 G A ---	---	TCAACACGCTTTTATTGCCACTTCTGGCTCCCTCGTCCAGGAAGATTCTTACCTTACCCGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCACITCTCTCTGACACTGCCAAGT TAAAGAAACCCCTGCTTGTGAGAGGGAGGGCCAGACAGG[G/A]AGGAATTCAGGGCATGTATG GCTCAGTCCCACTTCTGACTGCAGAGTATAGGGACCAGGGTTCCAACTTT

WI-7330	207	C T	---	---	AGGATGGAAGGAGACACGGGGCAGGAGAACTCTCTTCTGCTAAATCGATAGGAGTCAGTTTTGTCT TAAATGCTGACTACAGCCACTGACATGGTTGGCTGGAATTTCTCTTTAATTTGTGGCATATAGGTTT GTGACACAAGAAGTCATCTTTGGTGGCTAAGTTTTACTAAGGAAATAACTGAAAGATTAAAG TGAGAG[C/T]TGAAAGAGAAATGATAATGCTTCCAACTGTAGCTGTACAG
WI-9443	211	G A	---	---	TTAAAAACAGTTTCAGGTTGGTGAAGCAGAAAAGGATGTGATTACAATTTAAATGAATCAGTCACATT GCACAAATTAATCCTCTTGGCATCATACAACTGGGTTTTAATGGCAAATGATGACATCATAGCATGA CCAACTCATGGAAGGAGTCTAGAGTCCATCAGCTCACACCTGAGGGGAAAGGCACTGCAACCCA CTGACGAGAC[G/A]CAGAGACCTTGGACTACAGATGACACCAACATGCCACATT
WI-7166	59	C T	---	---	TCCTCAAAAGAGAAAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA[C/T]GGAT CATCAACAAGATTTCCTTGTGCAAAATATTGACTATTCTGTATCTTTCATCTTGACTAAATTCGTG ATTTCAAGCAGCATCTTCTGGTTTAAACTTGTTCGTGTAACAATTGTGAAAGAGTCTTCCAAT TAATGCTTTTATATCTAGGTACCTGTTGGTTAGATTCAAGGCCCCGAG
WI-7259b	189	T C	---	---	GCCTTCCCCAGGAAGCGGGGCTTGGCCTGGAACCTTCCAGAGAGGCGGGAGCAATTTTAGCC CCACCTGCTCCCATCTGCCCCCTGCAACAGCTGAGGCTGCTTCTCTCTGAGTTCTCTGGGCT GGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACAGT[C/T]GGGGGAGCAG AGCCAGCAGGTGGACAGGTGTTGCAGGGGCCAACCTTCCCCCTGGAGCTC
WI-7259	188	G T	---	---	GCCTTCCCCAGGAAGCGGGGCTTGGCCTGGAACCTTCCAGAGAGGCGGGAGCAATTTTAGCC CCACCTGCTCCCATCTGCCCCCTGCAACAGCTGAGGCTGCTTCTCTCTGAGTTCTCTGGGCT GGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACAG[G/C, T]TTGGGGAGCA GAGCCAGCAGGTGGACAGGTGTTGCAGGGGCCAACCTTCCCCCTGGAGC
WI-7322	275	A G	---	---	GTACTTTAGGCCTGTGGAGGTGGGCATTAGTGGTGACCCCTGCACAGGGTTTTCTAACAGATGAC CCTGTGAATCATAA TTTAAACCTGCATATATTTATAGCCAGTCACATTTGCCCTCTCACCCCTATATG GCCATAAAGCTGCTAAGCACTCAGGCCTCCCACTCATCAACCCCTTTGACCAGAGAAAGACACTC TGGTTCTCTATCCCCCTGTACATAGAGATTGTGATGGGGCCTCTGGCTG
WI-7685	46	T C	---	---	TCAGTTCTAGTCTCTCTGGGGCCACAGAAACTCTTTTGGGCTGT[C/T]TTTCTCCCTCTGGATCA AAGTAGGCAGGACCATGGGACCAGGTCTGGAGCTGAGCCTCTACCTGTACTCTCCGAAAAATCCT CTTCTCTGAGGCTGGATCCTAGCCTTATCCTCTGATCTCCATGGCTCTCTCCCTCTCCCTGCGGACTC CTGGGTGAGCTGTGGCTCAGTCCCCCAACAGATGCTTTTCTGTCTC
WI-563	87	G A	---	---	TGTGACCAATTGTTATTTAGAGGGTTTAAACAATGGCCTGACTATCACCTGATGGTGGCCAGAAATTC CTGGGGGAGGGCCTCCCTTGAJCCCTGATCATGTCTACCTAAGTGCCTACTCTAACAATACTACTCC TGTGGTATGGGATCCTAAGCCCAAAAGCTGAAATGAACATGTTCTAGCAGTACAGAAATCCATACT GCCCTCAGTAAAGGCAATTTTAAATCTCTTTGGATAACCCAGGGCACAT

WI-931c	191 C A ---				GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTCTTATCTGCTGTGTCAAAATGATCCTTCT GTTGCTGCACGTGCTACTGTTGATGGATTATAATTATGTCCAAAAAGGC[C/A]CGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-931b	81 A G ---				GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCTCCCT[AG]TCCCTCACCACACCTTCCAGTGTCTTATCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACGTGCTACTGTTGATGGATTATAATTATGTCCAAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-931	31 A G ---				GACCAGGGCACCAGAAAGCCACGGAAGCCAC[AG]GCCACTAGCCCTGAACCTTGCACACCCCTGGA GTTCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTCTTATCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACGTGCTACTGTTGATGGATTATAATTATGTCCAAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-10870b	91 C T ---				GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAGTGGGG[C/T]ACCTACTTAGAGCAGTGGAGTACCCTGAGTACGACCCCC TTAGCAGCAGAATTACAAGAAATCTTGGGACCTGTACTCTGTATACAAAATAAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTAAATAACGTTGCCCCCCC GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAGTGGGGCACCTACTTAGA[GA]CAGTGGAGTACCCTGAGTACGACCCCC TTAGCAGCAGAATTACAAGAAATCTTGGGACCTGTACTCTGTATACAAAATAAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTAAATAACGTTGCCCCCCC AGTTTATTCTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAGTCTT GGGAAATATTGGGCATTGGTCTGGCCAAGTCTACAATGTCCCAATATCAAGGACAAACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTCTGGACATTGCCCATGTATAATCCTCACTGATGATTTCAAGCTAAAGCAA AGTTTATTCTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAGTCTT GGGAAATATTGGGCATTGGTCTGGCCAAGTCTACAATGTCCCAATATCAAGGACAAACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCC[AG]TTAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGACATTGCCCATGTATAATCCTCACTGATGATTTCAAGCTAAA GCCTTGGAGTATATCTAACTGTGGCTCCACTTTCATTTTCTTGAACATTGCTATCAACTGGGAA GAGT[C/A]GTGACTTTATGCCAGTTTCCCTCTCAGATTTTATGACGGTGTGTTTTCTTTTGTGA TGCCATTTGAGGGATGATGTTCTTAAACTATGAAGTACTGGCTGTCTCTCTCCATTGCTGTTTCAGG TTAACAGCCACCATTTGTAAACACTTTGT
WI-7719b	281 T C ---				
WI-7719	163 A G ---				
WI-10396	72 C A ---				

WI-10673	94	C G	---	---	TCCCTTTATGCAACCAAGAGATATTTAATAACACCAATTACGTAGCAGGCCATGGCTCATGGGACC CACCCCGGTGGCACTCATGGAGGGG[C/G]TGAGGTGGAACTATGCAGTGTCTCGGCCACACA TCCTGCTGGGCCCTACCTGCCCAATCAATCTGCCAATAAATCCTGCTCTATTGTTGTCATCCTG GAGAATTGAAGGGGAGGTCAAGTGTGTTGTCATGATTGTCAGAACCT
WI-7842	57	T C	---	---	CACAGCCATGCCCTTGAGGAGCGGCCACCAGATGCTGAATCCCCTATCCCATTCTGTCGTATGAG TCCGATTTGCCCTTGAATTAGCATCTGTCTCCCCCAAAAAGAAATGCTATGAAGCTTTCTTTCCCT ACACACTCTGAGTCTCTGAATGAAGCTGAAGGTCTTAGTACAGAGCTAGTTTTTCAGCTGCTCAGAAT TCATCTGAAGAGAGACTTAAGATGAAGCAAAATGATTGAGCTCCCTTATA
WI-7721	145	A C	---	---	CTGCCATCATACGCCCACTGGAGTCCACACTTGAATTTGGCAGCTACACGGGTGCCATGCTCTGG AGGAGAAAGGGGGCCACATCCCAACCCAGCTGTACCAAGCCCGGGGAGGTGCAGCCCTTCTCTCC TGCTCTG[C/A/C]TCTGACTCTCTTTTGAGGTCCCTGTATGCTACCTCTGACTTCTGTTGGTCCCTCTG TGCTGCTCTCATCCATTCCTCTTACTGGGGCTGGGGCTCTAGCCCCA
WI-4767b	173	C A	---	---	TTCCAGTCTGTTTATCCTTTTCATTGTCAAAAAGATGCTCTTAGACTGAAATTCATAAGAGTTCCCT CAGTCTGGGTAATCCTAGATCTTCTATATCCATTGAGTGTGATGGAGTTGGAGAGGGTATGTTT CTTGCTTGAGAAATCCTAGAAAGCACAGGGATGAC[A/C/A]AAATCACTAAGGAATTCCTACTAAGA CTGCTCTAACCCAGAGATTTTAACCT
WI-4767	50	A G	---	---	TTCCAGTCTGTTTATCCTTTTCATTGTCAAAAAGATGCTCTTAGACTG[A/G]ATTCATAAAGAGTT CCTCAGGCTGGGTAATCCTAGATCTTCTATATCCATTGAGTGTGATGGAGTTGGAGAGGGTATG TTTCTGCTTGAGAAATCCTAGAAAGCACAGGGATGACACAAATCACTAAGGAATTCCTACTAAGAC TCCTCTAACCCAGAGATTTTAACCT
WI-7718f	222	C T	---	---	ATTGCACTGAAGTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAGATG ACTTGCAGATGGAAGAGGTGAAATGAAGAGGAAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAA[C/T]CATGCAGGAAGGAAACTATGTATTAAAT
WI-7718e	60	T C	---	---	ATTGCACTGAAGTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATTCGCAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAAT
WI-7718d	31	G A	---	---	ATTGCACTGAAGTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAAT

WI-7718c	91 C G ---	---	---	ATGCACTGAAGTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATCCAAAGGGGCGTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTCAGATGGAAAGAGGTGAAATGAAGAAGGAGCTGTGTGAAACAGAAAAATAAGTC AAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAT
WI-7718b	248 A G ---	---	---	ATTGCACTGAAGTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATCCAAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ACTTTCAGATGGAAAGAGGTGAAATGAAGAAGGAGCTGTGTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAT
WI-7718a	42 A T ---	---	---	ATTGCACTGAAGTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGC AAGGATTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGAT AGATGACTTTCAGATGGAAAGAGGTGAAATGAAGAAGGAGCTGTGTGAAACAGAAAAATAAG TCAAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAT
WI-7227d	99 G C ---	---	---	AGGGAATTGTGTTGCTCCTGGAGGAAGCCCGAGGCATCATTAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTCACTTTTCAGACAAGCTTTA[G/C]AGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCAAGAGGAGCTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227c	291 G A ---	---	---	AGGGAATTGTGTTGCTCCTGGAGGAAGCCCGAGGCATCATTAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTCACTTTTCAGACAAGCTTTAAGAGAAATGGACTCAGGGAAGAGACTCACATGC GGTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCAAGAGGAGCTGAGCTAAACAGTG TTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATGCAAT
WI-7227b	93 G T ---	---	---	AGGGAATTGTGTTGCTCCTGGAGGAAGCCCGAGGCATCATTAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTCACTTTTCAGACAAGCTTTAAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCAAGAGGAGCTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227a	24 A G ---	---	---	AGGGAATTGTGTTGCTCCTGGAGGAAGCCCGAGGCATCATTAACAAGCCAGTAGGTACCTGGC TTCCGTGGACCAATTCACTTTTCAGACAAGCTTTAAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCAAGAGGAGCTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7310b	234 A C ---	---	---	CCACAATGCCTCCACAGATGTCAAGGACTCCTGCTGCTCCTGGAGGTGGAGACAAGGAACCTCCG AAGAGGAAGGAAGAAAGCCGCTACTGCTATGTGTGATCCTTCGAAACAACTGATGCGAAACT TGAATCTGTTACTGAAATGAGGAGAGGAGACATGTGCTATTGAATGAGCCCAACACACTGTAAAT ATCCACAGACTCCCTCCCTGCCCCCATCCCAACATGATGATCTTGAGATTTC

WI-7310a	64 T A ---	---	CCACAATGCCTCTCCACGATGTCAAGGACTCCTGTCTGTCTGGAGGTGGAGACAAGGAACQI/A JCGAAGAGGAAGCAAGAAAGCGTACTGTCTATGTGTGATCCTTCATCGAACAACCTGATGCGAA AACTTGAATCTGTACTGAAATGAGGAGAGAGACATGTGCTATTGAAGTGAAGCAACACACTGT AAATATCCACAGACTCCCTCCCTGCCCATCCCAATGATCTTGAGATTTC
WI-7878b	162 A G ---	---	CCAGCAACACTACACCCCTTGACCTGGCTGGACTCCTATGATGGCTGCTGGTTGATAATAATCA GATCATGCCAAGACAGGGCCTCTGATAATCGCTTTGGCATGATTGCAATGGAGGCAATGCGTCC CTGAGGAGAAATCTGGAGGAGCTG/A/GJGTGTGATGAAGGTGTATGTTGGAGGGAGCACAGTGT CTGTGGGAGGCCAGGAAGCTGCTACCCCAAGATTGGTGCAGGAAACTA
WI-7878a	51 C G ---	---	CCAGCAACACTACACCCCTTGACCTGGCTGGACTCCTATGATGGCTGCTGJTGTTGATAATAA TCAGATCATGCCAAGACAGGGCCTCTGATAATCGCTTTGGCATGATTGCAATGGAGGCAATGC GTCCCTGAGGAGAAATCTGGAGGAGCTGATGATGAAGGTGTATGTTGGAGGGAGCACAGTG TCTGTGGGAGGCCAGGAAGCTGCTACCCCAAGATTGGTGCAGGAAACTA
WI-7381c	213 C T ---	---	CTCCACATTCACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTTTCTTTCTACC AGCCCTGCAAGTTTCCTCATGGAGCTCGGAGGAGCAGGCTGCAGGTTCTCGCTATGGTGAGATC AGATGTGGCCAAAGGAAGGAGCTCTGGTTCCAGAGAAATTCACAAAGTTCCCTCTGTACAGAGACA AAAGGCCCTC/TJGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381b	54 C G ---	---	CTCCACATTCACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTGCTTTCTTCT ACCAGCCCTGCAAGTTTCCTCATGGAGCTCGGAGGAGCAGGCTGCAGGTTCTCGCTATGGTGAG ATCAGATGTGGCCAAAGGAAGGAGCTCTGGTTCCAGAGAAATTCACAAAGTTCCCTCTGTACAGAG ACAAACGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381a	53 C G ---	---	CTCCACATTCACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTGCTTTCTTCT ACCAGCCCTGCAAGTTTCCTCATGGAGCTCGGAGGAGCAGGCTGCAGGTTCTCGCTATGGTGAG ATCAGATGTGGCCAAAGGAAGGAGCTCTGGTTCCAGAGAAATTCACAAAGTTCCCTCTGTACAGAG ACAAACGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-1017b	93 G A ---	---	AAATTGCTCTATTCCGACCCCTCATATTAATAAGAGCAATGAGAGCGAGGGAATTAAGACTCTCTC AGGTACTGACTGTGGGACCAAGAGAG/GA/GATGTAGATTGTACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTCTTCCCATTTACAAATAAGGAGACAAAAATTAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGTAGGTTTTGTCCC
WI-1017a	92 G A ---	---	AAATTGCTCTATTCCGACCCCTCATATTAATAAGAGCAATGAGAGCGAGGGAATTAAGACTCTCTC AGGTACTGACTGTGGGACCAAGAGAG/GA/GATGTAGATTGTACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTCTTCCCATTTACAAATAAGGAGACAAAAATTAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGTAGGTTTTGTCCC

WI-1795b	130 T	C	---	---	GAAGCAACGAGAAAGTATCTTTATCCCATCTAGATTATGCTGGGTTCTTCCAGACTCTACGATTA AATTGTATGCATGTGAACAACATGATGAGGTACTTATAGATCTGAGTCTTGTGGAGAAAGAAAGT/CJC GTCTACCAATTTTACCACAAATTCGTAGTACAATTTAAGTATCTCTGTATTATCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATT
WI-1795a	47 T	C	---	---	GAAGCAACGAGAAAGTATCTTTATCCCATCTAGATTATGCTGGGTT/CJC/TCCAGACTCTACGA TTAAATTGTATGCATGTGAACAACATGATGAGGTACTTATAGATCTGAGTCTTGTGGAGAAAGAAAGT GTCTACCAATTTTACCACAAATTCGTAGTACAATTTAAGTATCTCTGTATTATCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATT
WI-10616d	136 G	A	---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCCGACATCATGACCCGTTAACGTCCAGGCCATGT CCCACATAGAGAAAGCCTTTACTTCCAGCTCTCCATACGTAGGTCTGTCCTCTCTATCACATTGGCCA C/GAJTAGCCCTCCCTCCCTCCCTACAGGCCCTCTTCAGGGCCCCAGTCCCCCTCTGAGACTCCG ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
WI-10616c	136 G	A	---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCCGACATCATGACCCGTTAACGTCCAGGCCATGT CCCACATAGAGAAAGCCTTTACTTCCAGCTCTCCATACGTAGGTCTGTCCTCTCTATCACATTGGCCA C/GAJTAGCCCTCCCTCCCTCCCTACAGGCCCTCTTCAGGGCCCCAGTCCCCCTCTGAGACTCCG ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
WI-10616b	141 C	T	---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCCGACATCATGACCCGTTAACGTCCAGGCCATGT CCCACATAGAGAAAGCCTTTACTTCCAGCTCTCCATACGTAGGTCTGTCCTCTCTATCACATTGGCCA CGTAGC/C/TCTCCCTCCCTCCCTACAGGCCCTCTTCAGGGCCCCAGTCCCCCTCTGAGACTCCG ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
WI-10616a	116 G	C	---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCCGACATCATGACCCGTTAACGTCCAGGCCATGT CCCACATAGAGAAAGCCTTTACTTCCAGCTCTCCATACGTAGGTCTGTCCTCTCTATCACATTGGCCA CCACGTAGCCCTCCCTCCCTCCCTACAGGCCCTCTTCAGGGCCCCAGTCCCCCTCTGAGACTCCG ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
WI-1126c	52 G	A	---	---	CTCTATTCTCTGGGCACCTGCTTTCTTTGGGGGCAAACTTCCAGTATCATCT/GA/ATACTAATAAA AAACCCCTGAAGTCTGCTTGCATTTTCAAGATTCAATATATATCCAGATTGTTTCCAGCAAAAGAA AATTTTATTCTCAAGATATAAAAAATAAATAATTTAAATTTCAAGTTTCTCAAAAGGAATATGAAATT TGTTAAATGCAAAATCCAGCTGTAACTTTTTTGGACTGTCTTTTATTCTT
WI-1126b	230 T	C	---	---	CTCTATTCTCTGGGCACCTGCTTTCTTTGGGGGCAAACTTCCAGTATCATCTAATAATAAAAA CCCTGTAAGTCTGCTTGCATTTTCAAGATTCAATATATATCCAGATTGTTTCCAGCAAAAGAAATT TTATTTCTCAAGATATAAAAAATAAATAATTTAAATTTCAAGTTTCTCAAAAGGAATATGAAATTGTT AAAAATGCAAAATCCAGCTGTAACTTTTTT/C/GGACTGTGCTTTTATTCTT



WI-1126a	97	T C	---			CTCTATTCTCTGGGCACCTGCTTTCTTTGGGGGCAAACTTCCAGTATCACTGATCACTAATAATAAAAA CCCTGTAAGTCTGCTTGCATTTTCAGATTC/CAATATATATATCCAGATTGTTTCCAGCAAGAAAA ATTTATTTCTCAAGATATAAAAAATAAATATTTAAATTCAGTTCCCTCAAAAGGAATATGAAATTT GTTAAATGCAATCCAGCTGTAACTTTTGGACTTGCTTTTATTTCTT
WI-11183c	124	C T	---			TAGTGCTAAATTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTCACATAACATTT TTTATGACATACAAATGACCAAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTTAAATATTGGT ATGTGGTGCTAGAGTAGTAATGGAA
WI-11183b	192	T C	---			TAGTGCTAAATTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTCACATAACATTT ATGACATACAAATGACCAAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTTAAATTC/CAATTTGGT ATGTGGTGCTAGAGTAGTAATGGAA
WI-11183a	118	C T	---			TAGTGCTAAATTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTCACATAACAA TTTATGACATACAAATGACCAAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTTAAATATTGGT ATGTGGTGCTAGAGTAGTAATGGAA
WI-10770b	174	G A	---			GCTTGGTTTGCCTTAGTCTATTGTCTCAGTCTGAGTTCTCCCTTCTGCTGGCCCTTTTGTATTCA CCCATACCTCTATGCCCTGCTCAGACCAATTCCTCTATCTGGAGCGCTCTCCCTTGACTTTCTCCTG TTCACCAACCTTCTTTTATCTTCAGGACACTCA/GA/TTTCAATGCCACTCTCGTGACACTGCTCTCT TTCACATCTTCTGTGCTCCCTTTCCC
WI-10770a	49	G T	---			GCTTGGTTTGCCTTAGTCTATTGTCTCAGTCTGAGTTCTCCCTTCTG/TTCTGGCCCTTTTGTATT TCACCCATACCTCTATGCCCTGCTCAGACCAATTCCTCTATCTGGAGCGCTCTCCCTTGACTTTCTC CTGTTCAACCAACCTTCTTTTATCTTCAGGACACTCAGTTTCACATGCCACTCTCGTGACACTGCTCT TTCACATCTTCTGTGCTCCCTTTCCC
WI-9667b	82	C T	---			GATGACAACTTCTGCTGTGACCCCTTAGTCTTGTCTCATGACACTTTTCAATCTCTGCCCTTGATCATGG TTATCACTGGACA/C/TAAGCCACCTCCCAGCAGGCTTAGAACTCCATGAGTAAGGACCCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCAATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAAACTTGCATTCT
WI-9667a	68	G C	---			GATGACAACTTCTGCTGTGACCCCTTAGTCTTGTCTCATGACACTTTTCAATCTCTGCCCTTGATCATG GCTTATCACTGGACACAGCCACCTCCCAGCAGGCTTAGAACTCCATGAGTAAGGACCCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCAATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAAACTTGCATTCT

WI-10400d	189 A G ---	ACATTTTATTAGCAAAACAATCAGCAAAATAATAAGAAAGTAAATTGCAATTCAGACATCTGCTG GTTAACIGTTATAAGATGTTTAGCACACATGTAAGCACCTTACTAACACAATATTTTATTCTAATTT TCTTCCCTTACCTTTACTCTCCACCCCAAAATAAGTAAGTACCTATGIC/GJTGCCATGTAG TTTTTGGTTCATTTACTTGCAAATTATTCAAAGGCGTTAATGCATTATG
WI-10400c	166 A C ---	ACATTTTATTAGCAAAACAATCAGCAAAATAATAAGAAAGTAAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGTTTAGCACACATGTAAGCACCTTACTAACACAATATTTTATTCTAATTT TCTTCCCTTACCTTTACTCTCCACCCCA/CJAAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCATTTACTTGCAAATTATTCAAAGGCGTTAATGCATTATG
WI-10400b	165 A G ---	ACATTTTATTAGCAAAACAATCAGCAAAATAATAAGAAAGTAAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGTTTAGCACACATGTAAGCACCTTACTAACACAATATTTTATTCTAATTT TCTTCCCTTACCTTTACTCTCCACCCCA/GJAAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCATTTACTTGCAAATTATTCAAAGGCGTTAATGCATTATG
WI-10400a	46 T C ---	ACATTTTATTAGCAAAACAATCAGCAAAATAATAAGAAAGTAAATTGCAATTCAGACATCT GCTGGTTAACTGTTATAAGATGTTTAGCACACATGTAAGCACCTTACTAACACAATATTTTATTCTA ATTTTCTTTCCCTTACCTTTACTCTCCACCCCAAAATAACGTAAGTACCTATGTCATGCCATGT AGTTTTTGGTTCATTTACTTGCAAATTATTCAAAGGCGTTAATGCATTATG
WI-10809b	78 C T ---	AAAGGGCTACAACTAAGGCCAAAAACCATGAACGGTATAAGGAGGGTAAATGCAAGGGGAGACCC CACCTCTCACCAC/CTTAGAAAAGGGCATTTCAAGCACATTCATAGAGGCTTCATATACTGTTAG CAACAAATGGAATGATTAGCCCAAGGCAAGGGTATGGACCAAAAGTGCCCAAGTATGAGGCCACA GTGAATATCCACTAACGACCTTCTGGATGATGTACACATGACATAGGCTTAA
WI-10809a	33 C T ---	AAAGGGCTACAACTAAGGCCAAAAACCATGA/CJTGATATAAGGAGGGTAAATGCAAGGGGAGA CCCCACCTCTACCACCTTAGAAAAGGGCATTTCAAGCACATTCATAGAGGCTTCATATACTGTTAGC AAACAAATGGAATGATTAGCCCAAGGCAAGGGTATGGACCAAAAGTGCCCAAGTATGAGGCCACAG TGAATATCCACTAACGACCTTCTGGATGATGTACACATGACATAGGCTTAA
WI-7038c	266 T C ---	CGAGCTGGGATAAGCAAGGGGACCTTGGCGCTCTCAGCTTTCCCTGCCACATCCAGCTTGTGTGCC CAATGAATACTGAGATGCTGGGTGCTCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGCCAGAC AAGAAGACTGTCAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATTGAT CATTTTATATGAATAAAAGATCCTGCATTTATGGTGTAGTCTGAGTCC
WI-7038b	140 A C ---	CGAGCTGGGATAAGCAAGGGGACCTTGGCGCTCTCAGCTTTCCCTGCCACATCCAGCTTGTGTGCC CAATGAATACTGAGATGCTGGGTGCTCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGCCAGAC AAGA/CJGACTGTCAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATT GATCATTTTATGAATAAAAGATCCTGCATTTATGGTGTAGTCTGA

WI-7038a	31	G A	---	---	---	CGAGCTGGGATAAAGCAAGGGGACCTTGGC[G/A]CTCTCAGCTTCCCTGCCACATCCAGCTTGTG TCCCAATGAATACTGAGATGCTGGGTGCTCTCCCTTCCAGGAATGCTGGGCCCCCAGCCTGGCCA GACAAGAAGACTGTCAGGAAGGGTCGGAGTGTAAACCAGCATACAGTTGGCTTTTTCACATT GATCATTTTATATGAATAAAAAGATCCTGCATTTATGGTGTAGTCTGA
WI-3429b	64	G T	---	---	---	ATACGCTTCTGTCTGTCCACAGTGGAAACAGCACCCAGGTGGCCAGGGTCGGCTCCACACA[G/T] CCCTCAGCCCCCTTCAAGCTTTCATGTGTCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAAATACAGATCCCAAGTCTCCTCTCTCTGGATTGGATCTAGCAAGACCAGAGACGGTCTAGAA TCTGACTGTTAAACAAGCACTCCAGGCAATTCTTAAGACCAAGCACGGAGC
WI-3429a	62	C T	---	---	---	ATACGCTTCTGTCTGTCCACAGTGGAAACAGCACCCAGGTGGCCAGGGTCGGCTCCACACA[C/T]AG CCCTCAGCCCCCTTCAAGCTTTCATGTGTCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAAATACAGATCCCAAGTCTCCTCTCTCTGGATTGGATCTAGCAAGACCAGAGACGGTCTAGAA TCTGACTGTTAAACAAGCACTCCAGGCAATTCTTAAGACCAAGCACGGAGC
WI-6786c	151	G A	---	---	---	ATTTAGGACAGTGAAAAAAGGGATTATAAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTGGCGAAAGGATAAAGAGTGAGTGACGGTACCT GTGAGCCCCATCTTCT[G/A]TGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAATGCCACATT TTTTGGCAGGGGACACTCTTCTGGGTGCTCTATTGCTCAGTTTCATCAT
WI-6786b	111	A T	---	---	---	ATTTAGGACAGTGAAAAAAGGGATTATAAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTGGCGAAAGGAT[AT]AAGAGTGAGTGACGGTGA CCTGTGAGCCCCATCTTCTGTGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAATGCCACATT TTTTGGCAGGGGACACTCTTCTGGGTGCTCTATTGCTCAGTTTCATCAT
WI-6786a	106	A T	---	---	---	ATTTAGGACAGTGAAAAAAGGGATTATAAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTGGCGAA[AT]GGATAAAGAGTGAGTGACGGTGA CCTGTGAGCCCCATCTTCTGTGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAATGCCACATT TTTTGGCAGGGGACACTCTTCTGGGTGCTCTATTGCTCAGTTTCATCAT
WI-6711b	226	G T	---	---	---	GGCTATTTGTAATGCTTGGTTATTGACTCCAAAATTGAATAAGTATTGGGGAAGAATCCCTCACCT ACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCTAAACCTCAGTCCAACTCACTCTGAAT TTGATATACCTCCATTATTAATTTCAATACATCATTTGCAGAGAAAAGACACGGTGCCAACTGGGTT TGGTTGGTGCCTGCACACCCACA[G/T]TGGCAACTAAGTGTAATCTCTAAA
WI-6711a	36	T C	---	---	---	GGCTATTTGTAATGCTTGGTTATTGACTCCAAAAT[CT]GAATAAGTATTGGGGAAGAATCCCTC ACCTACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCTAAACCTCAGTTCAGTTCCAACTCACTCT GAATTTGATATACCTCCATTATTAATTTCAATACATCATTTGCAGAGAAAAGACACGGTGCCAACTG GGTTTGGTTGGTGCCTGCACACCCACAGTGCGCAACTAAGTGTAATCTCTAAA

WI-10613b	172	A C ---	---	---	ATTGTATGCCAAATCATAATACCCTGCATTCTAGAAACATACAGTGTAATAGAAATTTGAGCCATA TGGTGAAAATTTAGAAAGTATTATCTCTATATGTATATCTAGTTTAAATCAATGAATGTGATTT TTTGCAACTTTGACAGGCCAGGCAATTTTATTTGAC/CJGCCCTAGGAGGTTACTATAATTTAGA AAGGCTCTTACCTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-10613a	44	G A ---	---	---	ATTGTATGCCAAATCATAATACCCTGCATTCTAGAAACATACAGTGTAATAGAAATTTGAGCC ATATGGTGAAAATTTAGAAAGTATTATCTCTATATGTATATCTAGTTTAAATCAATGAATGTG ATTTTGTCAACTTTGACAGGCCAGGCAATTTTATTTGAGCCCTAGGAGGTTACTATAATTTAG AAAGGCTCTTACCTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-7587c	133	A T ---	---	---	GCCTAGTGGGAAACCTCAGGTAGTCTCCGGAAGATCTGTGCTTCCAAAGTGACTACCCTTGAAGC ACATCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA[A TJGGAATGAACCACTCCCTGCCCATTTCCCTATAAGAATATCCCAAGACCCAGGCAATTTTGCCCTCT TTCCACATGCCCTCCATATGCTGAGCCAAACTGCACCTGGGGCTGCCCTC
WI-7587b	81	G A ---	---	---	GCCTAGTGGGAAACCTCAGGTAGTCTCCGGAAGATCTGTGCTTCCAAAGTGACTACCCTTGAAGC ACATCCCTTCTG[A]ATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCCATTTCCCTATAAGAATATCCCAAGACCCAGGCAATTTTGCCCTCT TCCACATGCCCTCCATATGCTGAGCCAAACTGCACCTGGGGCTGCCCTC
WI-7587a	28	C T ---	---	---	GCCTAGTGGGAAACCTCAGGTAGTCTCCGGAAGATCTGTGCTTCCAAAGTGACTACCCTTGA AGCACATCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCCATTTCCCTATAAGAATATCCCAAGACCCAGGCAATTTTGCCCTCT TCCACATGCCCTCCATATGCTGAGCCAAACTGCACCTGGGGCTGCCCTC
WI-10681b	103	T A ---	---	---	ATGACTCAGGTGACAAAAGAGCATGCTCTAGACCCCATTTGACTTACGCAAACTCAATCAGCCAAC ACAGAAAAGCTAAAGACATCCTTTTTTAAAAAGCC[A]AAAGACAGCCATTTTAACTCTAATTCG TAGTTTATGATTTCTCAAAATTTCCCAACACACAGAAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTTTTGGAGAGGAGGAGTGACGCTCTGTTAAAAG
WI-10681a	41	A T ---	---	---	ATGACTCAGGTGACAAAAGAGCATGCTCTAGACCCCATTTGACTTACGCAAACTCAATCAGCCA ACCAGAAAAGCTAAAGACATCCTTTTTTAAAAAGCCTAAAGACAGCCATTTTAACTCTAATTCG TAGTTTATGATTTCTCAAAATTTCCCAACACACAGAAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTTTTGGAGAGGAGGAGTGACGCTCTGTTAAAAG
WI-7222c	126	G T ---	---	---	GCCTCTCCTCAACTGTCTGGACCCAGGCTAGGAAAGGCTGCTTGGATGATGCTGCTGCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCACCTGTTCTCAAGTTGGGGATGGG[G/TAATAA AGGAGGGGAATCCCTTGAACAAGAACTGGGGATAGTTATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAGGTTGATTTCAAAGACTCGAATTCATTTT

WI-7222b	255	G A	---			GCCTCCTCAACTGTCTGGACCCCAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCAACCCTGTTCTCAAGTTGGGGATGGGAATAAAGG AGGGGAATTCCTTTGAACAAGAAGAACTGGGATAGTTATATTTCCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGTGTAAGTTGTATTTCAAAGACTCGAATTCATTTCTCA
WI-7222a	126	G T	---			GCCTCCTCAACTGTCTGGACCCCAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCAACCCTGTTCTCAAGTTGGGGATGGG[G/TAATAA AGGAGGGGAATTCCTTTGAACAAGAAGAACTGGGATAGTTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAGTTGTATTTCAAAGACTCGAATTCATTTT
WI-8054d	41	C A	---			AAAGATGACACTTAGAACTGGATCAGCTTGGCCCTTCTCTT[C/ATTTATCTCCTCCCAAGTTCAAAATG CTTGCACTTTTAATAGCCAGCATTCTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCA CAATCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATTAGCCACTCTGCT TCCTGTCATAACGCCGCTTCCCTGGCGTACAGAGATCCTTGGCCCTT
WI-8054c	237	G T	---			AAAGATGACACTTAGAACTGGATCAGCTTGGCCCTTCTCTTCTTATCTCCTCCCAAGTTCAAAATGCTT GCATCTTTTAATAGCCAGCATTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCACAA TCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATTAGCCACTCTGCTTCC TGTCATAACGCCGCTTCCCTGGCGTACAGAG[G/TAATCCTTGGCCCTT
WI-8054b	148	T C	---			AAAGATGACACTTAGAACTGGATCAGCTTGGCCCTTCTCTTCTTATCTCCTCCCAAGTTCAAAATGCTT GCATCTTTTAATAGCCAGCATTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCACAA TCTCTTTGTAG[T/C]TTTAGCCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATTAGCCACTCTGCT TCCTGTCATAACGCCGCTTCCCTGGCGTACAGAGATCCTTGGCCCTT
WI-8054a	131	C G	---			AAAGATGACACTTAGAACTGGATCAGCTTGGCCCTTCTCTTCTTATCTCCTCCCAAGTTCAAAATGCTT GCATCTTTTAATAGCCAGCATTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAG[C/GJA CAATCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATTAGCCACTCTGCT TCCTGTCATAACGCCGCTTCCCTGGCGTACAGAGATCCTTGGCCCTT
WI-10854b	152	G T	---			TTCCACAAAAACTTCCCTGGCGGGGTGACTAAGATGAGAAGTGGGAGAAGTGGATAGTTTAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAAACACGAGACGATAGTTAACGCTCGGTAAGTTTAT ACGGTGTGCGAGGCAACA[G/T]GGAGAGGTACGGGAATAGTCTACTTCTCTTTTATTTTCTTG TTTTAGACACAGGGTCTGCTGTGTG
WI-10854a	102	C T	---			TTCCACAAAAACTTCCCTGGCGGGGTGACTAAGATGAGAAGTGGGAGAAGTGGATAGTTTAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAAACACGAGACGATAGTTAACGCTCGGTAAGTT TATACGGTGTGCGAGGCAACAGGAGAGGTACGGGAATAGTCTACTTCTCTTTTATTTTCTTG TTTTAGACACAGGGTCTGCTGTGTG

WI-9826b	127	G A ...	---	---	---	AATTTATATGTGAAGGGTTAGCAAACTATGGCCCACAGGCCCAATCTAGCCATGCCTATTTTGTG TGCTGATGGCTGTTGGTGTGTTGCACGCAGTTAGCCATTGTGACAGAGGCTGTTATG/AJGCCTT CAAAGCCAAAAAATAATTTACTCTCTGGCCTTGACGGGAAAGTTGCTGATTCAGATAATTTAAA GGCAGAGAAGATCAGAAGTGTGAA
WI-9826	125	A T ...	---	---	---	AATTTATATGTGAAGGGTTAGCAAACTATGGCCCACAGGCCCAATCTAGCCATGCCTATTTTGTG TGCTGATGGCTGTTGGTGTGTTGCACGCAGTTAGCCATTGTGACAGAGGCTGTTA/JJGGCCTTC AAAGCCAAAAAATAATTTACTCTCTGGCCTTGACGGGAAAGTTGCTGATTCAGATAATTTAAAG GCAGAGAAGATCAGAAGTGTGAA
WI-15986	60	T G TGGGTTTT	TTGTTTGTGT	TGACATTATAT	AAACGTAAAA GAAAATGT	CGGACACGTGTATATACAAATACAGATCGTATGGGTTGTTGTGTGGGTTTTTTTTT/GJTTAC ATTTCTTTACGTTTATATAATGTCAGCATTTCAA
WI-8655	29	A G AG	AACTGCAAA AGGAAACCAG	CCACCTGGGGC TCCC	CCACCTGGGGC TCCC	TTCAAGTAAGTCAAAATAGGAAACCAGAG/AJGGGAGGCCCAAGTGGGACAAATCATGGCTACCCC TCCCCAACAGAACAGGGGAGGAGGTGGCCCTACACCCTTTAT
WI-8170b	259	G A ...	---	---	---	GCACCTCTCTCTGAGCAACAGGTACACTTTTTTCTCTAACATTGATCTATAACACACAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGTAAGGTTAG CATTGGTGGAGAGATTACAAGGTTAAGATCATGTGTCCTCAAAAGTGCAATCCTATCAATCAGAA ATAAAGGTAAAGGGCCCTCAAAATGAATCTACGGGAAACATAACACAAGA
WI-8170a	204	T A ...	---	---	---	GCACCTCTCTCTGAGCAACAGGTACACTTTTTTCTCTAACATTGATCTATAACACACAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGTAAGGTTAG CATTGGTGGAGAGATTACAAGGTTAAGATCATGTGTCCTCAAAAGTGCAATCCTATCAATCAGAA A/T/AJAAAGGTAAAGGGCCCTCAAAATGAATCTACGGGAAACATAACACA
WI-8172	136	C G GACA	CCTTTATTAA ATTGTTTCTT	GAAGAGAAAT GTAATACCTGT AAAGGTAC	GAAGAGAAAT GTAATACCTGT AAAGGTAC	CAGGATTCCTTAAGTCATCTTCCAATACCTCAGGTACATGGTGAAGAGTCACCTGTTAAACACGAA ATCTAACCATTAACAAGCTTTTAAATCCTTCGGTAACCTCCTTTTATTAATAATTTCTTGACAT A/C/GJAGTACCTTTACAGGTATTACATTTCTCTTCCACCGTTTACA
WI-8183	56	G A TGC	TGAAATAAAA ACAAATTTCTGT	TGTGTTGAAAT CAAACTGC	TGTGTTGAAAT CAAACTGC	AGCAGGGTTTGAAATTGATCCCTTATTTACATGAAATAAAAAACAATTTCTGTGC/GJSCAGGTT TGATTTCAACACAGTTGAATCTGTAAAAACCAAGCTCGTTTCTGTGACGAGCAAAATATCCACAAT ATTTAAACTGCAAGCACCATGC
WI-14149	83	C T ...	---	---	---	GCCTTATTGGGATTGCAAGCGTTACAAGGTTAAAGACAAAAACCAAGCATGGGATTTTGCCTGGAAAT ATTAGCGTTAAAGGAG/CJTJGAGTTGAGTCAAAACACGGG
WI-8712	44	G A G	CACAGGGAAG AGGTAGTGA	CAGGAAGCCTG ACCATCTC	CAGGAAGCCTG ACCATCTC	TCAACAATGACACTGTGAACAGCACAGGGAGAGGTAGTGGAG/GJGAGATGGTCAGGCTTCCTG TTCTTAACAGCAGAGCCCGACCAACCTAGAAAGCGCCTCACCTAGCCTCTTAAT

WI-8827	22 C T	TOOCTGGGAG ACTATGG	GGGATTAGGAT TTTAGTGTTCA C	GGTGCCCTGGGAGACTATGG[C/T]AGTGAACACTAAATCCTAATGCCCATGCATTGGAAATTAT CCGACTATTACTTTCTTTAGTTCTTCTTATCCACCAAGTCTTCT
WI-8833	51 A T	TCATCCATGCC ATTCTCTG	CCTCACACATT ATAGGGGCA	CTCCGGCCTCTTAAAGCTCTCTGTAGACTGTCTCTTCCATGCCATTCTCTG[A/T]TGCCCCCTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAACCTGCTTGTGCATAAAAGGTCAGCTATGT
WI-8377	63 A G	---	---	ATTTTAGCCATGTTGGTAAAGTTTCAATTTTTCAGTACATGGGTAAACCCAGGCCCTTTCCCA[G/T] TATATCCAGGTATGCTACAAGTTCTTTTAACTCTTATCAGAAAGTTATTATTACTGTTTCTTAGAGAG GCTACCAGGCTAAATTCACCTAGTTGGTTTGTCTAATGTCCTCATTTATTTATCCTGAAGCTCGTG
WI-8850	21 A G	GGGACTTAAC CTTTGGCT	CAAAACAGCCA GGCAGG	GAGGACTTAACCTTTGGCCT[AG/C]CTGGCTGGCTGTTGGCTCTGGCTTGTCTGTTTGGTTCTT TCCTCTACTGGTCTTCTTGTCTTGGCAGCCACCTATGCTGCTGT
WI-8853	79 C T	CCCGGGCATTG AGGATA	AGTCTTCTCTGA GCCTTCCAT	ACTTTCTTGAGCTGAGCAACCTCATCTCTTCTGTTGATAACGCTGGTTAATCCCCGGG CATTGAGGATA[C/T]ATGGAAGGCTCAGGAAGACTTCATCTCAA
WI-8865b	52 A G	---	---	AGGTGACTGGAAATCACAGGCCACAGACTGAGGAAGACAGTATGTCGAACA[A/G]ACAACATGCT TCGGACTTACCAAAGGGAGAGTCGAGCTTTCCATATAA
WI-8865a	42 T C	CACAGACTGA GGAAGACAGT CA	GGTAAGTCCGA AGCATGTTG	AGGGTGAAGTGAATCACAGGCCACAGACTGAGGAAGACAGTCA[T/C]GGTCGAACAAACAACATGCT TCGGACTTACCAAAGGGAGAGTCGAGCTTTCCATATAA
WI-8895	32 A C	---	---	GTGCCACAAACCTGGACACCAACCAACAGAAT[A/C]CTCCCCGCTCTTTGAAATTTCCATTAAAGAGCA CAATGGGGTAATTATACCAGGGATGCTCCAATCGCTCTTTC
WI-8456	93 G C	---	---	CCTTTAAAGTCACAGTCAACTCGACTGTGGACTGATATATTTGTGAAATATAATAAAACTCTTTTC AAGGCTCCCATGCTTGGATGTCACA[G/C]TATGTCAAGTTAATAAACAATTTCTAAGTGTCACTC TCAACTTCTGTGTTATCTTGCCATGGTCCAGTAACAGTTTACACGGCAGACCAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACCTCCCGTCTGCTCAGTCACCCAC
WI-8496b	157 A G	---	---	TTTCATCATCAAAAAGTTTCTTTCCATAGAAAGATGGTAAT[G/A]TTGTATCAGTGCATATTTCTATGAAA ATTCTATCTCAAGTAACTAGCCTAGAAATCAGAGACAGCAGTATGTCAAGCTAGTATACAAGTCA AAGACACAATGCTGCCAATGCA[A/G]TTAGTATATAGAAATAATACGCAGCTGTAGAAAAAGTCT GTGGCCAAAGTGGGATAAAACAGTAGCAGTGCAC
WI-8496	41 G A	---	---	TTTCATCATCAAAAAGTTTCTTTCCATAGAAAGATGGTAAT[G/A]TTGTATCAGTGCATATTTCTATGG AAAATTCTATCTCAAGTAACTAGCCTAGAAATCAGAGACAGCAGTATGTCAAGCTAGTATACAAG GTCAAAGACACAATGCTGCCAATGCAATTAGTATATAGAAATAATACGCAGCTGTAGAAAAAGTCT TGTGGCCAAAGTGGGATAAAACAGTAGCAGTGCAC
WI-14153	28 A G	GTGCAGGAAG GCCAGC	AAGGGCAGGA GGGGA	CTGCAGGTCTATGTGCAGGAAGGCCAGG[A/G]TCCCCCTCTGCCGTTGTACCCACATCCACAGAGCA GCCCTAGTGCCAGGTGCGAGCCACTGCCACCCACGGCACACGGGAACAGGACCCATGCTGCTG

WI-12108	40 C T A T A	TGAAAGGG TTAAACTCAA	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTATTACTTTCTGGAAAGGGTTAAACTCAATATC[CT]GAAATACTTTTCATTATACCAGGT CAAGAAAAATGCCACAGCCAGAAAAATTTATTTTAA
WI-5989	29 G A C A C A G G C A	CCACAAAGGT CACAGGCA	GGGTATAACAG AACCGTATGTA GG	CAGGCAACGTCACAAAGGTCACAGGCA[G/A]CGTACATACGGTTCTGTTATACCCCATATATTAC CCCTTCATGTCTAAAGAAGACATTTCTCTTAGAGATTTTCATTTTAGTGATCTTTAAAAAAAT CTGTGTTAACTTGCCTCCATCTTTTCTTGGTGAGGACAC
WI-12201	61 C T C T G C A T G	CCCACTGATCA CCTGCATG	CCGACCACATA CCTGGC	ATAGTCTTTTAGCCTTTTCTGGAGTGTTATGTCCCAAGCCACTGATCACCTGCATG[CT]GGCCA GGTATGGTGGGGGTGATGGACGTGGTTGCAGCCCTCCACTGCTCGATAAAGGC
WI-12018	31 A T T C T G A C T T	GGCAGGACG TCTGACTT	GGAGAGATGAC AGAAACAGAG AG	TTTTATCTGTCAAGGCAGCCTCTGACTT[A/T]CTCTCTGTTTCTGTCATCTCTCCCCACATACCA ACTTCTCACCATGATGATTATACCAATAATACAGTTCCTTATATAGGGGCTCTGGAAAAATTAGAC AGTGAAGCATGTTGCAG
WI-14162	57 A G C T C	TGGCTCGCTG CCTC	AGGGATCAAA GAGAAAGGC	TTTTTCGTTTGTAAATGATCCGAATGCTTGAGAAGAAACCCCTGGCCTCGCTGCCTC[A/G]GCCCTTTT CTCTTTGATCCCTGAGTTGCTGAGATTAAAGATGAGGTCCCAATGAGAGCTACCAAGATGTAGTCG AGCGG
WI-15407	92 A G T T	CATGCCCTTA AGGATTAAGT	TCTTTTCTCTT TGGTAGTGTGG	AGCATGTAAGGAGCAGTTTATTGATTGGTATATTCAGGTTTCTAACCAGCTGAAAAATTCAAATA CATGCCCTTTAAGGATTAAAGTTTAA[A/G]CCACACTACCAAAAGAGAAAAAGTTTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109 T C A A T T	GTTGAGTATTT GTTCTGCTCAT	GGGAAGGCTG GTACATATTGG	TCTGATGTCATTTATTGGCACAATAAATTATCTGATACAACATGGTGCTAGACATGGCTACACTTTA TACTTTGTGCATTTAGTTGAGTATTTGTTCTGCTCATAATTT[C]CCAATATGTACCAGACCTTCCC
WI-12326	25 G A C A	GACAGACTTC AAAAGCAATT	AGGTTTGAAAA TATGTATTAAG TACTTTGT	CTGACAGACTTCAAAGCAATTAC[G/A]CTTCCAGAAATACAAAGTACTTAATACATATTTTCAAAG CTGTTTGCAATTCAAACAAAAGTTAGCGTTTGTAAATCAAAATTTGATAACCCGACTAAAAAT
WI-12361	63 C T	---	---	TTAAATCCACACTGAAGTCTGGAGTATGGGGGGATATAGGAATTTTCAGCATATGTATTAT[C/T] TGAACATAATTTACAAAAGTGAACAGTTGGAAGGTACTTATAGGTAGACCTGAGGGTCTGTTACC
WI-11305	87 C T A T C A C A C C A	CAGACACAGC ATCACACCA	GACCTCCCGT GGC	ATACTGGTTTAATCCATGTCAAATGTAGTTTACAAAGGGAAGGACAAGTACCTTTGTATAGAATAT ACAGACACAGCATCACACCA[C/T]AGGGCCCCACGGGAGGGTGGGGGAGACACATTTTCCCTGGG AAAGG
WI-11321	67 A G T T T	GGGAGGAAAA TCCAATAAAT	CATTGGGAAT AGCTAAACCTT	ATTTTATATGAAGGTTTCTGGTGAATCTTTTAAAGCAGGGAGGAAAAATCCAATAAATTTTTTAA[ A/G]AAGGTTTAGTATTTCCCAATGCTATTTAATACAAATTGAGGTAGGACGTTAAGTCTTATCAGA CTGTGTACTGGAGCCCCG
WI-11324	40 C G T G T G C C C C A	GGATAATCA TGTCGCCCA	ATCAAGCTTG GGCTCT	AGCATACTGCATCTCCTTTATGGATAAATCATGTGCCCCA[C/G]AAGAGCCCCAAAGCTTGATGACAT TCTGTAAAGTTACACAATGTATCTGAAGAAGTTATCTGTCTTGTCC



WI-11352a	69	T C G	AGCAGACGAC ATAGTGGAAA	GACCTCTCGTA GGACACTTACG	TGACACATGGTTCTGTTTCCAGAAAGGAGAGAGATCATCTACATAAGCACAGCACACATAGTGGAA AGT/C/GCTAAGTGTCTACGAGAGGTGAGATCATATCCATAGAAAAACAGCTCTCTTTTACTTGCA CACTTA
WI-11371	84	C T G	CAGCTGGAG ATTCTGATTCA	GCCCCGCTGA GCAC	TTAGCCCCATGCTGTCTATTGCAATACCTGTGAAACCTATGAAAACTATACCTGCCAGGGCTCAGCTT GGAGATTCTGATTACG/C/GTGTCTCAGGGGGCTGGACATCCATGTTTGGGAAGAGTTGCGCGGGT GATTTCGATGCGTATAT
WI-11385	75	T C G	ACAGAAGACT TTCATATTCTT	GATTCATTCT AGTCATGGTCA TATTTT	CTTAAAGCATTATAGTTTGGCCTGATGGTGACACAGAAAGACTTTTCATATCTGTTTAAAAAGTC TCTTCAGT/C/JAGGAAAAAGCTACAGATTTAAAAAATATGACCATGACTAGAAATAGAAATCAGC
WI-11388	88	C A A	TGTTGAAAT ACACGTAAC	TGCCTTGATC CAAGTTAAAT T	TCATGTGGCCAGTTAGCTCAGTTGGTTAGAGTGTGGAGCTCATAAAAAATTAAGAATGAATGTTTG AAATTACACGTAACCTAAGTTC/C/A/TATAATTTTAACTTGGATACAAGGCATTGTTATGCTAAT
WI-11392	55	T G A	GGTATGTTG CTTGAACCTTA	GTACATTCAG TGTTTGTAAA AAG	TTCTATCATCCATTAAATGGCAGGTATGTCTTGAACCTTAATAAATAC/T/G/C/T/T/T/TACA AAACACGTGAATGATCTTTCTTGTGAGAAGGGGAACACTGAGTCTCCGCTCTAGATCCATTAACTGT CATACTCCTTCCCCAGA
WI-11396	52	A T T	TTTGTTTGG AAATGGTGT	AGCTTATTTT ATATTCACCCA TC	AAAGAATAAGATGGCATTTGTTTCAAGTTAATTTTGTGTTTGAATGGTGTGTTTAT/GATGGGTGAATA TGAAAAATAGCTTACCTCATCCCACTCTAAAGGTAGTTGGTGAATTTTGAACCGTTGTCAAT
WI-11441	100	C A C	TCCCCACCA CAGC	TGCCAGGCCT TATTTG	CTGTCACTTCTCCCACTAAACCGTGAATCCAGTATGTCTGGCAGCAGCTGTCTGTCTTGTGGTG TATTCACATTACTGAATCCCCCAACCCAGC/C/A/JCAAATAAGGCCCTGGCACAAAAGTAAGCTCTCC ATTTTGTAGAATGAAT
WI-11466	26	T T T	TGAGAAGCCA TTTATTTTGA	GTTTATTGTTA TAAAAATGAC CTACAACTT	ACTTTGAGAAGCCATTTATTTTGCAG/C/TCTTCAGTCCAAAAAAGTCAACATTTTCAGAAATTTT TATATAAGTTGTAGGTCAATTTTATAACAATAAACCTTCTATTTATCTATTTATCTCTCACATACATTT CATGTATCCTG
WI-13364	35	A G	---	---	TTTTCTTTTGTGCTCTTTTATTTAGTAGAAGC/A/GJGGAACAGTTGTCAATACTACCTTCTGTGG TCCCCTGTTAGACAACATACCTTTCTTTGAAATGTAAATGTCA
WI-11276	41	A G	GGCAGCCAGG AGCAGAC	TGTACTGAGGA GCGGTG	AGGCAACACTGCTTTATTAGGCGGGCAGCCAGGAGAGAC/A/GJACCGGCTCCTCAGTACACATT CCCCACCCCTGCCGTGCTGCCCACTCAGGCTGGGATGGAGGGGCGAGCTAGGTCTGGAA
WI-12210	76	A G A	ACTGGGAAA CAACTATTGC	TGCTAGTTTGC ATATGTTTTCC	ATTGGAAACAACCTTAATAATTGTCATCTACATATAGAAAGCTGCTTTGAATAACTGGGAAAAACAA CTATTGCAT/A/GJGGAACAACATATGCAAACTAGCATCATTTGTCTCTAGA
WI-14186b	88	A G	---	---	AATGGTCTGGTTTATTGAGAAGCTGTTGGTCAATTTGATGGAAAGACACATACGGGTACAAAATTACA GGTGGTTTGTGTTTCAATACATG/A/GJTACAAATCATTAGAGTCTTTACAAGTCAATAGAGTCTTTGGAT TTT

WI-14186a	52	C	T	A	GGTCATTGAT GGAAAGACAC	AACATAACCA CCTGTAATTTT GTACC	AATGGCTGGTTTATTGAGAAGCTGTTGGTCATTTGATGGAAGACACATAC/TGGGTACAAAATT ACAGGTGGTTAGTTCATTACATGATACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66	A	G	G	GAGAACACTT GTGGGCTT	GGACCTATCAG TCCATGTTTGA	ATTTTTTTGGCTATAGTTCAGTGGTTCTAAAACCTGAGCTTCGAAGAGAACAACTTGTGGGCTTAA/ GTTTCAAACATGGACTGATAGTCCACCCACAGATTTCTAACTGGTAGGTCTGGGGTG
WI-12345	37	C	A	A	GTGGCAGGAA AAAGAGGAA	TTGCAGAGGGG TTCAGG	GGAACAGACCTGATCCACGTGGCAGGAAAAAGAGGAA/C/A/CCTGAAACCCCTCTGCAAGTATTCTCT TTCCTGACCAGCTGGGCTTGGCACCTTTGTGAGATTGCAAAA
WI-13416	71	C	A	A	AAATTTTGG AAGTTTTTCAG	AGTGTTTATAG TTCAATGAATA	GAAAAGGCTGTAATTTTATTTTCAAATTTTGGAAAGTTTTCAGAAAAAAATAAAAATGACAAGAACA CATA/C/A/AAATATTGAAATATTCAATTGAACATAAACAACCTTAGCAGAGGAAAGGGACTTTTGAT
WI-12310	46	G	A	A	TTATCCCAAG TATAATTTTA	TGTTTAAATAT GTTTGGTGCT	TTTGAAAAGATGCTGAATTTATTCCAAAGTATAATTTTAAAAAGCTG/A/TTTTAGACCCCAACATA TTTAAACATCTCTTACACATACAGAAATTTTCAAGTTTACAAATATTCCAGAAGGCCATTTTCTTTAAGCAG T
WI-12086	72	C	T	T	CCGGGAAAC TTTGATTT	GGAGTCTTCGG GTCITGG	GAACCGAGCTTTATTGGAGCAAAAGAGTGTGGACACTGTTTACAACAAAAACGTTTCCGGGAAAACTTG GATTT/C/T/CCAAGACCCGAAGACTCCTCCAAGTTCACACTGTTAGTAAGGTCAAATTTGGGGGCAGA ACAGGAACATGCCTTAGCT
WI-11549	102	T	G	T	GGCATAAAAGT TCATAATATTG	GGAAAGTCTGT ACAAATCCCC	ATGCTTCACAGGTGTGTAATTTGTTAAGAGTTTGCTATCTAAATTTTCATATTTATTGGCATAAAAGT TCATAATATTCTTTTATGATCTTTTAAATATCTG/T/G/GGGGATTTGTACAGACTTTTCCTC
WI-11585	79	T	C	A	TGGGTTTGCAA AAACAAAA	CCATGCTTCAC TGATACITTC	TTAGAAAGGAAAGAAATAAAACACGGTAATGGGAAAAATCAGTTTCAGAGGTAGGAAGGAAAGCTGGGTT TGCAAAAAACAAA/C/JGGAAAGTATCAGTGAAGCATGGCTAGAACTAGAACTCCAAAGCAGGGGTAGAGT TT
WI-11604	68	G	C	---		---	TTAGTTGGTTTCCCTGAAACCTTATGCTGTTTATTTTAAACCAATAGGATGTTCCAGTTTACCAGCATTT/ G/C/JAGAACTAGGGACTTTTCCATGAAAAATAATTAAAGAGCTAAGGAAATTCAGCGCTCACCATTTTTC TTTGTTACTCTGCAGTT
WI-11614c	108	C	A	---		---	CAAAATCAAAAAATTGAGGAGGCAAAAGAACAGAAAGTAAAAATCCAGAAGACTCAGCTGCTTGAGGCGAT GTTCCACCCCTGGACTTGCCAACTTTCAGTGTGAAACTGCA/C/A/JATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11614a	60	A	G	C	CCAGAAGACT CAGCTGCTTG	AGGGTGGGAA ATGCC	CAAAATCAAAAAATTGAGGAGGCAAAAGAACAGAAAGTAAAAATCCAGAAGACTCAGCTGCTTG/A/GJGG CATGTTCCACCCCTGGACTTGCCAACTTTCAGTGTGAAACTGCAACATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11626b	83	T	C	---		---	TTGATTTTACTAAGGCTTCCACTGGAAACATGAAGGTAGGATAAGTGTACAGGATAATATATCTCAG ATATTTTTAAAAATAAA/T/C/JACTTAATAATAAGAAAAATTAGCCATACCACATTTGTTCCATTTGCTAG AAGAACAATTTGGCAATGA

WI-11626a	39	G A G	T C A C T G G A A C A T G A A G G T A	G T G G T A T G G C T A A T T C T T A T T A T T A A G T	T T G A T T T A C T A A G G T C T C C A C T G G A A C A T G A A G G T A G [G/A] G A T A A G T G T A C A G G A T A A T A C T C A G A T A T T T T A A A A T A A A T T A C T T A A T A A T A A G A A A T T A G C C A T A C C A C A T T G T C C A T T T G C T A C A A G A A C A A A T T G G C A A T G A
WI-11627	23	T C	C C T T C C T T C C A T T G T C C T C	C A T T T G C A A C C C A T C T C A A G	A C C C C T T C C T T C C A T T G T C C T C T [C] C T T G A G A T G G T T G C A A T G G G A A G T A A A G C A A A A A G G G A G A T G A G A A A T A C T G A T G C C T T T T T G T C T G G C T T A C T T C C A T T C G C A T G T C A A G T C C A T C C A T G
WI-11636	61	A G T C C T	G G A C T T A A A A A G A T C T G C T T A	A G A A C T T G C T A A A T A T T T A T G T A A C A C T	T C A G A A A T G T T G C A A G C A A A T A C T A T T T G T A A G G T G G A C T T A A A A A G A T C T G C T T A T C C T [A/G] T A T A T C C A C A T A A C T C T A G T G T T A C A T A A A A T A T T T A G C A A G T T T C T G T G A C A G G T G C T C A G T A A A C A C T T T G A C T C C T T T T T G G T A
WI-11537	119	C G T	A T T G C T C A T C T T A C T C T G A C C A	G A C C C A G C A A A A A G A A T G A T T	G T A C C A T T C T A T G G T G G C A A A T A A G C A A C T G T G A G T A A A C G A G G C A G C T G A A T A A A T T T A C A G T A T A C A A T A T T A G A G A A T A T T A T G T G C A A T T G C T A C T T A C T C T G A C C A T [C/G] A T A A T C A T T C T T T T T G C T G G T C C A G G A C C
WI-11654	37	G C T G	G C C A A A A G A C T A T T C A G C A A	G G C T C T C C C A G G A C A G T T T	A G T A G A A C A T C A G T G C C A A A A G A C T A T T C A G C A A C T G [G/C] A A A C T G T C C T G G G A G A G C C A C T C C A G A G C T A T T T C T A A G A C T T T C T G T G T T T C A T A C T C T A C A G A G T T C A C A C T C A T A T T T C A T A T T T T A T T T T G G G T G T T G G G T
WI-11656	28	G A A A	A T T G A T T T A G A A G G A A C T G C	C A A G G C T T T G T C C T C A A G T A A A	A C C T G A T T G A T T T T A G A A G G A A C T G C A A [G/A] C T T T A C T T G A G G A C A A A G C C T T G C C T G C A G T T G T T A A A T G C C T G A A C A A T C A G A T T C C A G C T G G A T
WI-11680	55	T C	...	...	A C A G A T A C T T T C C A C G C A A C A T T T C T G A A A T G A A A G C T T T G A T T C T C C C C T T T [T/C] T T G C A T A A A G G C T G G G A A G G T G T T G G C C A G A C C G T A C A T C T T T T
WI-11696	47	T C A G G G A C A G	T T A T C A C A G C A G G G A C A G	G G C A T T A G A G A A G C C A A C C T T	G T C C A A G A A C A A A G A T A C T T T G A C A T C T T T A T C A C A G A G G G G A C A G T [C] A A G G T T G G C T T C T C T A A T G C C A C C A T C T T G T G T T T C A G A A T C T T T C A C A T T T C C A C T T C G C C
WI-11702	69	T C A G C A G	G A A T A A T A C T G A A A T A C C A	A G A A C A A C T T A A G C A A A T T A T A C T G A A A	T T A C A T G T G T C A A T G G T G A C A T A C T T T C A A T A A T T A A A A T C G A A T A A T A C T G A A A T A A C C A C A G C A G [C/T] T T T C A G T A A A T T G C T T A A G T T G T T C T A G A A A A C A C T G C T A A T T T T T T T T C T G C A G A
WI-11706	60	T T C T C T T C T	T G G C T G G A A T T T T C T C T T C T	A T C A C C A A A G A A C A A A T T C C A	T G C T G A T T C A T C G C T T C A C C A T C T G G C T G G A A T T T T C T C T T G T A C A A T T A T T T G C [C/T] G G C T G G A A T T T G T C T T T G G T G A T T T G C C C T T G C T G C T
WI-11709	105	T A T T C A G T T T G C	A G A A G C T T G C T T C A G T T T G C	T C A T T C T C T A A T T T A C G G G A	A A T A T C A C T C A T A T C A G G C A T G T T A T A A A A T G A G A G A T T A T G T C C T T T T T G G C A T A C T T C A T C T T C T T C A G G A C A C A G A G A A G C T T G C T C A G T T G C [T/A] G T C C C G T A A A A T T A G A A A A T G A A T G G C C A G A T G G A T G G A A A
WI-11710	103	C A C A G C T T T C A	G C A C C T A G C C T G C A G T T T C A	G T G T G G A G G A G G G A G G A G	T T A T T A C C A T C A A C C T G T C C C A G C T T T C A G C A C A A C A G C C A C A C T C T A G A C A G C C T T C A C T C C A G T C C A T T C T G G C A C C T A G C C T A G C T C A G T C T C A G [C/A] C T C C T C C C T C C T C C A C A C A C T C C T T C

WI-11715b	123	C T	AGCTT	AGCTGGCTGC	TCCCATCCTG TGGCT	AGAATGGAGCTGTGGGAGGGAGCATGCACACAATGTAAACAGACAAAATGCATTACAACGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTCTAGCCAC AGGATGGGACTGGGGAAGA
WI-11715a	49	A C A A A		GCACACAATG TAAACAGAC	CATTACACCAC AGTTGTAATGC A	AGAATGGAGCTGTGGGAGGGAGCATGCACACAATGTAAACAGACAAA/CJTGCATTACAACGTG TGGTGAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTACAGCCAC AGGATGGGACTGGGGAAGA
WI-11727	43	G C T C A A C A		AACAATCCTT AAAACAAC TA	CCTGTGGTTTG TGTTGCAG	CTGGATTTCCTATACCTAACAAATCCTTAAACAACTATCAACA/GJCTGCAACACAAACCACAGGC AAATGAAAACAGATGCCCCAGACAGCACCCACCACCATGGACACAC
WI-11728	16	C G ---			---	TTTTATTATCAAACTC/GJCAATTCATTTACAAATGTAAAGTTATCATCAGTCCCATCCACTTT CTCCCATCTTATCTCTCCCAACCCTACAGTTCTCTCCCTACAAACCGGGTTCGAAA
WI-11758	61	A G T C G C T G		ATCTGTGGTTT TCGCTG	TGATTGGCCCT GTGGTCTA	TTTTCTCTTTTATTAAAGTCGCTATACCTAAGAGGAGAACTCTGTGGTTTCGCTG/GJTAG ACCACAGGGCCAAATCACCACAGCTTCTGTAGAGAACATGGAGAGTGCCAAAGATCACCATCA
WI-11295	37	A G A T A T A A		GCCTCACAAA GTATTTCTAA	AAAAGTGCTCA TCTGTGAAC TC T	CCGGCCTCACAAAAGTATTTCTAAAATATAATTTGCT/GJTAGAGTTACAGATGAGCACTTTTCA CATTAGGTGATATGCAAAACAATCACTATTTGGCTCAGCAGGAAACAGACTTTT
WI-11773	93	T C ---			---	AGCACATGATATCTGCGTGGAGTTTCTGTAGCTCAGCAACACAGAGTCAGAGATTAAAGAATT ATTTATTGCCCTCTCTTTTTCGCCCT/GJGTGATTGTAAATTAGGGAGTCAAGGCCAAGTTATC
WI-11282	42	C G G C A G G G A A		GGCTCAGAGA GCAAGGGAA	AAAACTCAGA CTGTAAATTTT GTGTG	CATGACAACTCTTTTATTAAATGGGCTCAGAGAGCAAGGGA/CJGACACAAAAATTTACAGTCTGA GTTTTGGCGCAGAGACCCCTCTCCACCTTTTTCATGCCCTGTGTGTACACACACACTGTCCAAAGCCTC AGA
WI-11790	28	A G A A C C T C T G		CCCACTTACC AAACCTCTG	CGGTAGGCGAG GCTAAGC	TAATTCACCCCAACTTACCAACCTCTGT/GJGCTTAGCCTCGCCTACCGTACACATGCTCAGAGCAC TTACATTAACTACAAATGGGCAAAATCATCTAACACAAAAGC
WI-11879	61	C A A G T A T A C A		TCATCTAATCT GTGAGGTATTT	GATAGTTGAAC CTCTTCACITT ATAAAAA	TTTTAATCCCAAGCTTACAACCATCTTTTTCATCTAATCTGTGAGGTATTTAGTATACAG/CJAGT GATTTCTCTCTCTCTTTTATAAAGTGAGAGGTTCAACTATCCAGACAGTCCCATCTA
WI-12469b	91	C T A A G T T A A A		GTITTTAATGT GGTATTAGAA	CAATTTTCAGA TTGTCTATAGC AAAC	TTTACTAATTTCCATTCCTCCCTTTTATAGTTTTTAAATGTGATTAGAAAAGTTTAAATTTACAT ATGTGGCTTATATCTATTTCTA/CJTTTGACAGCACAGTCTTCAAAGTTTGTCTATAGACAATCTGA AAATGGGTCTGAAC
WI-11906	52	A G A T C T G A A		TGTTATAACAT CAAAGAAAGA	TTAATTTCTGC AGTTCCCTCA	ACATTTAGTAGGAATGACTTTGTGTTATAACATCAAAAGAAAGAAATCTGAAT/GJTGAGGGAACTG CAGAAATTAACCTTCAGTCTAATCTCAGAAATGCCAGAGTAAGATGAACCTTTACAG

WI-11909	78	A	G	TTTGTTGGG TGGTCAAG	CCTCCTCTGAG ATTTTCTGAAT AG	GCAGTTCTCTGAAAGACAATGGATTGTGGAGCATACTGAAGACTATTCCTAAATGGCTATTTGTGTTG GGTGGTCAAG[A/G]CTATTTCAGAAAATCTCAGAGGAGGACAAAATGATAGTGCACCTGCAGCCAGCTCG GACTGGCTTGCAGAGTC
WI-11806	60	T	G	CATGAAGAGT GGGCAGTTCA	TCTGTAAAGC CAATTTTATAT ACTAATAA	AAAAATACCATTTAGCATCAATTTGCCCAAGTTTGGCAGGCATGAAGAGTGGGCAGTTCA[T/G]GTT TTATTAGTATATAAAATTTGGCTTTACAGGAAGCATTATGG
WI-11946	31	C	A	---	---	CCCTAGTGAATACAACCTTTTGCTCTGGAGAC[A/G]CCAGCTAGTCTAAGAAAACCTTCTCTAGGCTGAG CTCTCTGGGAATCTAAGATAAAGAACTGAGATCTCTGGGAAGAGGGAA
WI-11965	65	T	G	TGAAGATCAG ATCTCTGGTTT ATT	CAGCTGTGGTG AATGTTGAT	ACAAAATTCACAAAGTACAACACTGCTTTATTTTCTTGTGTTGAAGATCAGATCTCTGGTTTATTAA[T/ G]ATCAACATTCCACCACAGCTGAAGGAAATTAACCTGAACCT
WI-11027	90	T	A	TGCCCTACTAC GCTTTTAAAA A	TGAGGAAATGT GTTACAGTATT TTTATT	ACCTATTTTGAACCTGCAGAAAGGGCAGGACAAAACAATCACCTTCATAGATTTTCTGGGAAATAT TGCCCTACTACGCTTTTAAAAA[T/A]AATAAAAATACTGTAACACATTTCTCTCATTTCTCTACGA ATACTTCTTTTGTATTTGCAATTTCTATGGCATACACAGAGGCACCTCTCTCAATGCCCTG
WI-11049	95	C	T	---	---	TTCTGCTGAAGATCACAACAAATTTCAACCTCTGTGTTCAAAATAATTAAGGATCTTTGTACCTTT GTGTTATTTCTGTTTCAACTAAGGAC[T/G]AGACTTCAGAGGCATAGCTTCCCTTTGTAACGTTTTT AAACATCTTTTCAATTTGTAGGAAGGAACATTTCAAAAGCCCAA
WI-15488	69	C	T	AAAGGACAG CCAGATATCA AC	TTTCCATCTTA TTTCATTTCTG TAAC	CAACATTTATCAACATGGTAGGGAAAAAGTTCTCACTCTGCACATATAAAAAAGGACAGCAGATATCA AC[T/G]TTACAGAAATGAAATAGATGGAAAAATTTTAAACAAATTG
WI-13654	49	A	G	AACAGTTAAT GAAACACATC CGT	GGCTGGTGAAA TGATGTCAT	TGCTCAATTTAATGTATAATCTCCAACAGTTAATGAACACATCCGTA[A/G]GTATGACATCATTT CACCAGCCAGCTACTTCATGTGGCAGAAAAGGTAACCTTTTCCCAATTTTACAGACAAAACCCAGT
WI-11070b	135	C	T	---	---	ATGAGACCTGCTTTGAACGTTAAACGTTTGGATAATGGAAAAGGAGCTAGGACAATTTCTTGCTT TCAAGTAAAATTTGTGACTGAGCAGAAAATCAGCCAGCTATCTT[G/T]GGTGCAGAGAGGTACTCCAA C[C/T]GTGGGGGTCTGTGACTTCCACGTCACCTGGGGATCCAAACAGAGGGAA
WI-11070a	110	G	T	CAGAAAATCA GCCAGCTATCT T	TTGGAGTACCT CTCTGCACC	ATGAGACCTGCTTTGAACGTTAAACGTTTGGATAATGGAAAAGGAGCTAGGACAATTTCTTGCTT TCAAGTAAAATTTGTGACTGAGCAGAAAATCAGCCAGCTATCTT[G/T]GGTGCAGAGAGGTACTCCAA GTACCGTGGGGGTCTGTGACTTCCACGTCACCTGGGGATCCAAACAGAGGGAA
WI-12020	121	T	C	---	---	AATCTTTTATATTTCCAGCTGTTGAGACAGTATTTTGAGGGCTGATGTTACCTCTAGCGGCGAAACC AGAGCCAGCTATTAAAGCAGCCAGAAAGCTACAGTAAATTGAATACATGACCATT[T/C]CTCTTTTAGC ACGTTCTTTGTTCTCTCT

WI-11076b	142	G A ...	...	CATGGTTCTGCCAGCTTACAGGAAGCATGGTGGCATCGGCTTATCTTCTGGGAGGCCTCAGGAA ACTCTGAATTATGCGAGTAGGCAAGGGGAGCAGGCATGTCACATACCCAGAGAGGAGAGAG AAAGAGAG[G/A]AAGTCCACACATTTTAAATGATGAGTCTCTCAAGGAACCTCACTCACTGTGCAT G
WI-11076a	106	T C AGGCA	TCCTGCTCTGG GTATGTGAC	CATGGTTCTGCCAGCTTACAGGAAGCATGGTGGCATCGGCTTATCTTCTGGGAGGCCTCAGGAA ACTCTGAATTATGCGAGTAGGCAAGGGGAGCAGGCAT[G/C]GTACATACCCAGAGCAGGAGAGA GAGAAAGAGAGGAAGTGGCACACATTTTAAATGATGAGTCTCTCAAGGAACCTCACTCACTGTGCAT G
WI-14263	49	T C	CGCAGAAAA GGCATAITCA	ACCTTTAAAGTTTCTCCCACTACTCCCGCAGAAAAAGGCATATTCAA[T/C]TGTCCTCATACTAAATT TTTGAATAACCTAACTCCCTTTTGTTCTACTAAGAGAGGTTCTTTTTGGCTACAAGTAACA
WI-14267	28	T C ...	...	AATTATTGCTGAAATTAGGAAGGGAGCA[T/C]TGAATGGGAAGGGGAGGTTAGAGAAGACAGAG ATTTAAAGAAAGCAAGTACCAITTTTCCAAGTATAAAACTCGTA
WI-13892	50	G A TAGAAC	CTTTTCATTT TGCTTTTAAA	GATTGTTTTTATTCATTCCTGCTTTTCATTTTTGCTTTTTAAATAGAACA[G/A]CTTTGATTTTTAGTA TATGACATCATCATGAATTTTTTCTCTACTTTGTTATTTAGGCTCCACCTCAGTAGTTTTGACAA AGGTAGATGAGTTCA
WI-15288	108	C G TCCCTCTCTC	CATGAGAGGA TCCCTCTCTC	ACCTCTTTCTGATGACACTTGTACCTGTAAAGGGTCTAGAGAGAAAGAGTAGTAGACTCCTACTTTGC TACAAATTCAGGATGCAGGGCATGAGAGGATTCCCTCTCT[C/G]TCCAAAGGGAAGAGCTTTTGGC
WI-13951b	88	G C ...	...	AATAATGGAAGAGGAGTGAACAAAGTAATGAACAAA[C/T]AGACCCCCAGATCAGAGGAAGAG GCTTCTTGTTAACTCTGGAGCA[G/C]ATTCAAGCAGCAATATTACTGAACACTTTGCTATGTGCTG G
WI-13951a	39	C T CAAAA	GGAGTGAACA AAGTAATGAA	AATAATGGAAGAGGAGTGAACAAAGTAATGAACAAA[C/T]AGACCCCCAGATCAGAGGAAGAG ATGGCTTCTTGTTAATTCTGGAGCAGATTCAAGCAGCAATATTACTGAACACTTTGCTATGTGCTG G
WI-13264	25	G A TTGCCAT	AAAAAGGCTC TTGCCAT	GAGACCAAAAAAGGCTCTGCCCAT[G/A]ATTCCCGTCTCTCCCTCCTGACTGACCCCAAGTGTCTT ACAATGAACATCCCTCAGCCCCATGGCATGGTGATCCCTCTCTTTGGGATCTGTGAATATAACCA ACTGTCTTGCAATGGC
WI-13960	39	A C TGATAGA	CATGAAAGGA CAAATTTGCAT C	TTATTTGTCATTAGCAAAAGGAAGTTAAATACTGATAGA[A/C]GATGCAAAATTTTGCTTTTCATGCA TTTGTGGAGCAAGTACTAATTGTTCACTGTCAATTTCCCTCACAAGGAGTTGAGCCCTTAGATGAC
WI-15843	62	C T CAG	ATCTTATAACC AAGAAGCCTT	AACTCTTTATTTAGCTAGCCCCAGTGACTTTATGCATCTTATAACCAAGAGCCCTTCAG[C/T]AG AGCAAGTCTGAGCCAGAGGTTTATACACTTTTGCTTCAGGGTCCACCAGGAACCCAGGCTTGCTTGGCT

WI-13983	52	G A	TCTCTCCACT CCITTAACCT	CAATACTCTCT TAGCCCACTGG	TTGTGATCTGATTTCCGAAACATAGAAATCTCTCTCCACTCCTTAAACCT[G/A]CCACTGGGCTAA GAGAGTATTGTACAGAATATGCACTCACTGACTTAACAGAAATTAGAACATCCAGGCACCTCACTGAGA
WI-13850	51	A G T T	AATCTCAGGG TCACAGCTTTA	TGTTCCCTGAC AATGTTTGTA	CATGAATCTCAGGGTCACAGCTTTATTTATAGATTTTAAACACAGCCAT[G/G]TTACAAACATTTGT CAGGGAACATTTACAGAAATAAATAAGATGGACTTGCAGGTGTAAGAGATTACACTTCA
WI-15295	27	G C A	TGTCAGTTTGA ATGTATTCCTG	TGAATAGTTGG CAAAGGAAA	AGATGTCAGTTTGAATGTATTCCTGAT[G/C]TTTTTCCCTTTGCCAACTATTCAATTATGACCATCTTTTC CTCGTCAAGTGACCTGCCATCATCAAGAAAGAGGCCCCGAAATATAGTGAAGCTCA
WI-14284	55	C T	---	---	ATTTCAACAAATCCAGAACAGGTTCTCACAGCTTTGAGCCTTTAGTGCAAAACA[C/T]TATGCCAT GCGGGAATAAATGCTTATCCAGTGGAGCGCTCCCTGATGCAATTGA
WI-14288	85	G C	CCGCTGCTATT CCCAGAT	GGTCTCTTCC ACCAAATCTT	ATGACCAGACCAGAGCCCCCTGTTCTATATGAAGACAAACAGGTGGCCATACCTTGGTGGAGGGATA CCGCTGCTATCCAGAT[G/C]AAGATTTGGTGAAGGAGACCATGACAGATGACAAACGG
WI-13522	33	C T	TGATGTAGTTA CCCCACTAAT	CATAATATTG AAGTCAGTGGT	TTTATTTTGATGTAGTTACCCCACTAATACAAC[C/T]GAGAACCCTGACTTCAAATATTATGAGAG AAATTAATCTCCAGGGAATTTTGCAGAGAAGATAATA
WI-13529	42	T C	CACAAACATT TATTGAACAG	TCTATACACTT CTCACTCTCTT	AAATATGATTCCTATCCACAACATTTATTGAACAGTTACCA[T/C]AAGCAAGAGAGTGAGAAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGCTCCGAGGGGTTATAGTCTAACACAGGGGAACCAACCTCTC A
WI-13859	84	G A	---	---	TTATTTGTCAGAAATTCAGAAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAAGTTTACTAC TTTGAAAGGAAACTA[T/G]AACAACAAGTATATATTCAGGAAAGGACTCCTAGAACTTGAGCA ACA
WI-13536	29	T C	---	---	TGAAAGGATACAGAAAAAACTCAGCGAAG[T/C]GAAAAAGGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCACAGCTCCAGTTGCTCTCTCCAGTCCCATTTACATGGAGTACACITTAATTTTCTCAGCA
WI-13373	52	G A	---	---	TTTTATTGTTTGTAGAAAAACAGGCTCTTTAACACTGAATAAACATCTCACT[G/A]AACTGTCGCTC CTAGATTACAAAAAGTCAAAACCAATTTCCCTTTGACGCCGGCCCTTGAATCTGACATTCAGATCAAGTCAC CGTAATAGAAACCCAGAGCT
WI-13477b	61	A G	---	---	TTGGTTTTTAATACCTCTGTTGGATAAAAGGACATTTTTCATTAGCTTGTCTCAA[A/G]GAC AGAGAAATAAGATAAAATTAACCTTAAAGAAATTAATAGAAAAATTAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT
WI-13477a	32	A G AAG	TTAATACCTCT TGTTGGATAA	GAAGACAAGC TAATGAAAAA	TTGGTTTTTAATACCTCTGTTGGATAAAAGG[A/G]CATTGTTTTTCATTAGCTTGTCTCAAAGAC AGAGAAATAAGATAAAATTAACCTTAAAGAAATTAATAGAAAAATTAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT

WI-14297	86 A T G	AATGTTGGGT ACTTTTCCAA	TGTGCACATTC AGAAACATTTT	CTGACITTAATTAGCATGCAATGCAATTAATTCTGGCAATAAATAATATGTGCAGTTATAAAAAAT GTTGGGTACTTTTCCAAAG[A/T]AAATGTTTCTGAATGTGCACACTAGAAATATATGCAGAAATCCTTT AAACAGTCGACT
WI-12229	89 T G AAA	CATGTGCACA AAAAGAGTAA	ACATGTGAAT GTCCCAAAAA	TCCATGTAATAATTCTCAACAGAGAACACTATCTTTAAATGAAGGATTTACCATTAAAGAAATCAACA TGTGCACAAAAGAGTAAAAAT[T/G]ACCMAAAATTAAGATTTTGGGACAATTCACATGTTT AAAAAT
WI-13582	43 C A	TGCAATCTAG AGACTGGGA	TCTGCGCAGTT AGATTCCA	AAGGCTGCCCCCTTACTGGACCAATGCAATCTAGAGACTGGGA[C/A]TGGAACTCTAACTGCGCAGAG AAATCAAGACCCGATGGTGTGAATCTGGGGCAGCTTCAAAATTTCTGCCTCCTAAAAACATTTTCAC CCAAATTTTCAATTATGGC
WI-13857	28 A G ---	---	---	TCTGAGTTGATAAAATGCTTTTCTGAAAC[A/G]TACATTTTAGGTATCTGGCACAATTAACCAAATGT CTGCCATTTTGTGTAGCTTTTCATACAGTACAGATTTCATTGATGTCGCTCCACATCTG
WI-15809	77 T G TGTAAATGCC	TGTTTCTGT TGTAAATGCC	TAAGGTAGCTA ATTCAATGTTT GTAAA	GTTTTAAGTTGCAGAGATGTGAATGGTTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTCTGTT GTAATGCC[T/G]TTTACAAACATTGAATTAGCTACCTACCTTAAGTATTGAAGAGCTTCCATT
WI-15892	123 A T ---	---	---	TTAATCAGTCTGTCTCAAGAAGAACAGGACTTGATCAAGCTCCAGCCCTCACCACCTATCAGCA TAGCAATTTAAGGATCAGAGCTTTGTTTACATTTGTCTAAACCAAGAGAGAA[A/T]GGAATCA ACTCCACAGATCAACATGT
WI-15801b	81 T G AA	CATACTCCACT CTAGCTGCAGT	AGAAGAGTGG ATGGGATGC	TCITTTATCCAAAGATGGGAAGCGCATTTTCATTTGGCTTGAATGAGAAGCTTCATACTCCACTCTA GCTGCAGTAATAC[T/G]GCATCCCATCCACTCTCTCTCTTTTGTGACTGAAACTCTTCAAGAAGCT GCTGAATGCTCTCTC
WI-15801a	24 G A AATGGGAAGC	TTTATTCCAAG AATGGGAAGC	TCATTCAAGCC AATGAAAATG	TCITTTATCCAAAGATGGGAAGCG[A/G]CATTTTTCATTTGGCTTGAATGAGAAGCTTCATACTCCACT CTAGCTGCAGTAATACTGCATCCCATCCACTCTCTCTCTTTTGTGACTGAAACTCTTCAAGAAGCT GCTGAATGCTCTCTC
WI-13763	59 T C GCAGIGAT	GGCTGGACACT GCAGIGAT	CCACACCTGC CCCT	GCTCGTAATGAGACAGAACGCTACAATCTGTTCAACACTGGGCTGGACACTGCAGTGAT[T/C]JAGGG GCAGGTGGGGCAGGCTGGGGCTCTGAGCCGAGGACAAATGTCATGGCAGAGCTTCCAGAA
WI-13578	48 T A AACC	TCAATAAAGA GCAGAAAGAA	CAGTGTGTAAG AACATCTTTT GTC	TTTTTTTTTGGTGAGTGTGCTTCAATAAAGAGCAGAAAGAAACCTT/AJAGACAAAAGATGTT CTTACACACTGAGCTTACAGTACCCCAACATGATATTTGCTTTTCCCGAGGGCAAAAAGA GAGCTTCCCAGAAACCTC
WI-13789	62 G A AGGGAG	TTGGATGGCTG AGGGAG	CAGTGGCTTC CTCTGTTT	TCCAAGGAAAAAGAAAGAAACCAATCAGTGAGAAAACTCAAGAAATTGGATGGCTGAGGGAG[G/A] GAACAGAGGAAGCGCACTGGGGCTGGGACTGAATATGGACAGTGGATGGTAGGGTCTCACTCTTT GAGTCCCT
WI-13594	66 G A AGC	TTTTTAACACA GATCACAAA	CCTTTGGGCA GTACTTTT	AATAACAAGTTTAAGTTCGAGCTGCAATGTTGGCAATGCAGGTTTTTAAACACAGATCAAAAAAGC[ G/A]TGACAAAAAGTACTGGCGCAAGGACAAAAATAATGCTAAGAAATTAGGCCAAACAGCTGC



WI-15625	40	C T	---		---	GTTCTCCCACTACTCCCGCAGAAAAAGGCATATTCAA[C/][T]GTCCCATACTAATTTTGAATAA CCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTTCTTTTGGCTACAAGTAACA
WI-13367	84	G C A		CCACTGAA GACTCACCAG	TCCCACCCCA CCCT	GTCTCACTTTCTGTCTAGGCTGTAATTTTTCAGTTTAAACAAGTTTCTTATGTGATTGTGGCCACACT GAAAGACTCACCAGAA[C/G]AGGGTGGGTGGGAATACTTAATCAATAATTTGTGGAAATTTACCCGAT GAAATCCAGTTATTCCCT
WI-13600	26	G T		TTAATGAGCC	CATATTGAAAA TTGTTACTAGA	CTCACATTTAATGAGCCCAAGCATCCATG[C/][T]CCATCATCTAGTAACAATTTTCAATATGCACATTATAT TATACTGGAAACAAGAAATACGGATTGTGTAGGGAAGAGCATAGAGGACCACCATCAGCAACCCCTCT TGATCCCTTCTCTACCC
WI-13602	89	G T		TCCATTCTGGA GACAACACA	GCATACCTCAT GACAATATTTA ATATTAAAT	GATAGGAAAGAAAGAAATGAAGTCAATAGTCTTAGCAAGCCCACTAGCTCAAGGAATAGACAGCCC CTTTCCATTCTGGAGACAACACA[G/][T]AAATCTATTAAATATTGTCATGAGGTATGCACCT GCCCC
WI-13650	76	A T		AAAGATTAC AATATTTCACT	CAGGCTAGGAT ATGAAGAGTA GTTTT	GCATTAAACATTTAAAAATTTCTGAGGGATATTGATGAGAACTATGATGAAAGATTACAAATATTTTCA TTTTAAAAAC[A/][T]AAAAACTACTCTTCATATCCTAGCCTGATGACTTAAAAAGTTACCGG
WI-14319	83	C T		CAATCAAGG CACAAAGCTA	CCAAATCATCT ATATTGTTGCA TG	TGTTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAAGATAAAAAAGGAATAGCAATT CAAGGCACAAAGCTAAG[C/][T]ACATGCAACAATATAGATGATTTGGGGTGGGACAGTACAGAATT
WI-13528	80	A G		CAATACATT GCATTTTCCTA	CATGATACCAC AGTTTCTCTG AA	ATTGGATACATGCTTTAAAAATGGTAGCTTTTAACTGTAATCAATACATTTGCATTTTCCCTAAAA AAAGAAGACATTT[A/G]TTACAGAGAAAACTGGTATCATGCAAGGAAAAAGCAGAAAAAATTT
WI-13909c	93	A T			---	ACTTAACTGGCTTATCTCACGGTAATCTATTCTGTATTTCCAGTGAAGTTTCATCTTCCCTCACACT CTCTTCAAACCTCGAATATCTTTTTC[A/][T]GAGATGCTAGCTAGTACCCACTGCAACATCTCTCAA
WI-13909b	80	G A		TTCTCACACT CTCTTCAAAC	GCAGTGGGTAC TAGCTAGACAT CTC	ACTTAACTGGCTTATCTCACGGTAATCTATTCTGTATTTCCAGTGAAGTTTCATCTTCCCTCACACT CTCTTCAAACCT[G/A]AATATCTTTTTCAGAGATGCTAGCTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86	C A			---	TTTTTATTGAATCCAAATGTAGCAAAATCATTAAAAACAATTTATAAAGGGGACAGAAAAATTAAG AATCAACATCATCTCGAC[C/A]ATGGAACTTTGAAAAGGCATGGCAGTGGAGACCAGTAACATA
WI-14323a	78	T C		ACAGAAAAAT TAAGAATCAA	GCCTTTCAAG GTTCCCAT	TTTTTATTGAATCCAAATGTAGCAAAATCATTAAAAACAATTTATAAAGGGGACAGAAAAATTAAG AATCAACATCAT[C/][T]CTGGACCATGGAACTTTGAAAAGGCATGGCAGTGGAGACCAGTAACATA
WI-15389b	104	G A		AGATAATGAA ACATCTGCGA	GATGAGGTGAT TCCCACACT	AAAATTGACAATAACACTAGCTTGTCTTTTGTCTGTTTGGAGACTACCATTTATCAAAATTTATTATGT AATACACTCATCCAGATAATGAACAATCTGCGAAAA[G/A]AAGTGTGGGAATCACCTCATCTGTGC

WI-15389a	33	G A T C	AATCAACTAG CTTGCTTTTGG	TTTGAATAATG GTAGTCTTCCA AA	AAAAATTGACAAATCAACTAGCTTGGCTTTTGTGTC[G/A]TTTGGAAAGACTACCATTTATTTCAAAATTTATT ATGTAATACACTCATCCAGATAATGAACATCTGCGAAAGAAAGTGTGGGAATCACCTCATCTGTGTC
WI-15747	88	T C A G T G T T	TGCTTCATTT AAACTAATTT	CATAATTCACC AAAAGTTTCA TAATTT	TGTAATCTGCTTACAGTCTTTGCAAAGACAGACATATGTTTTGCATAAAGATATAAATGCTTCAT TTTAAACTAATTTAGTGTTT[C/J]TTTAAATATATGAACCTTTTGGTGAATATGAACCTGTACCAAAAC C
WI-13752b	117	C T	---	---	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTTAAGTCTGGATATACTTGGCTTGCAC[C/T]GGACACCTTTTACG GAGGATTCGGGACAACT
WI-13752a	106	T C A G T G T G G A	CCTTCTCGTTA AGTGTCC	CCCTCCGTAAA AGGTGCC	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTTAAGTCTGGATATAC[T/C]TGGCTTGCACCGACACCTTTTACG GAGGATTCGGGACAACT
WI-14339	102	T G T T A C	CCCAATCAAA CAGTACATGA	TCCAGATTTCT GGAAACCG	AATCATTTAATGAATGTTCCAAACACACCCCTTCACTGGGCTACAGTAAATTTCACTGGGATGGAAG CAGATGAACCCACCCCAATCAACACAGTACATGATTAG[T/G]CGGTTCCAGAAATCTGGATAC
WI-13744	115	C T A A A C T G A A	TGGTGCCTGAAC GATAAGCACA	AATCAGGAAA GATAAGCACA GC	TGGATGGATGGATGAGGCCACCTGTGTTCACAAAAACACGTAATGGAACCTTCATGCAGCTTTAGAT TTCTTTTGGCCAGCTAGGAGCTTGTGTATGGTGTGTAACAAAACTGAA[C/T]GCTGTGCTTATCTTTC CTGATTCT
WI-14061	68	C T	---	---	CTTTGACTATATTGTTTTTCCAAAAATAGGACTATGTGTAGAAGAGAGCCCCCGTACATACCTTAT [C/T]AACCATTTTCATCCACCATTTGTAAAAATCTCATCTTCTGGGCTGGATCTCAAAAAACAGAT
WI-15719	69	A C C A T T C A G C	ACCTTTTCATC CAITCAGC	TGATACTTGGC AAGAGTTTTAA ATT	TTACAGTTGGATTAACTACACACTACCACACTGAATATACTGAATTAACCTTCAACCCCTTTCATCCATTGAG C[A/C]AATTTAAAACTCTTGCCAAAGTATCATGAACCTACGAAGAGGAGATAAGAGATCTGATC
WI-13810	106	T C A A C T T	CTCTAAATCG ATACATCCAA	GAACTGATGCT TGCTGCTAAT	TAATCCATCAATCTAAAAATCACACATACTAGATCAAAACAGAGTACCACAGTATGCTTTTATTTTGGCA GGTATTAAATGGTTCTCTAAATCGATACATCCAAAACTTT[C/J]AGTTAGCAGCAAGCATCAGTTCTTC
WI-15736a	27	G T C A C A	ATTTTATTCAC ATTAAACTTG	GTTCTTTGATA TGTGGCTTAGT TTT	GGATTTTATTCACATTAACTTGCACA[G/T]TAGCAAAAAAATCAAAACATAAAAACTAAGCCACA TATCAAGAACAATATACATAGAGATTGAAATTTCTCAATAGCATTTGGAAGGTATTTCCATAAATA
WI-13785d	72	G A	---	---	TCAAACTGCACACTATAAAAGTCTTTAAATGCAGCAGGAGATGTGAAGACACACAAATGAAC AAGTGC[G/A]TAGTGACACATAGCTGTCAACACACAGTG
WI-13785c	56	A C	---	---	TCAAACTGCACACTATAAAAGTCTTTAAATGCAGCAGGAGATGTGAAGAC[A/C]CAAAATG AACAAAGTCGTAGTGACACATAGCTGTCAACACACAGTG

WI-13785b	40	C G	---	---	TGTTGTGACAG	TCAAAACTGCACACTATAAAAGTGCTTTAAAATGCAGCAG[C/G]AGGAGATGTGAAGACACAAAATG AACAAAGTGGTAGTGACACATAGCTGTCAACAACACAGTG
WI-13785a	27	T C	GGCTT	ACTATAAAG	CTATGTGTAC	TCAAAACTGCACACTATAAAAGTGCTTT[C/J]AAATGCAGCAGCAGGAGATGTGAAGACACAAAATG AACAAAGTGGTAGTGACACATAGCTGTCAACAACACAGTG
WI-13793	88	C G	ATAGG	TCAGCCTAGAT	TTTGTTACT	AGAAACCAAGTATATCATAGGCAAAATAAAAATAGTTTTACCCCAATTGATACAACATAAAGGGATTT TACATTGAGCCTAGATATAGG[C/G]AGTAACAAATCCTCTGCCCATAAATCTATGACTTG
WI-13794	52	A G	TTCTTTCTC	TTCCACCCCT	AGAAATGGGCTC	TAGTCTCCTACAAATCCATCAATCCATTTCTCTCACCCCTTTCTTCTC[C/J]TACAAGGTTAAGA GCCCATTTCTTCAACAACAAAACAAACATAGAGCAAT
WI-15729	35	A G	GTGTAAGTGC	CTTTGAACCAT	CTCAGCTTCTT	TCATTTAAGTGCACCTTTGAACCATGTGTAGACTGC[C/G]GGGCACTTTAGAAAAGAGCTGAGACTGAA AAGTCTGTCTTGTACITCCAAAGGAAGGTAAAGTCCCTGTTTGACAGCCCGGGCTGCTCATTTGTTA
WI-13424	66	G A	C	ACCCTATTCTT	TTTTTCTCCC	GTCCTTTGCACAAGTCTCCCAACTGGTTTGAGTTTCCCTCTGAGGTTTTTACCCCTATTCTTC[C/G/A] TAGACCCCTGGGAGAAAACACATGTGAAGTGGCTCAGGACATGAGGCAGGCCGTTTCAACAAGAT GCTGGCTAAGGGGCTTC
WI-14085	29	T C	AATT	GGTCAGAGGC	CAAGCTGAATC	AACTGTCTTATAAAAGGTCAGAGGCAATTT[C/G]AGATCCCAGATTCAGCTTGTCTCATAAAAGAT TCAACTTCAAGTAGCACAATTTCTGTCTGCTTTTAAATCCJGAACATTCITGAAGCAGCAA
WI-13446	22	G C	TCACATCA	GCCATGTTCTT	AAGGGAATCA	TGCCATGTTCTTTCACATCA[C/G]CCTCTGATTTTGATCCCTTTCTGCTCTGTAATTTTTTCTTC TTCCCTTTTAGGGCCTAGTCTGTTTAGAAATCTGGTTTTTGAGAGTAGTGAGCCCTTTTACTTTTTT CTGACTGCCTAAT
WI-13725	56	A C	TGGGTGCC	TGAGCACATA	CCTGCTGTCTC	TCACACAAAGGCATTTGGAATGTCACTTACACATGGTGAGCACATATGGTGCC[C/J]GCCCGAG ACAGCAGGATAAGTTTCAAAAACCTTGACCAGGCAGGTTAGAGCAAGGCAITGGTTCAGGATG
WI-15702d	107	T C	---	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAACCTGTAAACAA[C/J]ACTAATGGGTTCTTTGAACAAAATAGTTT TGA
WI-15702c	101	T C	---	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAACCTGTAAACAA[C/J]CTGTAAACAATACTAATGGGTTCTTTGAACAAAATAGTTT TGA
WI-15702b	90	C T	---	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAAC[C/J]CTGTAAACAATACTAATGGGTTCTTTGAACAAAATAGTTT TGA

WI-15702a	48 G C	AACAAATAA AGGCTTTCAA AAAG	CCTCACCCCTT TACCCC	CAAAATGTTTATGAAGAGACTCCGAAACAAAATAAAGGCTTTCAAAAAG[G/C]GGGGTAAAGGGGTG AGGAAAGCATGTGAGAGAAACTGTAAACCCTGTAAACAACTACTAATGGTCTTTTGAACAAAATAGTTT TGA
WI-13831b	113 T C	---	---	TTTTTTTTTATGGATGCACGTGTACATGTTTATTTAGCGAAGGTGACTTGGAAAAGGAGATTCACAT ACTTCCACTGTATCCTCCGGGTAAAGTTTCCCTCTCTCTGTTAGAT[G/C]GTCTCCATGTTACAGTCAAC TATAAAACATGGCTCA
WI-13831a	56 G C	---	---	TTTTTTTTTATGGATGCACGTGTACATGTTTATTTAGCGAAGGTGACTTGGAAAA[G/C]GAGATTCA CATACTCCACTGTATCCTCCGGGTAAAGTTTCCCTCTCTCTGTAGATGTCCCATGTTACAGTCAAC TATAAAACATGGCTCA
WI-13806	62 G A	---	---	TGATTGAGCTTAGAAAGGAAGTCATGTTGAAATCAGAGAGAGGCCAAAACACTAGGCCCTCAGGT[G/A]C CCATTAAAGCATGCTGTGAATGCAAAAGGAAAGCTTAAAAAAATTTTTTAAGGGTGACTCCAGTAAAC CAT
WI-14372	86 A G	---	---	CACATTTTCAGCAAAACAAATCGAGGTGCAAAACAGGGTTTATTTACATTTAATATATTAACCTGGATTT TTTGCAAAATAAATAGGG[A/G]TTCCTTTAAATAACCATCTCCTCACTTCATGGCCAGT
WI-14373	95 A G	---	---	AGGCTGTTTTTGGGCTGAGGCCCCCAACATGACAACGTAAGACTGTAACCATGGTCACTGTGAGTT ATGAGCTAGGAACCTTGACGAAACCA[A/G]CACATATACAATCATCTCCACCTCCCAACGCCCTT ACTTTCACAGCCTCTGCA
WI-14078	61 C T	AAAGAAGTAA ATTAGGAAGA GCAAGA	TGTGTGCATGT CTCTTACTGC	AGAAACCGAGAACTCAAAGAACCCACATGGTGATCAAAAGAATAAATAGGAAGAGCAAGA[C/T]G CAGTAAGAGACATGCACACAAATCGAAACAAAGGGCATGGAGGAAGGACTTTAGATGGTCAG
WI-14083	47 C T	AGACTTGAGA GCTTAAACA ACACT	GCTACTGGAC CTCTAAACTAC TGA	TTGCTACATAACACATTACTCCAGACTTGAGAGCTTAAACAAACACT[C/T]ATTTGTTATTTACAG CTCAGTAGTTTAGAGGTCAGTAGGCTTGGCTGAGTTGTTGCTTAAGGTCTTACAAGGCCAA
WI-14085	31 A G	CATTTATTTTC ATGTGTAAGA AGAAAAA	CAGTCATGTC ACGTGCTAGTT	TGCATTTATTTTCATGTGTAAGAAGAAAAAC[A/G]TAACCTAGCACGTGAACATGACTGCATGGATAC ACGGCTCAGCACGAGGCTAAAGTCAGAAAGTGAAGTGAAGAAAAAATAAGCATGTTGATTTAAGTGAAA TAACAGAACAGGAGGCCCTT
WI-12169	121 G C	AATAAAACTT CCTATTTTCTT TTGCTT	GGGTTCTGAGG TGAAAGAAAA A	GTCAAAGGTTGGCAAAATTTATTTCCACTTATCAAGAACTTACAAAATATTTTGTTCATTTCTTAA TTTTCCACCTTTATTGCTAAGTTATAAATAAAACCTTCTATTTTCTTTTGTCTT[G/C]TTTTTCTTTCA CCTCAGAACCCCTTA
WI-15705	50 A G	GCAGGGAGAT TTTAGACTGA ATC	AGCTGTAGTCG TCAAATACTCT AGAA	TTGTTTTTATTTGGGAGAAATGAAGGAGGGAGATTTTAGACTGAATC[A/G]TCTTAGAGTATTT GACGACTACAGCTCCTCTCTCTTTGTACTACGGAGACCCTGCTTATAGCCCCAACAGGAAATCTCTCA TCTGCGGTTGCCAGACAG



WI-14631	82	G A ---	---	---	TGAATTCAATGGACAGTTTGGCCTCTGTTTAGTGAAACCCCTCACAAGCACTCTGCATAGTCGGCTTT CTGCTCTCTTTAAACG/AJTGCCCTGGTTCCCTCTGCCCAAACCTTTTAGGATTGGCCTCCTCAGGGCCTT GTCCTGA
WI-6053	24	A G ---	---	---	ATCACCACCGTGTCTAAGAAACAAC/AJGJTCTTCATGTCCAACTCATATCCCGGGACCTTTGTCAACTG CAGTACACTTCCTGCATTGAACCTGGCTTCTGGAGGGAAGCCTCCTAGAGGCCAGGTAAAGGGGTGC AGCAGTGAAGGGTATATCTGGGCTGGCCAGTTGGAACCAACGGAG
WI-15964	99	T A CTGGAGGTA	GACTTCTCCAC CCTCTTGC	---	CAGAAACCTCTCTGTGTAATAAGCTGATGCTAAAGTCAGAGCAGTCCAAAGGCAGGAGGCTGCCTT GGGAGGTAGTAAGCTCTCTGCTCCCTGGAGGTA/AJGCAAGAGGGTGGAGAACTTTGGCAAG
WI-12075	103	G A GGCAC	CCCTTCTTTC TCTTCTTC	---	CAGCTAAAGGATCACTGCAGCTAAATACAGATAGAGAAGCAACAAGCCAGGCAAAATACCCCATCAG AGACAGTGACAAGAGCAGCTGGGGCAGGGGAGGC/GA/GAAGGAAGAGAAAGAGGGGAGGAG CCT
WI-12179	96	G A TGGAGGTCA	TCGAATGACCC TGATAGTGC	---	TAATTTAAACACAGCCCTTCCACATAGTGGGTGAGGCATCTGCACATTTTCTAGAGGACATGA ATAGTGATGTGGAGGTACGGTGGAGGTCA/GA/GCATCTACAGGGTCACTCGAGGAGGAACAG
WI-14651	49	C G ATTGT	GGAGATATTGA TCTCATTTAAA	---	CACAAATAGTGAAATTATCTGAGCAAGAAATCATCTCATTTAAATGT/C/GJAAATAAGTCAGAA AAAGATCAATATCTCCCTGCTCAAAATGACACTCCCAATTTTACAGGTAACCACTGTTA
WI-14666	105	T A ---	---	---	AATGTGGACTTTCAACAAGGGTTTAAACTAATCTAATACTTACAACTTACAAACATTCAGAGCAT TATAACAAGAAATTATTACAGGCAGCTAATGATTAAAT/AJAAACCATGAAAAAGAAAAAATCTG ATCTAGATGTCAGCAAAATGGGCTGAGACTGT/C/TJGTCTGGTAGATGCAGTGTGTGATGTTCTAC TCTATTACAAAAATTAACAGAAATATGGCTTCGCTTGTGCAAAATGTTATATCACAGTC
WI-13967	103	A C AAATAAAAA	TTGTGTTTTCA TCTCCTAAAAG TG	---	AATTTAATAGCAGCTCTGTGTTGTGATTTTAAAGAACAAAGATAAAATAATGTCATTACGAGTCATTT AAAAAATAAAGACTACAGATACAGAAAGAAATAAAA/A/CJACTTTTAGGAGATGAAAAACACAAA
WI-14408	60	T A G	TTAATTGTGTA AAACTCATTTG TTACTTT	---	TTAATATTTAGCAAAAGTTATTGCAACAGGTTGAAATGCAGACACACTATTACAGGCTGT/AJAAA GTAACAAATGAGTTTACACAAATTAATAATATTAAACACATACCTATGGAATTTGTTGAATGA
WI-13683	47	C G ---	---	---	TTTTGTGTTAAGAACAGCATTTTGAATAAATAAACCTATCTGCCCATG/C/GJTTTACAGCCTTTTAAAT TTGTAATATTATATAGTCGTTTATGGTACATATTGATTGTC
WI-13910b	63	C T CGTCT	CATTGAGATAA AGCACACTTAT CAC	---	TTAGAAAACCTGATAAAGCAACACAACCTTTTGGGAAAGCACCATGGCACGTCCTTTGTGCTA/C/TJ GTGATAAGTGTGCTTTATCTCAATGAAGCAACCCCA
WI-14635	22	G A ---	---	---	ACATGGCAGATACAGAGTGTG/C/AJCTTTGAAGACCACCACTGACCAGGAAATGCCACTTTTACAA AATCATCCCCCTTTTCATGATTGGAACAGTTTTCTGACCGTCTGGGAGCGTTGAAGGGTGACCAGC ACATTTGCACATGCAAAA

WI-16002	59 T C	GATAACATAA AATGATCATG AGAAATTC	GCCATCTCCTC TTTGACTTTT	CCAAACATTTTAAACCTATGACTGGTCATTGATAACATAAAATGATCATGAGAAATTTCAIT/CJGTTA AAAGICAAAGAGGAGATGGCTAATGCATGCTGGGCT
WI-15361b	101 A G A	CCCAGTTGAAC TCAAGTCATC	AAACTAAAC CTTTGTGCCTA AAA	GTGGAATTTTATTAGCCATCAAAATTTCTTCACACTCAATACTGTTGAACAACAAGATAACACAT CTTCTTGCTCATCCCACTTGAACCTCAAGTCATCA/GJTTTTAGGCACAAAGGTTTTAGTTTTCTCGG GAAATCAAGTTTTAACCA
WI-14759	73 T C	GCCTTTGACTT GTGCGG	TCCCACTGC OCCC	TGAGTTACAAACAAATGAGCAACAAAGTTAGAAAAATGGTTTTATTCAAACCTCCTAGCGTTTGACTT GTGCGGJ/CJGTACTCAAATGGGGGCGAGTGTGGACGGGAGGATTGCAACACAGAGTTTCATACTG CAA
WI-12535	50 A T	CTAGGAGGGTT GAGGTGTAGA TAT	GCTCCACGAGA AGAGAGGAA	TCCCTAACATTATTTCAGGTGGTGAAGGAGGGTTGAGGTGTAGATATJ/TJCTCCTCTCTTCTC GTGGAGCCTTACTGAAGACAGGATCGCCGTTCTTGTTTATCAGCTGAGAAGGGCAGTCTCGGCATC TTAAAGACCTGCCCTCC
WI-13805a	112 G A	AAAGGCACAC GGGGAA	CTCAGCCTGCC TTGACC	TTCCATTCAATTATGCTTGGCTTTACCAATTTTTTATAGCTATTGGGAGGCAGGAAAGGGAATTTTGGC CCCAGAAACCATGAGATTTGGGTGAGAAAAAGGCACACGGGAA[G/A]GGGTCAAGGCAGGCTGAG AGTCACATTCTCCAGACCTC
WI-12340	18 T C	---	---	ACACAAATATAATTCCTATTCJ/CJGAGTGATTAACCACTTTTGTGTTTAGAACCAACAAAACTAC AAGAAAAACATTTTCAAAACCTTTTTTTCAGGCTGA
WI-14808	52 T A	ACCCACCACA CTACCCTGT	GAGGCATCACA ATGTTAAGATT TT	CTTTGAAACACTTTTAAGCAAAACAGTTAAAAAGTACCCACACACTACCCCTGTJ/AJAAAACTTTAAG ATTGTGATGCCCTCTGCATCAATTTTATAGAAAAACAAAGAAAAACACAACTGAAGGGCCCCCATGTA
WI-14816	29 A T	---	---	AGTTAAAAAAATCGAGTCAGCATTTATJ/AJAAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAAATGCATTTATTTTGTATCCCAAGCCCTGAACACATGAAAAAATATTTACTAAAGGAATGTTG ATTACCAGCTACGACTTTC
WI-12542c	71 G T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCTCATCCATGTGAGGGCTCTAGATC ATGJ/GJTAGGTGATTGATACAAATACGATCCATAA
WI-12542b	70 G T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCTCATCCATGTGAGGGCTCTAGATC ATJ/GJTAGGTGATTGATACAAATACGATCCATAA
WI-12542a	45 C T	GCTATTAGGC AAACTGAACA TTTTAA	TCTAGAGCCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCTCATCCATGTGAGGGCTCTAG ATCAIGGTAGGTGATTGATACAAATACGATCCATAA
WI-12173	57 C T	GGATACAGCA GTAAAGATA CAAAA	CCACCTCTAGA ATGTATGCTCT ATAA	CACCTAAATCATCTAGAACTGGGGATACAGCAGTAAGAATAACAAAAATCCTGCJ/CJCTTATA GAGCATACATCTAGAGGTGGGAAAGAGGCAATAATA

WI-14836	28 T C ---			---	TCTTTGGAGGATAGAGACAGAGTGTTT/CJGTTGATTTTCGTTTCGGTTTCAGTTGGTTGTCATT GGTTTTGTTTTTGCTAATTTGCCACCCTATAAAAGCAGTGCCACCCAGAGGCAG
WI-14856	60 A T A A		TGGTGACAG GAAATACTT	TTTGTTTGCTA CTTTTACAAA CITT	ACATTTCCTTATGATAGCAACAATAAATGATGGATGGTGACACGGAAAACTAATTAATTAATTA AGTTGTAAAAAGTAGCAACAAAAATGAGTATATACTATAAGTGATAGAGGATGATATATGAAAAA GGCTATAAAAAGCTCCAAA
WI-14863	61 G A ---			---	ATGGCAATTTACTTTATAGCAATGAACAAATATTTGTCAAAGGGCAAAATATTTTGTGTG/CJAJAG TTAATAAAGTTAATATCTTTTACCACAAAGCTAGAGGTCAACAGTACCACTATTATTGATTGCCACT ACCTGGC
WI-14867	46 T C A		GACATTCCAA GGCTCTCTAAG	TGGGCTGCAG ACACTC	TTTTAATTAAACGTAAAAAGGCAGGACATTCCAAGGCTCTCTAACA/CJGAGTGCTGCAGCCCCA TTCGCTTTGAGATGTAATGTTAACCCAGGGTGA
WI-14733	98 G A A		CCAAATTGAC AGATATTCTGC	GATGAGGTGAG GCCATTATT	ACGGAGTCGTCCTGATGATTTCTTGTCAAAAAATGTTTGCCTGATTCTTAATCATGAAGAACAATT AGAAAAATCCAAATTGACAGATATTCTGCA/GAJAATAAATGGCCTGACCTCATCAAAAAACATCA ATGTCATGAAAAACACAAAA
WI-14898b	79 A C ---			---	TTTTGTACCTATTCCTGTTTTCAGTGCATGTACAGGAAGAGTTGTCTCATAGGTGCCACTAAGGAAA ACTTTCTCCAT/CJJAAGCTGCCTGCTGTGCACGTTTGCCTGGGCTTGTAAACCCCTGGTGTGCTCT GCCTGTGTTCTGCTT
WI-14898a	50 A C CA		CATGTACAGG AAGAGTTGTCT	AAGTTTTCCTT AGTGGACCT	TTTTGTACCTATTCCTGTTTTCAGTGCATGTACAGGAAGAGTTGTCTCAT/CJAJAGGTGCCACTAAGG AAACCTTCTCCATAAAGCTGCCTGCTGTGCACGTTTGCCTGGGCTTGTAAACCCCTGGTGTGCTCATC TGCTGTGTTCTGCTT
WI-14907	48 G A		GGCACACATT GGACTCTGAC	TCTGCTGCAAG GGGAAT	TGGTATTTATTTCCGACATTACTGTAGAGGCACACATTGGACTCTGAC/CJAJATTCCTTGCAGCAG ACATTTGTGAAGCTGCTGGTGGCACACCCCATCAATCAGTGACTCCTGCAGTGCAGAGGGGCCACATG CAGCATGCTCAGTGIG
WI-14911	52 G A C		CCAATACATT CAGTTCTGGT	CAAAACCAGGA AAAGGACCTT	CTAGAATCTGGGAAGTCCAAGCTCAGTGCAACCAATACATTTCAGTTCTGCTGTC/CJAJAAGGTCTTTTC CTGGTTTGCAGACAGATACCTTGTCTGTATCCTCACATGGCAGAGAAAGAGAGGAAGTAATCT
WI-14913	88 C A ---			---	CTGATGCTTTGACATCTGGGGCATTGCTGTCTCTAGAGAGACTACTTCTCTGGGACCCAGCAATTTC TAGTGATAGTAGAGGACTCA/CJAJCCTGCACGTGCACCTTTTCATATACAGATCAACCAATCCCAAAAC CTACACCTCCAAACCCT
WI-14914	66 G C A		CTGGACACAG TTTTCTCTAGC	CAAGCCAGGA CAATAAATTC	ATTTCCCTTGGTGTGCTGTAAGCCTGTGAAGTCAATGCATCTGGACACAGTTTCTCTAGCA/G CJGAATTTATTGCTCTGGCTTGTGATGGCTTTCACAGC
WI-14926	49 T C ---			---	GTTTATTTTCAAAATGACACATCCAGATTCCAGATTGAAATGGGCACCTTAGCGAA/CJAJCTTGTGGACCACA AGACTTGTCTGAGAACATGTTCAAAAGACAGTTTCAAAATAAAAAATTTCTTAAATCAGGTCCA



WI-16083	89 C T	ATGTTAACA CAACATATC	TGAAAAAGATT OCAGCC	GCATCTTTATTACCAGAACTCATTTATGTCTTAATCATGTTTAAATATATATAAGCATGTT TAACACAAACATATCAAGGAT[C/T]GGGCTGGAATCTTTCCATCTATAGAAAAGCACTAACCATC CATTAAGCAG
WI-14930	55 C T	GGAGAGTCC CTCATGGAT	CACAACCAACC AATACCGC	CAGTCTGTGTTCTGGAAACAGCTCTCCTTTCCACAGGAGGAGTCCCTCATGGAT[C/T]GCGGTATTG GTTGGTTGTGGTGATTTGGGAGCAGAGGGAGAGCAA
WI-14946	47 T C	---	---	TCAATACTGAAGTGTCAAAGTGGTCTATTTGCCCCAGACATAACA[C/T]CTCTAAATCATCTCTA GATCAGGGGAGTCAATAAGGACCATTAAGGCTCATTAACACAGTACTTTATGGAAGGATT
WI-15987b	80 A G	---	---	ACATTAAACAGCACAAATTAAGGGTCCCAACGAGGTTGGTAGTGCTTCCACTATGTGAGGACAC TAAGAAGATGGT[C/A/G]TCTATGAACCAAGCTGCCGTGCCATGCTCTTAAACCTCTCAGC
WI-15987a	32 C T	CACAATTAAA GGGGTCCAA	GGAAGGCACTA CCAACCTC	ACATTAAACAGCACAAATTAAGGGTCCCAACGAGGTTGGTAGTGCTTCCACTATGTGAGGACAC TAAGAAGATGGT[C/A/G]TCTATGAACCAAGCTGCCGTGCCATGCTCTTAAACCTCTCAGC
WI-14948	56 T C G	AGGGAACCTG CTAACTTGCA	GATGATCTTAC ATCAGTTGTG GA	GAATAAAGTTCTTATGGCGTTCTTCAGGGAACAGGGAACCTGCTAACTTGTCAAGT[C/T]CCAACA ACTGATGAAGATCATCTCTGACCATAGCGAACCTGTAAAGCTTGTCTGTTCCCTCCAGCTGA
WI-16100	52 A G	CAAAAGCTA TTTTCTACAC TTGA	ACAGGAATGTC AGAAAACAGT ATATTAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAAGCTATTTTCTACACTTGAC[A/G]GTAATATACTG TTTTCTGACATCTCTTATCAACTCTCTGAAAATC
WI-14958	83 A G	AATAATTTAT CTCTTCTTTT CAAGGG	AATGCATTGAT TTGGGTTTTT	GTGATTGATCTGTAATATTGGGATTTATTTCAACTTAAATTCGAAGATGAAAAATTAATTTATCT CTTCTTTTCAAGGG[A/G]AAAAAACCCCAATGAATGCAATTTTTCAGTTTCTCCAGGCTTTGAACTGC AGCAGAAAATTCAGGA
WI-14976	35 C T	GTGATTTGCT TCGTCAAAG	TCAAACATAAT CTTCCATTCTA AGC	TATTTTTTAATTTGTTGATTTGCTTCGTTCAAAG[C/T]GCTTAGAATGGAAGATTTAGTTTGAGGAG GGGCAGGTTTGGGGTAGGCTACGCGGGCATAGTGGCCACAAAGAAGATGCCCATCTCACACCTGGAG ACGTCCATGAGCACTCG
WI-14981	31 G T	TCAGTGGTGT TATTGGATTT	CACCTCTGACA TAATACTAGC ATAAA	TAATTGATTCAGTGGTGTATTGGAATTTT[G/T]TTATGCTAAGTATTATGTCAGAGGTGGAGAAT AAAGAGGAAAAAGAAACAAGTGTGGCTCTCGCATCAACGACCTGATCTTGTACAGGAAGTTTTTGA GAGCTCACAAA
WI-14992	80 C T	TGCATTAAAT GAAGCTGCAG	GCTATGTGCTC AGCTTTCCT	TGATTACATTTTAAATCATGCTACCAGCCCATTAAGCCAAATTCAAACACCACCTCTGCATTA AATGAAGCTGCAG[C/T]AGGAAAGCTGAGCACATAGCACCCCACTGATCGGAAAGAAAGCTA
WI-15002	72 T A	---	---	AAATCTCTTCTTTCACACACAGATGAACCTTTAATAATTACAAATGCACTGAAATGCCTTCTCTTGA TTCCCT[A/T]TCAGTTTAGGCTCAATGGGCTCTCTCCTCAAGGCTGGACCTCAAAAGGCCAGTT
WI-15000	90 G A	GACAGAAAAA GACTCAGACT GTCTAA	GTTTCTAGTTC TGCACAAACTT CA	TCAAGCCAAATATCTGCAACAATAACATGTATTGAAAGGTATAGAAAATAAACAGATGATGACAG AAAAAGACTCAGACTGTCTAAGT[A/G/A]TGAAGTTTGTGCAGAACTAGAAAACAAAAATCCACCT

WI-12323	68	G A	CACAATACCTT CATGTACCTAT	CACTGGACATA TTCCTACTG	ATTTGTTGATGTTGGTTAAATCTTATCTCTTTTATACACAATACTTCATGTACCTATGAAATAA G/AJACAGGTAGGAATATGTCAGTGCAGAACAGAGGACTCACACCTGTGCATAGACAGCACC
WI-14683	91	A T	AAGGACGAT TAGTATCTAA	GGCATGTCCCA GTGTTTT	CATAAGTTGCAATTTATCAGTCCACGCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA GGGACGATTTAGTATCTAAACA[A/T]CAAAAAAACACTGGGACATGCCCCCTGAATTGCAAGT TGGAGTTCGTAAGAATCTAC
WI-13470	100	C A T	CCTGCCCTTAT ATTGGAATTC	GGGAGACCATG GGTCTCT	ATTTGTTGTTTATTTAGCACCTGAATTTAGGCAAGAGAAACATTTCTACCTGAAGACTCCATGCAGT CAAAATTCCTCGCTTATATTGGAATTTCTA[C/A]JAGAGACCCATGGTCTCCCCAAGTGAGGAAGCC AGGGCACTCAGCCCTTC
WI-14712	38	T A CA	TGAATGCTTCC AAGTACAAAT	TGAAAGTATGT TGTATATGGTA TTGTGA	TTTGGTGCTACTTTGTGAATGCTTCCAAAGTACAAATCA[T/A]CTCACAAATACCATATACAACTACT TTCAATCACAACTCAAAATATAAAATAACCTACAAATCACATTGC
WI-13712	40	A C TCTATTG	TTTACTTTGTT GTCATTTTAT	CCATAAGGCTCT CACACTTTTCT TAT	TGGGATACCCCTTTACTTTGTGTCATTTTATTCTATTG[A/C]ATTATTAAGAAAAAGTGTGAGACCTT ATGGCTTCTGCTTATTGGCAATATGCAATATAATATTGTGTGTTTAAATTTATGCAT
WI-16163	35	C T A	TCGGTGATGC AATTGAAATA	GCTGCCAATTA CATTAACTTAC AA	TCTAAGATTTTACTCTGGTGATGCAATTTGAAATAA[C/T]ATTGTAAGTTAATGTAATTTGGCAGCAT GCCCAAGTTTAAAGAGGACTATTCTTTTAAACAAAGACAGTGTCTGACATTTATTTCAGGT
WI-13453	88	T A TC	AATGCACAAA ATCTTGCTCT	TCAGATTTTAA CATCTCTTCT AGCA	TTTTTTTATTGCAATTTGAGTGTCTTATTATATTGGGAATTCAGTGTATTAACATTTGTACAAT GCACAAAATCTTGCTCTCTTC[T/A]JGCTAGAAAGAGATGTAAAAATCTGACCTAGTTGAACAGTCTT AATGAACCTCATTGTCCAT
WI-16167	58	T C GATTTT	CGCACTCTAA ATTAGAGATA	TGCTCGTGGTG AATAAGATG	CGGATAATATTATGTACCGCACTCTAAATTAGAGATAGATTTTTTCTGATATACATTT[C/C]ATCTT ATTCACCAGCAGCAGCACACACGACAGTAGAACAGTTCACACCTGATAAATTGCACAAGATG
WI-14482	17	G A ---	---	---	GCAGAACCAATTAATAA[G/A]AATCTGCAAGTTTCCCCAAGAACTCTGGAACCATAGTGCTAAT GCCCTTTAAATCGATACTAAAGGAGAGAGAAATAAAGGACTGCTTGATGTGACAGTCACTGGT
WI-15069	81	T C ---	---	---	TGTAGTCTTCAAAAGACATGTTGGCAGATAGCCAGGCCATCTACTGTGTATTCCAGTATCATGTAC GCACATAAAAAAT[C/G]GTGCTGCTGCTGTGAGTGAACCATTTGCTTAAGATAAA
WI-16156	97	A C CCGAGATCGC	TGAAGATTAA CCAGAGATCGC	AATTGTGTGCA TTTTGAAGAGA	ATCTGGTATTGTGTATCCCAACAAGTATACAGAACTACTATAAAACCAACCCCAACCTTCAATA TTACACTAATGAAGATTAAACCCAGAGTCGC[A/C]TCTCTCAAAATGACACAAATTAAGACG
WI-15012	59	G T ATGT	GCAGCAAGAT TACATCAGTA	CTCCAAATAGC CTAGAGTATAG TAAGGT	CATGGCAGCAAGATTACATCAGTAATGTAATATATACAGCTTTTTCATTGAAGCTTT[G/T]TACCT TACTACTCTAGGCTATTGGAGTGTCCCCAC

WI-15100	74	G A ---				TCTATTACAGCCAGAAATAACCAATTATTTCCAAATAAGCAAAATTTGGAACAGACTGGA GTGAGAAC[G/A]GTTCCACCAAGCCCTCAAGACAAGATGGACACGGCAGCTGGTTCTGGGGT GCATTTCTAGTGGACTTTAT
WI-14492	92	A T AATTACT	CCTTTATTTG CCAAATATAA	GTCACCATGTT ATATTTCTTT TAAGAC		TGGTACAGAATGTTAAATTACAGCAGGCGAGTATCCAGTTAAATAAAATTTAAACCTTTATTTT CCCAATATAAAATTACTAAATAA[A/T]GCTTTAAAGAAAATATAACATGGTGACAGCTTT
WI-12002c	89	T C ---				TCCTTAATTTTATCGGAATCCAGGACACAACAAGAAAACACCCCAAAACCCACATGGAGACAGAAG ACGAGACACAACCTCCTCCCGAC[T/C]GCCTCCCTGCTCTAGAGTGGGACAAAGTGGGGTGAGAC AG
WI-12002b	68	G A ---				TCCTTAATTTTATCGGAATCCAGGACACAACAAGAAAACACCCCAAAACCCACATGGAGACAGAAG AC[G/A]GAGACACAACCTCCTCCCGACTGCCTCCCTGCTCTAGAGTGGGACAAAGTGGGGTGAGAC AG
WI-12002a	30	C G GGACACAA	TCGGAATCCA	TGGTTTTGGG TGTTTTCTT		TCCTTAATTTTATCGGAATCCAGGACACAAC[A/C]G/AAGAAAACACCCCAAAACCCACATGGAGACAG AAGACGAGACACAACCTCCTCCCGACTGCCTCCCTGCTCTAGAGTGGGACAAAGTGGGGTGAGAC AG
WI-15116	96	C T GTTGCAAGTAA	GGGAGCCCTA GTTGCAAGTAA	CCTGAATATGC AATTATTTATT ATGACA		TTTTCATTTATTTTCCAGAAAAGAAATCACATTTTCAGTAACAACCTTACATATAGAAATTAACCTTTG TTCTGGAATGGGAGCCCTAGTTGCAGTAA[C/T]GTGTCAATAATAAATTAATTCATATTCAGGATTTTG TGAATAGGTGATTGGGA
WI-12578	37	C T AATGGGAA	GGCCTAAAGG	TCAAGCGACCA CCAACAC		GCAAAAGCAAAGCTATGAGGGCCTAAAGGAATGGGA[C/T]GTGTGGTGGTGGCTGTACTTGGT GCTTGTGTGCATGGAGCAGAAAGTCTTCCTGGTCCATGCAGGGCGTCACATAATTTAACTGCACATAAT TTGGGCAAACTGTCATTG
WI-15153	40	A G GCAATTGCA	CCCTTATGTTG GCAATTGCA	AACCTCAGATA AGTGCAGTGC T		ATTTACAGTTGGCCAGATCTCCCTTATGTTGGCATTGCA[G/A]GAGACACTGCACCTTATCTGAGGTTA GAAAAAATGATAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAAAATTAACCTTTCTAA
WI-15215	84	G C TCAAATGGG	TGGCTTTAGAA TCAAATGGG	CCAACAGGGGA AAAAGTCA		CCTTTGTCTCTGAACCTGGGACCAAGGATGTGAAATAATTTTGAATCTGATGCAGGTCGAGGTATGGC TTTGAATCAAATGGG[G/C]TGACITTTTCCCTGTGGTGGAAACTCTGTGAGGGTTTGGCA
WI-15225	80	C T C	CTTGAGGACCT AGAAAGCAAA	TTTGATTGGCA TAATCACTCC		AGGAAAGAGTGGTAAAGCAAAGCGCATCATTTGGATGGAATGATTATGTGTACAGACACTTGAGGAC CTAGAAAGCAAAAC[C/T]GGAGTATTATGCCAATCAAAATGCAAGGTTGGAGATATGCTAAAA
WI-15152	51	G A ---				AATTGCTAGTGCAAATGGACCCAGAAATTGGAAGGGCTATGTAACACTACACA[G/A]TATGCACACCAC AGCCTGTGAGTGCACAGATCCTCTTGTGCATTCAGCTTTCTTAAAAACACATCAAAAGGCTGCA
WI-15123	55	C T TAGGATG	TGTTAGTGACA GACAGATAAA	TTGCTTAAGGG CAACACAGAC		TGACTGTATACCAAATGCTGTGCTTAATGTTAGTGACAGACAGATAAATAGGATG[C/T]GTCTGTTT GCCCTTAAGCAATTTACAACCTCACTGGGGAAGAAACAGACATGCAAAACACGAGATAAACACCAAT

WI-15182	49 C A	GCACAAACCAG GGCAAAATA	GCAATGGGTTAA TCCAGCA	GAGACTGCCTGTGACACAACACTAGCTAGTGCACAACACAGGGCAAAATA[C/A]TGCTGGATTAAACCC ATGCTAATGGGTTACCTTTATTAGTAATCATGGTGCCCTCATAGCATGGTCCAGATCCG
WI-15198	38 T C	GGGCOCTGGC CACTATG	ACTTATCCGTC AGGCAGAGTAG	GTGGACCTCTACAAGTACCATGGGCCCTGGCACATATG[C]CTACTCTGCCTGACGGATAAGTTGGC ATATGGTTTCAGATTGCTTGCTGTACACAGTCCAGTTTCCCTAGAGACTAGTCCGACTCTCTT
WI-12601	42 T C	CATTATTGAG TATCTTGCTT TGAT	GTTGTAGTCT ACATGCTTAGC TAGAC	TCAAGTGGTAAATAGCCATTATTAGTATTTCTTGCTTTGAT[C]GTCTACGTAAGCATGTAAGACT ACAACATTACGACCCATCTCTTCAAGAGGAAGCTGGTATTATGGAAAAACAATTTGTCAATTCAGAT T
WI-14510	104 A T	TGGCAAAATA TGCATAACAA AA	TTGAAAATGGT TAAACTGGCA	ATGTTGAGAGTAAATATGCCCTACATATTTAGTGTAGTAAGTACACCCACAGATATTTTTGGGAGAAAGAG TTGTTTGCTTTTGTGGCAAAATATGCATAACAAAAT[A/T]GGCAGTTTAAACCATTTTCAAGAGT
WI-15239	57 T C	CATTGCAAT AAACACCATC A	GGACCTTATCT GTGGACTCAGG	CAGTGTGATGACATTTCAATGGGAAAAAGATTGTGCATTTTGCATTAACACCATCAT[C]CCTGAG TCCACAGATAAGGTCCCGGAGAAAGGGGCTTCCCTCCTTCTCGCTGGGTGACGTTCCCGAGCGAGT GAAGCCTTTTCTGGAATG
WI-12634	52 T C	GCATCATATG AACTGTCTAGC AGT	GGACAAATTGT AAACATAGCT AATAGC	ATGAGTTTATAAACTGGAGACAGCGCATCATATGAACCTGTCTAGCAGTATTA[C]GCTATTAGCTA TGTTTACAAATTTGCTGAAAGGGTCTAGATGTGTACACCCAGAAAGTGGTATTCCTGA
WI-15249	34 T C	GGGCTTGACAC AAGATTCTAA AA	GGAAAGCCAG AGATTTTAAAC AA	TTTGCTTGAAGGGCTTGACACAAAGTTCTAACTT[C]TGTGTTAAAACTCTGCTGGCTTCCCTGGCTGG TGAGGAGGCACAGGCTGGGGTCTCAGGTATCCACTGGTGGCCCGCATCTGTTCCCTCCACTCCCGAG CCACATCTTGGCTCT
WI-12159	28 C T	AAGACACCGT GCAATGTC	CCCTCTCCTCA GTGCACIT	CTGTCCGGGGAAGACACACCGTGCAATGC[C/T]AAGTGCACCTGAGGAGAGGGGGTCTGTGACTC CCAAACCTCGAATATTTATGAATCTAAGTCCAGACGCGAGTTTCACCGGAGATCTGC
WI-12648	41 A G	CCTAGTGGCAT TAAGGATGC	TTGCTACTAAA AGTGGACATCC T	TCCCCAGATTGTATGGAAATGGCTAGTGGCATTAAAGGATGC[A/G]GTAGGATGTCCACTTTTAGTAGC AACCGATGTTAATTCACACTACTCCCATGTTAGGTGCTTTACTTGGATTATCTCATTAAAAACCCACA
WI-12684	64 G T	CATGCTGTAA ACAGCTGTGC	GGAACAACAA AGCCTAAATGG	ATGAGAGGTAAGTGTCAACAGTAGGCTTAAAAATATTCAGTAAACCATGCTGTAAACAGCTGTGC[G/ T]CCATTAGGCTTTGTTGTTCATTAGAGACACAGGAGGAAAAATTTAGCATAAATCTT
WI-15260	75 G A	AAAGGATGAA GCTAATCATG GA	TCCTCCAGGG AGCTTGC CCTTCCACCAT GATTGTGA	TTTATAAGCTGAATGAAAGAGGTGACACAGCGGACACTGTCTAAGTGGAAACAAAGGATGAAGCT AATCATGGA[G/A]GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGATGAGCTGGAGAAATTA TCCTG
WI-15325	39 T C	CATGTGGCTGG GAGGC	AGCTTGC GATTGTGA	AAGGTTAATGGACTCACAGTTCCATGTGGCTGGAGGC[C/T]TCACATCATGTGTGGAAGGCAAAA GGCACATCTTACATGGTGGCAGTCAAGAGAGAAATGAGAGC
WI-13936	123 C T	AGTTGGCATTC AATAGCCTAT	TGAAACTCCCA CATGGAGTT	TATTTAGTATTCATCCATGGCGCTTCTCACTCCCTATACATTCACAGGGTTGAGTAGTCTACCC CCATAGGTTCAGAACCTATGACCTGTATCTTCAGTTGGCATTCAATAGCCTAT[C/T]AACTCCATGT GGGAGTTTCATAATAA

WI-14528	62	T	G	TAAAT	TTTAACTTTT TCTGGATGGTA	CTCGATTAGCA CTTATTATAAA AATTAAAA	TATGCTTTATTGAAGAGAAATAGGCTATTATAATATTTTAACTTTTCTGGATGGTATAAATTTGJTT GAATTATAAATTTTAAATTTTATAATAAGTCTAATCGAGACATCACTGGGTATAATTGA
WI-15347	74	C	T	AATT	GACTTCAAAG GAAAAGAACCA	TCACGCCCA AGTCTTTG	TATTTCTTCGGTTTCGGATGCAAAACAAAAATTTTAAAGAAAAATGTGACTTCAAAGGAAAAAGA ACAAATTTTC/CAAAGACTTGGGGAGTGAAGGCAGAGCCCTGGTGCAGATGGACGAGGTCTGCAGA GG
WI-14546	95	C	A	GGACTCA	CCAATTTCTAG TGATAGTAGA	AAGTGCACGT GCAGG	GTATTTCTGATGCTTTGACATCTGGGGCATTGCTGTCTAGAGAGACTACTTCTCTCTGGGACCAGC CAATTTCTAGTGATAGTAGAGGACTCA/C/CTGCACGTGCACCTTTTCATATACAGATCA
WI-15353	37	G	A	---	---	---	TTATTGGCTGCTCTCTGTAATACAATGTGGTGAACAC/G/AJCTTAAATCAGGACATCTTCCACCTTG TTTTGGCTCCAGTTGACTGCAAGACCAGTGTGAGGCACATAGGCTGATTAAATCAGTGG
WI-14580	100	G	A	GTCTTGA	CATCCCATCT GTCTTGA	CCGACCAAGAT CCCTOC	AGAAATTTTCTTTTTTAACAGGACAAGTAACAGATTACATCAAACTTCAGAACTTCTCAAATAC CTAGTTATTATACACATCCCATCTGTCTTGA/G/AGGAGGATCTTGGTGGCTTAACA
WI-8540	73	T	C	GGCTTA	GGCCTGCATT GGCTTA	GCCCTTCTTT TCAGGCAC	CCAGCTGGAGGTGGAATAATGCGGCAACCCACAGAAAAACACAGACTACACACAGGCCCTGCATT TGGCTTA/CJGTGCTGAAAAAGAGGGCCGACCTCTTGATAAAGATGCT
WI-8039b	97	T	C	---	---	---	AAGTAGAACACAATAGATGGCTCAAAAATATCAGAATGCAGTACGCACATCAGAGTAAATACTG TTTGGTAAACTTGTTCAGTTAAATATGTAT/CJGTGCTCGTGCATGTGATTAATATCCTTCT TACCACAGTCACTTAAAGAACCAAGCTTAGGACTAGGACACACACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTGAGATGATGATTTAATGCCGCGAGCCGACACCCACA
WI-8039a	87	T	C	---	---	---	AAGTAGAACACAATAGATGGCTCAAAAATATCAGAATGCAGTACGCACATCAGAGTAAATACTG TTTGGTAAACTTGTTCAGTT/CJAAATATGTATGTGCTCGTGCATGTGATTAATATCCTTCT TACCACAGTCACTTAAAGAACCAAGCTTAGGACTAGGACACACACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTGAGATGATGATTTAATGCCGCGAGCCGACACCCACA
WI-8044	107	C	A	---	---	---	CACAACATTCAGAAGTTTCTGCAATGTGCTTCTCTGATGTCTAAAAAGATTTGAGCTTTGACTAT ACGATTTCCACACACTGAACGCATTCAAGTTTCTCC/CJ/AGTATGGATCTCTGATGATTAATA AGCCCCGAATTCGGCTAAAGGCTTCCACACATTCAAGACATTTGTAAGGTTTCTCCAGTGTGGAC TCTCTGGTGTGCACAAGATGGAATCGGCTGAATGCTTTCCACACT
WI-8550	32	G	A	ATGCAACAAG	GGGAACATCA ATGCAACAAG	TTTGTGGCTTG AGTTTACAAAT	CTTACTACATGGGAACATCAATGCAACAAGTA/G/AAATTTGTAACTCAAGCCACAACTTAGTTA ATAATCATGGTTAAGGGACATTGCCAAAGAGCAACTGATGCCCTCAGTGAA
WI-8057	87	T	A	---	---	---	TATTAGATAAAACCCCTTTGTTCCCGATTGAGGATGTTTAAATTTGCTTCTTTAAACTCTGTGACTTTT CCTGGTTCAAAAGGACAGT/AGATGGACAGCAGGAGTGGGGTCTGAAAAATGTAATCTTT GTGTCAAGGCACCTCTGTGGCTCACAACCTGCCCTGTGAGGGATGCTGCCCTCCAGCCCTAAAG ACACTAGGGCTTTCAATGGACGGGGTGTGAAGCAGCCAGATGTTAAGG

WI-6192	91 A	GACTGCTAAG GATTTAAATTTG GAT	TGAAGTGTAG ATGGCTAAGTA TTAAAA	AAGAGGAACAAATTAGCTCAGTCCAACATGATTGGCAGTTGGCATAATCTAGTGAAGCAAGTGTCT GACTGCTAAGGATTAAATTTGGATAGTATTTAACTTAGCCATCTAACACTTCAAGCATAAAC
WI-6194	105 T A	CACATGGCAA TGATAATAAA GAAA	TCTATCCTCAG AGTGTAGTCTG CA	AAGTGATGTCTCTACAAATACATTTCTCAAACTCAAAACATCATGCTTGAATATCACTGAACCT GTCACCAAGAAAGTACATGGCAATGATAATAAAGAAATTAJATGCAGACTACACTCTGAGGATAG AGCTCTAAAGAGTAAACAAATGGAATTTGGAAAAATAGGAGTAAA
WI-6213	164 C T	---	---	CATATGCTGCTTTATTTCTGAAGGATACACTGAACGTTAGATGATAATAGCTAATGACAGAAATGT AGAAATGAGGCATCAGCTTCTTAACCACCTCTACAAAGATGTAGTATGTATTCATTACATGTTT ACTTTTGATATTGCTCATTTACTATGTTCTATATAATATGATAATACAGTAGGTAGGTGATCC TGCAATTCAGGTAAGCGGTAGGTGGAATCCAGATTTCTCTTGAGGAAAA
WI-6217	131 C T	---	---	CGGGTTAAGAAATACCTTTAAATTTAGGTAATAAGCTCAAGGAGGTGGGCTGTCATCTGTGGTG TCAGTCTTCTGGCCCCCTGGCTGTCAAGTGTGCTCCAGGGCTTGACAAGCAGCTCATTCAAAG[C/T] GGCCACCATGGCCCTAGGCTGCTCAACAAAGTCCAGCAGCAATCATGGCGTTCTCGTATATCTGATCC AC
WI-6238	175 G A	---	---	ATAGCTTTATTTGTCAACGAAGGCTACACGGGATCACTCTCGTTTGTGTTTATGCTTTTTTTTC TAGAAGGTATCTACATCTGCATTTATTTACAGCCTTGTGGTATTACACAGTCAAGATACAGTGTTA GAAACACAAAAGTGTGAGAAAAAACTTCTCAAAATTTGAGTCCAGACTTCAGGAAATGATT TCCACATGTAAGGCCAGAGTCTCCAGTGTGGTCAATCCAGAAAGCCTTG
WI-6272	86 C T	GCATTTATTCA GGGAAAACCTT TAA	CTGTTTTTGA GAAGACAAAG AA	CTTGATTTAATCAGGGCTTTGGGTGCATAGGGGATTAGTCACGTGCACAGTCATAATAATGCATTTA TTCAGGGAAACCTTTAAATCTTCTTCTTCTCCAAAACAGCTGCTGGAAACACCTCAAAATTA GGGATGTTCTATCTAAACACCTTTACTGAAACTTTGATTCCTTTGGGCCAGAGGAAGTCTTTACTGTAG CAGAGGACTTAATGCAATGCCTATTCGGGCAATAAATGAATACTTGTGATGCATTCATACAGGCAAGAA TCCCAGCATCCCAGAGAAGCTCTGTCTG[C/A]CTGCAAGCCATGGCTGCAGACATCAGGGAAGCT GGTGAGTCTAGTCTCGCCTCTCGATTTCCTGCCAGCAGTCTCCTCTCTCTCATTTCTTCTGGCCC TCTG
WI-6303	96 G A	CCCAGAGAAG CTCTGTCTGC	CAGCCATGGCT TTGCAG	ATGCTTTTGCATGATCTAATATTGCCTTTTTCAGAGCTCTGCTGGTAAAAAGTGGGTGCCATACA AACAGTCCCTTTTCAAGCCCGGTGTGATGCATCCTGCCAATCAATCACTGTAAATGTCCAATTGCCA AACAGGTCAACCGTGTCTCCATGAAAAAACTGGATAAAGAGTTGCTGATAGTAGT[C/T]CTGGTT CTTCCCTTACATCTTTTGGGGGA
WI-6315b	193 C T	---	---	ATGCTTTTGCATGATCTAATATTGCCTTTTTCAGAGCTCTGCTGGTAAAAAGTGGGTGCCATACA AACAGTCCCTTTTCAAGCCCGGTGTGATGCATCCTGCCAATCAATCACTGTAAATGTCCAATTGCCA AACAGGTCAACCGTGTCTCCATGAAAAAACTGGATAAAGAGTTGCTGATAGT[C/J]AGTGTCTCGTT
WI-6315	187 T C	---	---	CTTCCCTTACATCTTTTGGGGGA

WI-6375	28	A G A A	GGTTATTGCA TATGAAATC	AATGTGAGATC TTTATTCTAAC CTTTTT	AAGGTTTATTGCATATGGAATCAATAG[A/G]TATCTTTTACAAAAAAGGTTAGAAATAAGATCTC ACATTGTAAAGGCACATATGAACAATTTATAGCAAGCAAGGGCAGTGAGACATCAACAA TTGTGCTCAACAGATGAAATTCATAACCTTGTTTCTGATAAGACAAATTCAAAACATACAAATCAAT TAACAACAATGTGCTTATCAGCTCCCTCCACCCCTATATTTAA[T/A]GCAACTGACAGTTTGAAG GACACCAAGACAATAGGGCT
WI-6409b	112	T A ---		---	TTGTGCTCAACAGATGAAATTCATAACCTTGTTTCTGATAAGACAAATTCAAAACATACAAATCAAT TACAAC[A/T]ATGTGCTTATCAGCTCCCTCCACCCCTATATTTAATGCAACTGACAGTTTGAAG GACACCAAGACAATAGGGCT
WI-6409a	73	A T ---		---	CTAATATAATCCTGGGCACATGGATTCCAAGAGAGATTTGCAGCAGATTTCAATATAGTTACTTAA CAGCTAAAATAAAGGGTGATTTAACTTACTTACAGAGTCACTAAATAATGGAGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG[G/T]TATCAACCTTCCCTAAGCATCTGTCTGGTCCG CAGC
WI-6523	165	G T GCTG	GCTAATCCAGT AGAGACTGAA	AGATGCTTAGG GAAGGTTGATA	TCTCTAGCCCTATTAGGCTACACTGTAGTCACCTTCTATGAGAGCAAGGGAAACAGGAAGATGGGC TCCGTGGAGTCCAAACAGGATGGAGCTCCCTGGTAGTCTCTCTTTTACACAACTTTCCCTGAGA ACTGTCCAGTCAGGTGGACCTTCAACAACACGACGCTAAACTCTGAGAGAAAAAC[G/G]CTG ACTTTCAGAAAGCATAAAGCTGAGAAAAA
WI-6554	195	C G ---		---	ATTGTAATTAATAATTACATGGGCTATTATTAAGGACATGTGTATGTTCCACTTTGTTTAAA [C/T]AATTACAAACATGTGGCTTAAAATAATGTACAGATCAATGTACAAAGTTTGAAAAATGGGCG
WI-6558b	68	C T ---		---	ATTGTAATTAATAATTACATGGGCTATTATTAAGGACAT[G/C]GTAAATGTTCCACTTTGTTTT AAACAATTACAAACATGTGGCTTAAAATAATGTACAGATCAATGTACAAAGTTTGAAAAATGGGCG
WI-6558a	42	G C ---		---	AACCAACAAAAACTAAGAAATGGGAAAAAGAAATGGCAGGTGAAGAACTCTTTTCAGAGAAATAAA AGTTGTCATA[T/C]JAGCAATGGATGCTGTGTCAGAACATACTGCCAATAAATTTAAGAAAAAGGA ACTCAATGAAGTTACTGTTATATAAAACAGGAGCTCACAGCAGGGATGTAAAGATTAATGGAAGAT ATCGTGAGCCAAAAAC
WI-6629	75	T C GTCATA	TCTTTTCAGAG AATAAAAGTT	TGACACAGCAT CCATTGCT	CTGCCCTGAACCAATCAGATTAGTTTAAATCAAAATCAATCAAACTCCAGCTGTTCTCTTGCTCTTT TTACTTAGCAAGGAAACCTTAGTGAATGCTACTTGACAAGAAAGAAAGTCAATTTCTCAAGCACA[ T/C]JACCCAAACTTGAAGGTGATTGAACCCAAAAATAATGGGTGGGAAACACCAAAATGAGGTGGAGGA ATGAGAAAGATGTGTGGCCAAAGCTATCTGTTATATTTTGATGTTGCCAAT
WI-6644	134	T C ---		---	TGCTAAACACCACCATTAATTAAAGGAGAGTACTAGGAAAAACTACCAACACACAGCATGTGAAACAGT TGGGCACGGTGGTAAAGGGACAGACTTGGAGCCACAGC[C/T]GGCTAATACACTGCAATATTTTA TGTTAGCAAAATTAGCTGGTCTGTGTATAAACCAGAGCGGTTATCTGG
WI-6690b	106	C T AGCCACAGC	CAGACTCTGG	TGCAAGTGTAT TAGCC	

WI-6690a	28 T C A G A G	AAACACCACC ATTATTAAGG	GCTGTGTTGG TAGTTTTCTCT	TGCTAAACACCACCATTATTAGGAGAGTTC/ACTAGGAAAAAAGTACCAACACAGCATGTGAAAC AGTTGGCAGCGGTGTAAGGGCACAGACTCTGGAGCCACAGCGGCTAATACACTGCAATATTTTA TGTTAGCAAATATAGCTGGTCTGTGTAACCAAGAGAGCGGTATCTGG
WI-6770	53 A G A A C A T C A C A	CAAAACCCCA AACATCACA	GCTTTGGAGT GTATAATAGTA TGAATAA	GATGTTTTAATGACACAGATCTCCCAAAGTAATCCAAACCCCAAAACATCACA[A/G]JAATTATTCAT ACTATTATACACTCCAAAGCAAAATACTTCAACTGCAATCC
WI-6686	151 A G A	GCATTCITCCA AAAACAAAGA	CCTTGTAGTG ACTATTCCAAT GTT	ATTCTGTAGGCAAAAGTTGAGCAAAATCAGCTAGCACTAATCTTGACCAAAATGGGTGAGTCAGCCTCA TCACAGAGATTTTTTTTTTAATTAGATGAAATTCACATTTAAACACATGGTAACCTCAAGCATTTCT TCCAAAAACAAAGAAT[A/G]AACATTGGAAATAGTCACCTACAAAGGAC
WI-6761	32 C A G	GATCTAACAG CTGCAGAATG	AAAAGCTGGG AAGGAAGAAG	CCTGAGAGGCAGATCTAACAGCTGCAGAAATGG[C/A]CTTCTCTCCAGCTTTTGTGAACAAAAAC AATTCCTAAGGCATCAGAAAGCACTGAGTGCAAAATGGGTGTCAGGTACAAGGTCTC
WI-6844	225 T C ---		---	TAAATAGTCCCACTAGCATTACGTCACCTTTGCATCATTAACCAACAAAGGTAATTCCTCCTTG GTATTTCAAAATGATGCATTATACAATAACGAAGTTAGAACTTAAATGACCCCTGATTAATATG TAACTGGTAATTTGTTTTAAAGCATAATAATTTGGTTCCTTCTTCATAAAATGGAATTTAAA TATTTCTCTGATAGTCTTGAGGTTC/ATCATTAATGAGTAGTGCAAAAGTGTG
WI-6824	112 A G ---		---	CGGTTTTGCTACACTTAATGGGTTTTTTTTAAGGATTTTTTTCAGGCTTTGTCAGCAACATCAA ACAAAAGGTACTGAGTACTCCACAGGGTACAGAGTGTGCCAA[A/G]CACCTTAGAAAAATTACAT GACACGGAGAAATGCGCTCTTGCTCCTTGAAAGAGCTTACAGTCTAGGATTTGACAACTCACAGT CTTAGGAAGTGGCAAAAGTAAGGCAAAATCTTCATCCCTAGAGCTATTGTG
WI-6889	139 T C A A T T C	GAAAAATGAG ATGCAGTTAA	TCACTTGTGG CTTTTAATTAT TCT	GTACAAAAAAGCTGAGAAAGAGCCCAACATGGAAGTGTCAAGAAAAACATTCTGATAGGTACGGACAA AAGAGTCTCTCAATCAAGGAGGTACATATTAGTTCTCACCATGCTAGAAAAATGAGATGCAGTTA AAATTC[T/C]JAGAATAATTAAGGCCACAAAGTGAACCTGTTGTTCTGGGGCCCTATGTTGTAGATT CTCT
WI-6911	216 T C ---		---	TCCCAGCTCATATTTATTGGGCACAGAGTGGGCACTCAAATATCTGATGAACCTGAACTGAA AAGAGGTCTCCTTAAACAAGATATCATCTCCGGAAGAGAGAAGTCCCACCATATAAAATGTATGAT CAAGTCCACAGAAAACTTGCTTCCCAAGGAATGTGTTCTAATTTGGTTTCAAAAGCACACTGGTTCC CACTTTACCACCTT[T/C]CATGACATTTGGACAATAGTACTACTCTTTCTAC
WI-9413	112 G C ---		---	GCCAGTCTCTAGTAAGTCTTAGGGACATGACCAGACAGAGCCCTGTTCTATATGAAGACAAAC AGGTGGCCATACCTGGGTGGAGGGATACCGCTGCTATTCCAGAT[G/C]JAAGATTTGGTGAAGGAG ACCATGACAGATGACAAACGGAAACAGTTTCTCAAAAAACAGAGGTATGA
WI-9557	74 C T ---		---	AAAAGCTTTAAAAAAAAGTGGTGTCTATCTTTAGAAACACTTTCAGCAAGATCAAGTAGCCCCAGCT ACAGCC[T/C]TGGTGCATCTTAACCCCTCTCCTTTT



WI-9617	37	G T	---	---	TGCTCTTTTATTTCACGTTTCAACACACGCGGTG/GTJGGCAGAGTCTACCAAAGTGCCCGCAG CGCACGCTTGGCGGGAAGGTCTCATTCGTCTGTCTCTATGACTGATTGAATTTGGGATGGCCAG CTOCAGAATGTTCCACGTGGGGCACTCTGTGGCAGAGAGGCTGAGCCCTGCCACACTGGCACCA AAGAGGTTGCACGATGCAGCTTGACGTGGGTCCAGCCGGGIGIGCTGTG
WI-9657	121	T G	---	---	AATGCTGGAGAAACATCAACATTGAGTTGACATTTGTTTGTCTGAAGTATAGTACCATCCACTAT CATGAATTTTGTTCATTACAAATGATAGAAAGCCAGATTCTCAAAATAAAGT/GJATAATCTT TGATTAATAATAATGTTTATAAATGTTTATGAAGCTCATTAAGATTATCTTTTAAAAAGTAAAAA TTTTAGAACATATGACGCTTTTCATAAATGCTTTTGATATAGATTGAGG
WI-13119b	114	G C	GCTGGGA	AAAAATTAAAC CAGGTGTGGTG T	CAGGGCTTGCTCTGCTCCAGGCTAGAGTGAGGTGACACAATCAAGACTCACAGTAGCCTCAACCT CCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGT/GCJACACCACACTGGTTAA TTTTTTAAATTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAAACAACCAACTAAC
WI-13119a	51	C G	---	---	CAGGGCTTGCTCTGCTCCAGGCTAGAGTGAGGTGACACAATCAAGACT/GCJACAGTAGCCTCA ACCTCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACCACACTGGTTA ATTTTAAATTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAAACAACCAACTAA C
WI-13112	71	C T	AGCTTTT	TTAGAAATTTT GTGATTATAT GGAAAAAG	ACAGGAATCTGAAAGTTACCAAGGCAATTTCCCTTTTAGGATCATAAAGACTACAGACTTTAAGCTT TTTT/C/TCTTTTCCATATAATACACAAAAATTTCTAAATATCCTTAAAAAGAAAAATATAAATAGT TTCAGTATGTTATGTAGAGTCACATACTATGGCAAAAATATTTTATTAAATTGAGGGAATAGGCCAAT TT
WI-12988	36	C A	CTCAGTACAA	CAAAGTGTA CTACTGATGCT GTTT	TGTTAACATTTTATTGGTACGTGCTCTCAGTACAA/C/AJAAACAGCATCAGTAGTGTACACTTTGAT AAAAAGGAATTTTAGCTTAGTAGAAAAAGAAAGCCCAAGGTGAGAAGTATATGAATATGTACAT CTTTATGGAAACTGTTTGTGTGACCCTTTATCTTCCCTGTGGATGAGATGTGCACACACAAAGT AAA
WI-13020a	108	G A	CTTT	CTAATAGTGG AACCTGAGA CTTT	TGCTATTTCATGACAGACACGTGAGACAAATATCTTTATTTTACAGATGGAATAGACCCAGACATT TTCAGTACTTTAACCACTAATAGTGAACCTGAGACTTTA/GJATCTGCAAGGGGTTTAAATAAT GCAAAATACATATATTTCCATTTTAAACCCATATTAAGTTTCCATTTCTTAATAGAAAAATGA TAAAAATGTTTCCCAATAT
WI-12837	87	A G	AAAGTCCA	CCATATACAT ATATCAAGGT GCCATAGGAA ATGCTGTTTT	TGTATAAAAAATCCAACTGTTCCACAAGTACATATGTCCTATGATTTTATGCATACATCCATATAC ATATATCAAGGTAAAGTCCA/GJ/TACAAAAACAACAGCAATTTCTATGGCCAGGTGTTCTACAGAAGT AAGACTGTGCAAACTTTATCGTATAGTCAATGAGATTGCACACTAAGGCCAGGATGAGGCAGAGCA AGTTGTGCTCA

L42611b	50	G C ---			GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTTCTCAGGTTGCCGTGTCGCTCTCCCTGACCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGGCCCTCAGCTTCTCTGCTCTATACCT GCCCATCTGAGCACCATTGCTCACCATCAGATCAACCTTTGATTTACATCATATGATTTACACCA CTGGAGCTTCACCTTTGTTAC
L42611	34	T C ---			GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTTCTCAGGTTGCCGTGCTCTCCCTGACCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGGCCCTCAGCTTCTCTGCTCTATACCT GCCCATCTGAGCACCATTGCTCACCATCAGATCAACCTTTGATTTACATCATATGATTTACACCA CTGGAGCTTCACCTTTGTTAC
WI-1172b	179	C T A	TGAAGAAATG GCTGATACCA	ATGTGCATTTT TCACTGCGAG	TGAACGTGTGGTTAAAACTAGGCAATTGGTTAAATCAATTTAAACACAGGCCCTAGAAACAGTG ACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTAATGTTCTTGAATACCATTTTCTGCTTTC AAAAGAAAGACATGAGGCTTCTTGAAGAAATGGCTGATACCAAGCTGCTGAGTGAACCAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1172a	17	C A ---			TGAACGTGTGGTTAAACATGAGGCAATGGTTAAATCAATTTAAACACAGGCCCTAGAAACAG GTGACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTAATGTTCTTGAATACCATTTTCTGCT TTCAAAAGAAAGACATGAGGCTTCTTGAAGAAATGGCTGATACCAAGCTGAGTGAACCAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1177	35	G C A	GCAGATTGGA AGTGTGAAAA	CACCTACATTT CTGAATATTTA GACTCTTT	AGAGGCAGATTGGAAGTGTGAAAAAATGAAAGAA[G/C]AAGAAAAAAGAGTCTAAATATTCAG AAATGTAAGTGTGCTGCTCAACTGTTCTTACCCACTTAATTTCTGCAATTTTGAACACTAGATTGAAT TCCCTTGCAAAACCCCTTGATCATGATACCCGAGTTAAACCGTTAATTAAGAGACATTAACATGG CCTGGTG
WI-1231b	141	G A ---			TCCATGTTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCCACTATGCATTGGAACATTCCTCATATTC CAACTAAGCAGGAGTGTTCACAATAAACACATAGGCTCTTTATTCCTCTTTCATTAATTTTCTT TCAC[G/A]TTATTCCTCACCCTGAAGCCCTTCTTCCCTCGTAGTGACATTTTAAATCCACTTTAC ACATTCGGACC
WI-1231a	126	T C A	GGCTCTTTAT CTCCTTCTTC	CGTTCAGGGTG AGGGAATAA	TCCATGTTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCCACTATGCATTGGAACATTCCTCATATTC CAACTAAGCAGGAGTGTTCACAATAAACACATAGGCTCTTTATTCCTCTTTCATTCATTC/TAAATTT CTTTCAGCTTATTCCTCACCCTGAAGCCCTTCTTCCCTCGTAGTGACATTTTAAATCCACTTTACA CATTCGGACC
WI-472	114	G C ACAGAAAAAG	ACATACATAT CCATTATACA	GACCTTCTTT TCCAGCCC	GAAGGCAGGACTGTGTTTGGAGGACAAAAAGTAAATCTTTTATCTTTTATTTTAAATTTTATTT TTTTTCAGGCATATAGACATACATATCCATTATACAAACAGAAAAAG[G/C]GGGCTGGAAAAAGAAAG GTCAAGTGAATTCAGATATTC/TAAATGCAAGGCTGACAAATTTGGGCTTGATT

WI-478	46 C T	GCATGTCGTG T TACTCTATTT TGTC	AAATGCCACAG GTGGCT	AAACCACTGCAACCTTCAAGGATGCTGTGTTACTCTATTTTGTTCCTAGCCACCTGTGGCATTTC CAAAATATGATAATCTGCGCCACCATACTGCTTTAAACACAAATAGAACTCTGGCAGCAAAATATAGC ATAAGCTTACTTCTAAATCAAGGCTACCATCAGTACCTTAGCACATTTAAAAAATAAAAAACCAAC ACTGCCCA
WI-533	29 T C	ATCACAGCAG AGTACCTTTCT AACT	CCTTCCAACT CTACACAATCT T	AGCCATCACAGCAGAGTACCTTCTAACTT/CJATAAGATTGTGTAGAGGTTGGAAGGAGGACACAGGA CTGTTCTGTTGGTATAATGACCCCTGTGTCCAGTTAATCCA
WI-601b	112 T A	---	---	TCACTTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAATGATCAATTTCAAATAAAGATGG TAGTGAGC/TJGAACAGAAAGAGGTTTTCATTGACTCCTAACTGAGTACTCAAAAACGAGCAGGTGCT TAGTGAGCGAACAAGAGGTTTTCATTGACTCCTAACTGAGTACTT/AJCAAAAACGAGCAGGTTGCT CACAGTCAGGAAGCAGGTTGCTGAGTACAGGAT
WI-601a	74 C T	---	---	TCACTTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAATGATCAATTTCAAATAAAGATGG TAGTGAGC/TJGAACAGAAAGAGGTTTTCATTGACTCCTAACTGAGTACTCAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTTGCTGAGTACAGGAT
WI-863	107 A G	CTCCTTCACAA CCTCACCA	CTTCCCGGTAA GCCAAGT	AACAAAACAGACACCCCTCGGCTTCTTCCACAGTCCACATGGGTGCCAAACAATCCACATTCTCT ACATCTCCCCACTGGGCTGCCCTTCAACAACCTCACCAJAGJACTTGGCTTACC GGGAAGCATAAA GCCAAAGCATTTAGTCTTTTATTGCAACATGGTCTGGCTGCAATAC
WI-919	36 G A C	ACTGCTTGCTT GTTGATTAAAT C	TTATTCTAATC CCACATGACAG C	ACTCACTGCTTGCTTGTTGATTAAATCAACCTAGCC[G/A]GCTGTCATGTGGGATTAGAATAAAATA AACACAAAATGAAGAACACACAGATTGCTAACAAAGCAGATTCTTTTCAAGGCACACGTAAGAT AATAACTTCAA
WI-991	37 A T	---	---	TGATTCAATTGACCCAAATAATAACTTCTGTACAT[AT]CATTATTGATTTTCAATATCACAAAAT TATGAGTGAGGGGATGATTGTTATCCCTATTTACAGATGAGAACACTGAGACTTAGAAGAAGTATCT TTCCCAAAGTCACAAAGTTAGTGACAGAGCGGATTCGAATCCATCAACTTGAATCCAGAGAAAAT GTTCTGCATCACTGTACAACACTGACTCCTTTTCTCCTTTGAAAACAAGGC
WI-1011	70 G C CCA	CAGTATCTGA AGTTTTTGCT CCA	AGGAACACCTA CAAAATGACTT CT	CTCCTGACCTGTTGCAGTGGATGTTTGAAGGCTCTGCTCAGTATCTGAAGTTTTTGTCTCC A/GCJAGAAGTCAATTTGTAGGTGTTCTGGGCGTTTTTGTGCTAGCTTTTCCATTTTCTTAATACACTGC CGTCTTAAGGGAGGGCTTGACAGACTTATCAGATGGCTGTTTGTGCTGCACTTCTGCACTGAAG
WI-5381	178 A T	---	---	TTCATGCAAGGTCCTAGTTCAGAACTCTCAAGAACTCAAGGAAGAAAGGCCCTAGAGATGACACCAGAA ATGAGAGTGGCTTGCTCATGAAATTTGGACAGCATGTTCCAAAGCAGAGGGAACAGCATGGAGAAGA AAATCATACTCTATCCACGTTGCAGAAACTGGCAATTAGTTTTGT[AT]TTACTAAAACACAAATGT TTAACTTGGGGTCCACAAAACAGGATATGTTGGCAATGGTATTTCTGTGATG
WI-5791b	76 G A	---	---	CTATGATTCCATCTAGCAAAAAGCAAGACTATTGGATAAGTTTTCACAAAGATGAGAACAGGTCCTA GAACCTCAG[G/A]ATCGAAAAGGAGTTTCATCTAGTCCATAGACCCCTATCTCACTGACCCAAAAGGTA AAAAATAAAATAAAGTAAAGAACTTACATCAGATTGTGCATTCTTATTTTGGCACCCCTGTTTGT TAGGAA

WI-5791a	44	C G ---				CTATGTATCCATCTAGCAAAAGCAAGACTATTTGGATAAGTTTTC/GJACAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAAGTTTCATCTAGTCCATAGACCTATCTCAGTACCCCAAAAGGTA AAAAATAAAATAAAAGTAAAGAACTTACATCAGATTGTGCAATTTCTTATTTGCCACCCCTGTTTGT TAGGAA
WI-5406c	120	C T ---				CACCTGCTGTTGTCCATGGGTGCCACAGACTCTCCAGAAGAGCCACTCCACAGATGCAACAGGCC TTTTGAAGGAGCCCGAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCC/C/JCTATGAGCCAC ACTTCTCATTTCCCTTAGAATTTCTTGACTCTGTGAAGAGGAAGGAAAGGAAGAAAAAGAGAGGCAA GG
WI-5406b	118	C A A	CCAGGATGTC AAGGTGAGAA	AATGAGAAGT GTGGGCTCAT		CACCTGCTGTTGTCCATGGGTGCCACAGACTCTCCAGAAGAGCCACTCCACAGATGCAACAGGCC TTTTGAAGGAGCCCGAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCC/C/JCTATGAGCCAC ACTTCTCATTTCCCTTAGAATTTCTTGACTCTGTGAAGAGGAAGGAAAGGAAGAAAAAGAGAGGCAA GG
WI-5406a	42	A G ---				CACCTGCTGTTGTCCATGGGTGCCACAGACTCTCCAGAAGAGGJGCCACTCCACAGATGCAACAG GCCTTTGAAGGAGCCCGAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCCCTATGAGCCAC ACTTCTCATTTCCCTTAGAATTTCTTGACTCTGTGAAGAGGAAGGAAAGGAAGAAAAAGAGAGGCAA GG
WI-5798	48	G C TG	TTTATTTCTCCC TTGTTTCTTT	ACTGTTAGAAA ACCAATATTTT TCAAT		CCATTCCTCTTCCCTCCCTCTCCCTTATTCCTCTTTTCTTTTG/C/JATTGAAAAATACTGGTT TTCTAACAGTGTGCTGGTATGGATACTATGTTATAACATGATAGTTCTATATGGGTATCA
WI-5415	54	T A TTT	TCTTCATGAAT TCATCTTTCAG	GGACTAATTC TGATCCGATCT		CCTGCTAATAATAATTAAGCAGCATTTGCTTCATGAATTCATCTTTCAGTTT/T/AJTAGATCGGAT CATGAATTAGTCCAGGCTTTTAGTTGTAATCGAAATTGGA
WI-5437	41	C T G	TCCAGAGAA AAATCCAAGA	AGTTTCTAAAC ACAAAATATG GTTTAAG...		TGTTTTAACCCAGGCAGACCTCCAGAGAAAAATCCAAGAG/C/JCTTAAACCATATTTTGTGTTTA GAACTCCTGTGGCCAAACCACCTTGATGTGAGTGAC
WI-5481b	131	A G CTGAGTCG	TGTCATTATG CTCCAAGTAT	TTACTTCCAGG CTCCAAGTAT		AAGCCAAATTCACATTAGTTGATGAATTTGAATTTTACAGTATCTAATGCATGGGCATCTGTTTCAAC TCTCTGTTTTCAAGAGGAGTAGTATATGCTGAAAAATCTATTTTGICATTTATGCTGCAGTCG/JGJA ATACITGGAGCCTGGAAGTAAAGACTTGGCTATTTTCACAATTA
WI-5481a	29	G A AATTT	CCAAATTCAC ATTAGTTGATG	CCCATGCAATTA GATACTGTAAA ATT		AAGCCAAATTCACATTAGTTGATGAATTTG/AJAAATTTTACAGTATCTAATGCATGGGCATCTGTTTC AACTCTCTGTTTTTCAAGAGGAGTAGTATATGCTGAAAAATCTATTTTGTCATTTATGCTGCAGTCGAA ATACITGGAGCCTGGAAGTAAAGACTTGGCTATTTTCACAATTA
WI-5492	38	T C ---				TCATGAGTCTTTCTTCAAGATGCTTGTAAAGTCCCA/T/CJCAAGAAAGGATCCCATGGCCTAAT GAAGATGTACCTCCACCTTAGGATATTTTGCAGACCAA

WI-5826	134	T C	---	CCCAATACITTT TTCAGGTGAA	---	TATTTTTTTTTCTCAATCCTGGAGCACACCATGCTCTTTCTATTTCATGCTTCACATTTATTTTTT TTTCACCTAGTTAAATGCTTTTCCCTTGATCTAGCAATGGCCAGTTTATACATATTTCTTAGT[C] TTTCAAAATTAATGCCACCATAGAAATAATTTCTAACCAACAGCCAAACAGCCTCACTCTTCCTT CCTGGTGCAATTTACTCTTTACAC
WI-5546	40	C T A	---	GGCACCAGCCT TTTITAGAGT	CCTGTATTTTA GCAAAACATGGG	CCTATAACCCCAATACITTTTCAGGTGAAAAAGGGAAAA[C]TACCCCATGTTTCTGCTAAAAATACAGG AGTATAACAGCATGACATGTTAAGGGAATTACAAATGCTTGAGGTAAATCTGATGTGGGAATAT TAGAAAAATTAAGCGAGAGAGGCA
WI-5552	97	C T	---	GGCACCAGCCT TTTITAGAGT	TGCACAAATTG CCCAGG	TGTTTGCTGCACCTCCCAACAAGTGTCATAGCCTCAAGGGTTTIGATTGAGCGGGTATGGGT GGGGCTATCGGCACCAAGCCTTTTAGAGT[C]TCCCTGGGCAATTTGTGCAC.TAGTGTGAGA TAAGTTGATTTAAACACCTCTGTGCCTCAATTTTCTACCTATAAAATAAGATAATAGTATCTAAAA AAAAAGAGAGAGAAATTAAGGTGGATAGACATGAATAACTCTGATGACTGGTTGTATCCCTGAA TCCTGCAATATACACATGATTCAATGAT[C]TCCATTTTGAATAATTAAGCTTTTGAATTTGTTTCCA ATG
WI-5836b	161	C T	---	---	---	TCGGGTATTAGGATGGGTTCAACCCTCGATGATGGGCGTTCAAGGAGGTGGGA[C]T/GACAC ATTACTCTCCAACCTGTTTCATCAGAACACTTCAACAGCG
WI-5573	58	C T	AGGTGGGA	GTTCATAAGG	TGAACAGTTGG AGAGTAATGTG TC	CAGGACCTTGGAGCCTTTGCTGTTTGCTCTCCACCTCACTCTTCTCTGCTGCCCATGGGTGGAGC CTCTCAGGCTTCCCTATGACAGCGGTCTATCTCTATATGGGCAATATCCAATGTCCCATTC[G/A] TTTTTGCCATTTCCCTGTATATCAAAACAGAGAGAGGGGTGG
WI-5850b	134	G A	---	---	---	CAGGACCTTGGAGCCTTTGCTGTTTGCTCTCCACCTCACTCTTCTCTGCCCATGGGTGGAGC CTCTCAGGCTTCCCTATGCA[C]TGGCTCTATCTCTATATGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCCCTGTATATCAAAACAGAGAGAGGGGTGG
WI-5850a	92	C T	---	---	---	TGCCTGATTGACACATAGTTATCTGACAGTAAATCATCTAACATCACAAATATCTTATTCTGCCTG TCACACTAAATTTGCAAGCATTCAAATTGATTGACTATTAAATGAGCATCGTGTCAATTC[A]T/CAGTGT TTAGGTTTCTCAAGAGAAATTATGCTGTTCTCTCTGTAACCTCAAGTA
WI-5612b	125	A T	TTC	GCATCGTGTCA	TTCTCTTGAGA AACCTAAAC ACTG	TGCCTGATTGACACATAGTTATCTGACAGTAAATCATCTAACATTCACAAATATCTTATTCTGC CTGTACACTAAATTTGCAAGCATTCAAATTGATTGACTATTAAATGAGCATCGTGTCAATTCACAGTGT TTAGGTTTCTCAAGAGAAATTATGCTGTTCTCTCTGTAACCTCAAGTA
WI-5612a	44	T A	---	---	---	TGAGAGCCAAATTTATCCGCAATAAA[C]TTCCTCCAAAGTCCCTCGATGGAGGCAATTCAGAAATCGGG GCAGGGGAGGCAGAGGTGAGACAGATGTGAAGAAC
WI-5636	26	A C	CCGCAATAAA	GCCAAATTTTAT	CATCGAGGACT TTGGGAA	

WI-5865c .....	103 C G ...	---	TTAGAAACCTCCATTATCTGCGATGGTACATCTTTTAAAGAACTTTTTTTCATTATGCATTG ACTGACTCACTCACTTGCTCTATCAAAAATTTAAAC/GIAAATAATTAATATTTTATTTACAGAGGAA CTCAGAAAGCCAGAAAAATGACCAAGACACAGTCCAGTCCATCTTCAAAAGGTCACAGTCCCTTCA GAGAAAGACAGACAACTAAATTAATCCAGG
WI-5865b .....	99 T A ...	---	TTAGAAACCTCCATTATCTGCGATGGTACATCTTTTAAAGAACTTTTTTTCATTATGCATTG ACTGACTCACTCACTTGCTCTATCAAAAATTTAAACAAATATTAATATTTTATTTACAGAGGAA CTCAGAAAGCCAGAAAAATGACCAAGACACAGTCCAGTCCATCTTCAAAAGGTCACAGTCCCTTCA GAGAAAGACAGACAACTAAATTAATCCAGG
WI-5865	165 T A ...	---	TTAGAAACCTCCATTATCTGCGATGGTACATCTTTTAAAGAACTTTTTTTCATTATGCATTG ACTGACTCACTCACTTGCTCTATCAAAAATTTAAACAAATATTAATATTTTATTTACAGAGGAACTC AGAAGCCAGAAAAATGACCAAGACACAGTAAJCCAGTCTCCATCTTCAAAAGGTCACAGTCCCTTC AGAGAAGACAGACAACTAAATTAATCCAGG
WI-5874	76 T G ACAGAAAA	CATAGCATGG ATAATATTAT ATATGT	CTCAGACATTCATTTTCATTAGTTGTTAAATTTTGTGTTTTCATAGCATGGATAATATACAGAA AAAAATTTT/GTACATATCAAAATGACTGAACCTTACTAGGTAGCAATTTGTTTGCAATTTGCT CATGAGCCGACGTTTCAGCTCTCAGTTTTTCCATC/AJTTTTTTCATAATTTACTCTCTTTCTGTC ACAATGTTCTGCTTCGTTATTTCAACTCTCATTTGCTGATTGGATGGTAGTCATAAAATATGGGTGATTG AGAAAAATAGTAAATG
WI-5752	36 A T TTTTCCATC	GACAGAAAAAG AGAGTAAAT ATGAAAAA	TTAGCAGAAACAACAAAAATGTCAACACACTGCAGTAAAGAAAGTGTTCCTCCGATAAATA/C/GJC CATTAGGTATTAGATAAGCATCCCATAAACATTTGTTGAAACGGAAGCCGAGTTTTCGATTACACACA GTTGCTGTTTTAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCGTCCACGAAA CATTGTTGAAAAACGAAGCCACGTTTTCCGATTACACACAGTTAGTTGCTGTT
WI-5760b	61 C G ...	---	TTAGCAGAAACAACAAAAATGTCAACACACTGCAGTAAAGAAAGTGTTCCTCCGATAAATAACCCAT TAGGTATTAGATAAGCATCCCATAAACATTTGTTGAAACGGAAGCCGAGTTTTCGATTACACACAGTT GTCGTTTTAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCG/GA/TCCCAACGAA ACATTGTTGAAAAACGAAGCCACGTTTTCCGATTACACACAGTTAGTTGCTGTT
WI-5760	187 G A ...	---	AAATCTGGCCTTTTCTCTTAGGAGGAGATTCTCACCATGGGAATCTTG/A/GTGCAGATTAGAT CCACCCCTCACTATTGAGAAGCTAAAGTGAAGACTACTCATTTCTCAGTCTTCCCTTGCTG
WI-5944	52 A G GGAATCTTG	TTCTACCATG AACTTGCA	GAGTTTTAATGAATCTGTTCCCTCTCTAAACCTCTGTTCCCACTTCACATTTCAGCAGATATT CTTTCATGGGTTATTTTGCCCAAGTCATGAGGAGATGCATGTAATTTGATCATTTCAAGAGTGTGAG TAATGCTTGGTAC/TJTTGCTCTGTGCGGTATCTGCTCCAATCACCATTCCACATTTATTTCTTATTAT GCTGAATGAAACGGTTATATTACAG
WI-5967b	148 C T ...	---	

WI-5967	165	CT	---	---	---	GAGTTAATGAATCCTGTTCCCTCCTAAACCTCCTGTTCCCCCAACTTCACATTCAGCAGATATT CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGATGTAATTTGTGATCATTTCAAGAGTGTGAG TAATGCTTGGTACTTGCTCTGTGCGGTATTC/TGTCTCAATCACCCATTCACATTTATTCCTATTAT GCTGAATGAAACGGTTATATTACAG
WI-6093	53	GC	---	---	---	GGGTAAAGATCCAGAGCCACAGGTGAACCTGCCGGTATTGAAGTCTTTGGGCCA/GC/GTCTGTAATG ATCTGACTTCTCCAGAACCCCTCTCTCTGGAAGTCCAACTGTGCACTGAGCCCATTTGAGGGA GCATTTGAACAAACCCAGCGACACTGCTGACATTTGACATTCAGCAACCTTGATTGACGGTGAC ACACCATGCTTCGAGAAGGAATGAGG
WI-6141	80	TC	AGGTACTT	AGCATCTACA	TGAAAACCCCA GAACAGTG	GACTGTGCTCAAGAAAAAATAATGAAAAATTGAATAATTAAGCACCTTCTTAATAAGCAT CTACAAGGTACTTATTC/CACGTGTTCTGGGGTTTCAATCCTCTCACCTTTTAGACTTCAGGAAAT CAGAAAAATGCATGAAAAACAGGATTGTTACATGCAGAGAAATAGGGGAGATAAAAAATTTGCTTTT CTC
WI-6450	45	TG	GGTCACTT	ATCTATATCT	CT	ATAGGACAGTTTTTCTCCAAATGACTTATTTCTATATCTTGTACATTC/GAGAAAGTACCACACATTTCA AACAAAGAGCCAGGCTATGCCAGGGTGGATTATTTTCACGGTCATGGTAATATGATGTAAGACTA TTTTACTGGCTCTCTTTATGCTATAAAACAAAGGATTTGGTCTATTCAACAAACATGTGCAATACAG CAGTTGTCATGCTCCTCTGGTACTAGAAATATAGTCTTTATAGAATATGTTGTTTAGAATAAGCCACA AATTATCTATAAAACAACAC/C/TAAAGGAACGAGGCTCAAAAGTGAACAAAAACGGCCTTAGTTTC TAAGTGAAGACTAAAGACGATATAGGAAAAATATAATCCGTGACCTCTTA
WI-7466c	141	GA	TTTGCTCTGG	TTTTCACAGTC	AGTCGCATGCC AATTTATAATT	GAACTATCCTTTAGTGGTCCACATTTTCTATTCTGATTCTTTGGTCACACAGGGACTTTCTGGGCT ATGAAATAGTC/T/CJATTTCAGTGAAGTATGTTATCATAAAGACATGCAAAAACCTTTTCACAGTCTT CCTGG/GJAJAATATCTCACAAAAATTAATTATAAATGGCATGCGACTTTCTGATTAGCCTGACAGG ATTGTTCCCTT
WI-7466b	80	TC	GTC	GACTTCTGGG	ACTGAA	GAACTATCCTTTAGTGGTCCACATTTTCTATTCTGATTCTTTGGTCACACAGGGACTTTCTGGGCT ATGAAATAGTC/T/CJATTTCAGTGAAGTATGTTATCATAAAGACATGCAAAAACCTTTTCACAGTCTT TGTCCTGGGAATATCTCACAAAAATTAATTATAAATGGCATGCGACTTTCTGATTAGCCTGACAGGA TTGTTCCCTT
WI-9814	104	CA	---	---	---	TGCTTTTAAAAATAACAATGACCACACCTGACACCATAGTCTGTCTCCATTTGCCACGCTTCCTC AGTAGAATAAGACAGGGACTTTGCTGGCTGCTATCT/CJATTCTCTCAGAGAGACACTTGGCCCT CATAGGCATCCATAGATAATTTGTTGAATGAATGCTTTTGCATATTGATTCCTACATTTGATACA TTCTCAGGAGGGACATTTGGCCTAT
WI-9720b	55	AG	---	---	---	CCTCTAACAGAAAACTTGACTTCCTCAACTCAAAATACCCCTTCTCTAATAATTTJ/GJAGTAACCA AAATATCTCTTCAAAATAAATTAATCTTTTAAATTAGAAAGCAACAGTGTAGAGGTAGTACATTCA CCACC

WI-9720a	47	A G	---	---	CCTCTAACAAGAAACTTGACTTCCTCAACTCAAATACCCCTCTCTA/GIATAATTTAAGTAACCA AAATATTCCTTCAAATAAATAATCTTTTAATTAGAAGAAGCAACAGTGTAGAGGTAGTACATTCA CCACC
WI-9825	123	A T	---	---	CACGCTCTAAGGCAGGATGGCTTATGAGATACCTTTGCGATGCTGCTGCACACCTTGAATCTGCC TGCTGGCTCCCTTACTTACCTCTCTGTCATGTCAGATGAAGGCTCAGGGTGTCTA/GAGGATTAG TAAGATCTCTTTCTAAAGACAGGAGAGATTATTTACAAGAAGAACTCACCAGGGTTAGTTGCATT TAAGAAATGCCAGTCTTTTGTCTGTCATCTTGAACATTAATCCACATG
WI-9748	74	C G	---	---	CCACTTCAGTAAATCAATTTGTAGCACCTTATTTCTAAAGATTCTAAATTTTATATGTTTACCCCTTT GTCATTTC/GTTCAGACCAAGTACATGTTTTCACACAGCCATCTTTCTTCCCTGGAATCTTTTCAGAAT TACAGTTATGATGCTCTTTTATATCCCA
WI-9943	91	T C	---	---	TGAGGCTATGATTGCAGATTTGTAGTGACTAATACCTTATTAAAGCAATTTCAATGTGTGGGCACTGTT CGTTGTGTTTATATCCATCTTC/GATTTTAAATTTTCTACTGAGCAGAAAAAATAATGTATACATT AACCTTTGCTCCCTATTGTACCTTTTAAATATTGCATTTTCACACCTTCTCTTTTGTCTATTAGGGA
WI-9891	39	T C	---	---	AGGGCCTTCACAGATCCGTCAGCTCAACACTGCCTCCTTTC/GAGTGAGCCTGTGAACCCACCAAGAC GGCTGGTCATCAGTGTCTCTCTCTTTCCGGACAACATCTTTAAAAAGAAAAAAGAGTGT CTTTGAATGTATCCATTTATCCCAATAATCTGTTTAAATAATCTCTTATTAGGCCAAATCCCAAT GTGCTGAAATATCTGCCAAGCATGTCATCTACACAAAAAGGGATTGCAAA
WI-9897b	84	C T	---	---	CTCAGAAATTTCAGATCTTCCCAATGTGATGATCTTGTCTCAACATCCTATTTTCTCCTCAAAAC ATTTATCTAGCCTGTATC/AAAGTCATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9897a	83	A T	---	---	CTCAGAAATTTCAGATCTTCCCAATGTGATGATCTTGTCTCAACATCCTATTTTCTCCTCAAAAC ATTTATCTAGCCTGTATC/AAAGTCATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9935b	115	C A	---	---	AGATAACCTGGAAAACTAGAAGAAATTAATAACGTGTGCACACCTCACCAGAACTGGAAGGAGT CTGACTGTGTTCTTATGGGTGCTTGACTGGCAGGGGGAGTTCAGACA/C/AAAGCAAGAAAAAGCC TGATATTAGAGGCACCTTGCAATA
WI-9935a	42	C T	---	---	AGATAACCTGGAAAACTAGAAGAAATTAATAACGTGTGTGCA/C/TJACCTCACCAGAACTGGAAGG AGTCTGACTGTGTTCTTATGGGTGCTTGACTGGCAGGGGGAGTTCAGACACAGCCCAAGAAAAAGCC TGATATTAGAGGCACCTTGCAATA
WI-9983	146	C T	---	---	CCTGTTAGGTGCCAGAGTCCATGCTCTTGCCACAATGTTAGGCTGCCTCCCATTTCTCTTCTTGA TCCCCAAACCCCAAGTTCTACCAATCTGATCAATGCTGACTAGGTGCTGCTGCTGAGGGTAA AGCATTATGA/C/TJAGACACAAAAAGAGAGGTAAAGTTGCTGCTCCTCAAGAGAGAGACATAA AAACAAATGGATCTGGAACTAAGTAAGGCTTCGAGGAGGAGGTGAGCAAGG



WI-10019	139	A	T	ATCT	TGATGTAATGC TATGTAGCAA	TTGATTACTGT GCTTAGGGA	ATATCAGTGGGTGAGTATACAGCAATCTATTTTGTATTTATTTATGTTGCTATATAAATCAATGGTTCTA ACATTCAAAATAAGATCTTTTGTCTCTGCTCAGATGCTTTCAATGATGTAATGCTATGTAGCAAAAT CTAATTTCCCTTAAGCACAGTAATCAAGGCCCTTCTACCCCA
WI-10020b	122	T	A	TTT	GGGAGAAAAG AAATCATGAC	GACTGTTAATT TATTTAATCAT TAGTCTGG	TTTACTTCATTGTCATCTTGACTCGTATTAATAAATTAATTAAGTAACTGGCTCTGAAAAGAAATTTAGGC ATGCATAGAGAAATAGCAGTGTATTTATTTGGCGAGAAAAGAAATCATGACTTTT/TA/AAAAATACC AGACTAATGATTAAATAAATAAATTAACAGTCTAGGTTCCGGAAAGTGGCTAAAGCACGCTAGTAGCCCT CCTTAGA
WI-10020a	39	T	C	ATAAAT	TGTCAICTTGA CTCGTATTAA	AAATTCCTTTC AGAGCCAGTTA AC	TTTACTTCATTGTCATCTTGACTCGTATTAATAAATTAATTAAGTAACTGGCTCTGAAAAGAAATTTA GGCATGCATAGAGAAATAGCAGTGTATTTATTTGGCGAGAAAAGAAATCATGACTTTT/TA/AAAAATACC AGACTAATGATTAAATAAATAAATTAACAGTCTAGGTTCCGGAAAGTGGCTAAAGCACGCTAGTAGCCCT CCTTAGA
WI-10064b	170	C	T	TTTACATG	CCCTTAGATAT ATTGTGATTGT	ACCTTTCIGAA GCCAGATTTC	TCTGAGTCTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGGCATTATAATAAT ATAATTTGCAGAGCATCTCTCTCTATGCACAGATATTTGGTGACACTCTGTTTAAATCCAGTATCC CTACTCCTTAGATATATTGTGATTGTTTACATG[C/T]GAAATCTGGCTTCAGAAAAGGTTAGGTGTT T
WI-10064a	54	C	A	CAGGGAAGG	GATAGCAGGAT GATAGCAGGAT	GAGATGCTCTG CAAATTATATT TATTAT	TCTGAGTCTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGGC[A/AT]TATAATA AATAAATTTGCAGAGCATCTCTCTCTATGCACAGATATTTGGTGACACTCTGTTTAAATCCAGTA TCCCTACTCCTTAGATATATTGTGATTGTTTACATGCGAAATCTGGCTTCAGAAAAGGTTAGGTGTT T
WI-10289	29	T	C	CAAACTCTT	TCTCCTGTCCC CAAACTCTT	ATTCTGTGT ATTGAATGGAA TTAA	CCAGGGATTCTCCTGTCCCCAACTCTTAT[C/T]TAATCCATTCAATACAACAAGAAATTTATAGAA TATGCACCAATGCCACAAAGACACCCCTATATTAGT
WI-1319	40	A	T	ATTCTTT	TGGCACTTAG AACATAGTTT	GCCACACACCC CTATGGT	AAGAAAATCCTGTGGCACTTAGAACATAGTTTATCTTTATJACCATAGGGGTGTGGCTTATCT TTTACCTGGCATGGCTTAGTCTGTTTATAATTTGGTATCTTTTGCCACAAAGAGTCTGTTCTGAC AGCTTATGATCTCTATTTAACATTAACACTGGTCAGATGTGTTTAAACCTGTGTAACCTGCAGC
WI-10316	104	T	C	CTCTT	CTGTTGATTTT CTACCTCTATT	GCTTTGGAATG TATCCAAAAGT TT	AGCAACGTGTACAACCTTAGTGAGGTGTAATCAGAAGCATCTATATTATTCACCAGTCACCAACCTG GACTATAGTCTGTGATTCTTCTACCTCTATTCTTAT[C/T]AAACCTTTTGATACATTCCTCAAAGCAT CATGGTCACTTCCAGTTATGAAGGATGTTTAAAGCCAGCC AGTGAGTTGTGCACAATTTTGGAGACATTTCTGTGACCCCAACTTAAACACACTCTCTCCACAC[C/T]AC AAAGTTAACACTTCAGTTACCAAGGTGATGATTGAGCAGA
WI-2572	61	C	T	...	...	...	

WI-10368	31 C T	TGAAGCAACC AGGCTTGGT	CAAGATATTAT ATTTATCTCT AAGAGGGG	GAGGAAGCTGCCTGAAGCAACCAGGCTTGTTC/TCTACCCCTCTTGAAGAAATAATATAATATCTT GAGATAGGAGGAGCAGCCTGAGGACAGCTGGGTTTGTCTACCCACTGGAAGCAGAATATCC TTCAAAGCTTTTCCAGTGAGTCATGTTGCTGCTAACTATATGACCCTGATGGATTGCCTTTCAGGG T
WI-10391	32 A G	CTGTCTCAGGT ATGACTCCCA	GGGAGTTAGGA GTCAAGAAGTT GA	CCTCCCGTTCTCTGTCTCAGGTATGACTCCCA/GTCAACTCTTGACTCCTAATCCCATCTCGGTG TCTGCTTCCCAGGGACGATCTGACAGCCTTTGCTTGCTGTGACAAACAGAACATTCGAGAAG TGATGCTGCGTGACCTCCAGGATA
WI-10567c	146 A C	GTTACCCAGA GTCTTCTAATA GCAA	TCGCGCTTCCA GTAGCT	AGCGATGAAATTTATATGTTATGCTGACTTACGCGGTGCTCAATAAATATTCTTTTTCATATT TTCCAAATTTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAGTTACCCAGAGCTT CTAATAGCAA/A/CJAGCTACTGGAAAGCGGCAAGAAATTTAACCCCT
WI-10567b	82 A C	GGGTGCTCAAT AAATATTATT CTTT	...	AGCGATGAAATTTATATGTTATGCTGACTTACGCGGTGCTCAATAAATATTCTTTTTCATATT TTCCAAATTTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAGTTACCCAGAG TCTTCTAATAGCAAAAGCTACTGGAAAGCGGCAAGAAATTTAACCCCT
WI-10567a	60 T C	GGGTGCTCAAT AAATATTATT CTTT	AAATTTCTGTT GGTGAAATTC TAG	AGCGATGAAATTTATATGTTATGCTGACTTACGCGGTGCTCAATAAATATTCTTTTTCATATT ATTTTCCAAATTTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAGTTACCCAGAG CTTCTAATAGCAAAAGCTACTGGAAAGCGGCAAGAAATTTAACCCCT
WI-11153b	84 C G	CAAACCTCAA ATTGCTTTAAG TACTTTA	AAATCCAA GTCAAGGCTT C	CGTTGGGAATATTTCTATCTCACCTAAATATG/C/AJGTGATTAAATATACATTTTACAAACTTC TTGCTTTAAGTACTTTA/C/GJGAGAGCCTTGACTGTTGGATTTTGGATTTTCTTTTCTTTAATA AAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTAATCTGATATCAGCATCCCTT TATGTATT
WI-11153a	33 C A	GGGAATATTC TATCTCACCTA AATTATG	GCAATTTGAAG TTTGTTAAAT GTAT	CGTTGGGAATATTTCTATCTCACCTAAATATG/C/AJGTGATTAAATATACATTTTACAAACTTC AAATGCTTTAAGTACTTTA/C/GJGAGAGCCTTGACTGTTGGATTTTGGATTTTCTTTTCTTTAATA AAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTAATCTGATATCAGCATCCCTT TATGTATT
WI-2616	125 T C	CACAAATGTA ACAAGAATTG ATCC	CCATGGCTGTA GTCCAGT	GTTGTGAAACTCCAGTATCATTCCCTCAAAACCACGCTTAAATCACAATCATTCTTCTCCTGTA GAGCTCAAACTCAGTCTGAATGAAATTTGCTGCACAAATGTAACAGAATTGATCCTAT/CJACTGGG ACTACAGCCATGGAGAAAGCAATGTAGTCAGCAAAATGTTAAG
WI-11163	58 C T	CAAGTGAATT ATGACCAAAA TGAGA	TGCTCTTTCA TTTGAGGTTTT T	TGACTCAAAGGAAACACACACAAAAAGTTTACCAAGTGAATATGACCAAAATGAGA/C/TJAAAT TTGTTAAAAAAAACCTCAAAATGAAAGAGACAAATATAGTTCAAAGATTCAGGTTCAATATTGT ACCTACAAAATAGGATAGTCATGGTTGGCAGACTTTCTTTCCCTTTCTTTTGT/GJCTCTTA GAATCCATTTTGTCTTTTGGCCAGCATTCCTCTCCCATATTTTAAAGGAGAGAAATTCACCTTTTCT CTGTTGGATGATCACAGGTTCTGCTCTTCCCAATCCAGAGGAGGCTACTATTACCCCATGGGGTCAT AGAGAGGATTAAACAGGGTGATGCCTGCAATGGGAATATTGAAACC
WI-10656	59 T G	---	---	---

WI-11169b	154 T G T T T T	TTAACCAAGA G T T T T C A T T C	CTAACTTAAA A T C C T C A T T C A A A A T A T A A	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTCTCTATCGAGAAAGCAATAAGTGAAGTAA CTGACTTGAAAAAATAAAGCCTAAAGTAGTGCTTTTAAACCAAGAGTTTTCATCTCTTTT TTTAAAAAAGAGCAGACAGT/GJTATCATGTGTTCTGATAAATTTTATATTTGAATGAGGATT TTTAAGTTAGCAT
WI-11169a	95 A G T T G A A A A A	AATAAGTGAA A G T A A C T G A C T T G A A A A A	AACTCTTGGT T A A A A A G C A C T A C T T	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTCTCTATCGAGAAAGCAATAAGTGAAGTAA CTGACTTGAAAAAATAAAGCCT/GJAAAGTAGTGCTTTTAAACCAAGAGTTTTCATCTCT TTTTTTAAAAAAGAGCAGACATTTATCATGTGTTCTGATAAATTTTATATTTGAATGAGGAT TTTTAAGTTAGCAT
WI-10685	25 A G ...	...	...	CAAGTGCTGGACCTGGATAGGTG/GJACCGGCTGAAGTTGGACAGTTGTTGGTTAGGTTGGAG ACCAAAATTCAGTCATCCTGTAATATAGATCTTGTTCTTTGGGTTACCACAGGGTCACTAAAG AGAGATGGGAGACAGTCTCAATCTTGCTAAATAATCCAAAATAGCCATGGGTTGGACAAAATAC AAGTTAGTGCTCTCTAATTTAATGGGCATA
WI-10686	133 C T A A G G	TGCCCTGTCC T A A G G	CAATCTCTAAA T T C A T G T G T A G A C A C A	AATAACCTGTGGCACAAGGCAATACTGAGCCCCATACAGAGTGTTTATGTTAATATTATGAAA AAAGTCAAGAGAAACAAGATGATAGTTCTGCTAGAACTGTTGAACTGATGCCCTGTCCTCAAGG C/TTGCTGCTACACATGAATTTAGAGATTGAATGAAATGGCAAAATTCAGAAAAAGGG
WI-11175	77 T A A	AAATGATTCTT T C T G C T C A A A G	CTGTTCTACA T T C T T T T G A A A A	GGTAGGATGATCTAGATGCCACTTACAGCCACTGAAATATATGCTCCCAATGATCTTTCTG CTCAAAGAGT/AJTTTTTTAAAGTTATCTACTTATTTATCTGCTTTTCAAAGAAATGTGAGA ACAGTACAAAATGIGTTCAGTATAGCAAAATTAATTAATAAAGTAAGAAAAAGGCCAATT TGGGC
WI-10694	144 A G T A T A G T T T C	TGCAAAATGCTT T A T A G T T T C	GGCATTTTGT A A G G A G G A A	TAGAGAGGCTTTTTCAGTTTCAGGTTGGAGGGTGGTGAGGTGAGATTCCTTTAGAACGACTGGC TATGTACAGAAAGATAAATCTGAGAAAGAACTCAGTTCTAAAGTTTCAGTCTTTGCAATGCTTTA TGAGTTTTC/GJTTCCTCCTTTACAAAAATGCCATCAATCCCTCAAGGAAAAAAGGCTTTCT T
WI-2716	23 T C C	TGAATTCATCC A G A A A A A C A G	TCCTTTTCTC T C T T G T T G T C A T T C	GTGAATTCATCCAGAAAAACAGC/T/CJGAATGACAACAAGAGAGAAAAAGGATTAAGGTTTTGT ATACGACAAGTGGCTCAAGCAATTTCTCTGTCAGTGCATGGAGCAGTG
WI-10719	115 T C G C C A T T C T A G	TGACTCTCAAG G C C A T T C T A G	GOACTGCCAGC A G C C	CAGGCCAACTCTGTGATTAAGTGTTTTAGAACAGACACCTCAGTCACACAAAGTTTCTTGTATGT GCCACCATAAACAGTTACTGGAGGATGACTCTCAAGGCCATTCAGT/CJGGCTGCTGGCAGTGCTT TTCCAGCCTGCTGCCATAACTAA
WI-10721	40 A G C T T G C C A	TGGCTCTGCTA C T T G C C A	GAAACTCCAC A T A A A T A A A T C T C A	CAACCAATTCAGATTTAAATTTTGGCTCTGCTACTTGCCA/GJATGAGATTTATTTATGTGGGAGTT TCTGAAGATTCCCATGGTAAATAGTATTCCTCTCCCTGCTTAGGTTTGAAGAGTTGAA

WI-11204b	88 T C ---			GCACGAAATTGATTAAATTGGCTGACITTTGAGGAGGAGAACAGGGAGTTGAGGTAAAGGGTG AAAAGAAAAAATTTACACCTTTT/CJATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTTGGGAAGAGATTAGTGAATCAGAAAAAATAGTCTGAGGAAAAATTTATTCAGAAG GCAACATC
WI-11204a	80 T A AACTT	GTAAAAAGGG TGAAAAAGAAA	TGATCACTTAA AATGTACATAA TACCTTT	GCACACGAAATTGATTAAATTGGCTGACITTTGAGGAGGAGAACAGGGAGTTGAGGTAAAGGGTG AAAAGAAAAAATTTTAAATTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTTGGGAAGAGATTAGTGAATCAGAAAAAATAGTCTGAGGAAAAATTTATTCAGAAG GCAACATC
WI-10732	80 C A ATTGGTTCAC	GCTGTGTCITC CATAACAGAA	AAGAACAAATG CATAACAGAA CITTTAA	ACATGTATTTCCCTTAGTGGTCAGCCTTCCTTACCCCAAGAAATATCCCTGGTTTATTTGCTGTGCTTC ATTGGTTCACCTC/AJTAAAGTTCTGTTATGCATTTCTTGAGTCCACATAGGTGTTAATCATTTCCA CACCACTCTGTTTAAACTGTC
WI-11206	127 A T ACTC	GGTTGTGTTTT CTGTATGTACA	GAGTGACAATC CTAATGGTGG	TAGCTTTTCTTTGTACGAGTGTCAATAAAGAAATACCACCTCTGTCACATTTTGTAAAAAGATAGCACAG AGAGAAGCATTACAGGGCACAGCACAAACATGAGGTGTGTTTCTGTATGTACAACTC/AJTCCAA CCATTAGGATTGTCACCTCTCATATATAGACAGAAATCAGTGGTGTGATTGAAATCCACACATGGA ATAAGTCTA
WI-11215	68 C T ---			GAAAAAAAGTTTTAATTTGGATTGCTTAGTTGCTTAAATTTGACCTACTTTTCAGATTTATTTTAGT [C/T]ATTTTCTCTATAATATTTTCTTGTAGTGATGATTTTCTATAAATTAAGGAAAAACAGATATTT ACACAGAGAAGACAGGATTGCTTGAATTAGTATAACATTTTATTTCCAAAGCCCATTCACCATGT TTT
WI-11219b	89 G A AGAGAAA	GAGAGAATAT TCCAAAAAGT	GGTCTCTAAT TTTCTACACT TTCT	ATGAAAAATGCATTAGAAGAAATTTGGAGGATAAAAATTTGAGAGAATATTTCCAAAAAGTAGAGAAAAA GAGACAAAGAGATGAAAAATAGGA[G/A]AGAAAGTGTAGAAAAATTTAGAGGACCATTTCTATACAG TCCAATATTTGAATAATAGTTATTTCAAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAAAACATCTC
WI-11219a	18 G A ---			ATGAAAAATGCATTAGAAGAAATTTGGAGGATAAAAATTTGAGAGAATATTTCCAAAAAGTAGAGAA AAAGAGACAAAAGAGATGAAAAATAGGAGAGAAAGTGTAGAAAAATTTAGAGGACCATTTCTATACAG TCCAATATTTGAATAATAGTTATTTCAAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAAAACATCTC
WI-11222b	136 G A GGCTGG	CATACCCTGC AGTTGTGA	CCTGGTAGCCA AGTTGTGA	AGCCACAGTGGAAATCATTTACACTACCGAAATCAGAAATGCTAAAAATTTGGGCTTTGGATTTTGT TTTTGTTTTTCCATAGACCCACCGTTGAACATTTGTTAAACATTTACCAGCATACCCTGCGGCTG G[G/A]TCACAACTTGGCTACCAGGAGAACCTGACACAGACTTCGTAATTTGCTTTTCAGGGCTACTGG AAAGCC

WI-11222a	25 C T A	GCCACAGTGG AATCATTTAC	TTTATGCCATA TTAATTCATTA	TTTATGCCATA TTAATTCATTA	TTTATGCCATA TTAATTCATTA	AGCCACAGTGGGAATCATTTACACTA[C/T]CGAAATCAGCAAAATGCTAAATTTGGGCTTTGGATTTT TGTTTTGTTTTTTCATAGACCCCAACCGTTGAACATATTGTTAAACATTTACCAGCATACCACCTGCGG CTGGTGCACAACTTGGCTACCGAGGAGAACCTGACAGACATTCGTAATTGCTTTCCAGGGCTACTGGA AAGCC
WI-10775	39 C T CACTC	TTATGCCATA TTAATTCATTA	TTAATTCATTA TTAATTCATTA	TTAATTCATTA TTAATTCATTA	TTAATTCATTA TTAATTCATTA	TTGCAAGTTTGTGTTTATGCCATATTAAATTCATTACACTC[C/T]ACATCATATTCTTAGCAAAATACA TCTAGACACCTGGCAGCTCAGTAAGGATATTCGGACAGTAATCATTTGTTATCATTTAGACATTTGCA GGAACCAACATATGGATGGATAAATGTGTTTAAATGAAGGCAAGCAATTA
WI-11226	165 A C ---	TTATGCCATA TTAATTCATTA	TTAATTCATTA TTAATTCATTA	TTAATTCATTA TTAATTCATTA	TTAATTCATTA TTAATTCATTA	TTGCATGCATTTATACGAAAGGAATTAATAATCTTCTTATAGTTGAATTTTAAGTAAAAATAAA GTTATACATATAATACAAAAAGTTGTAAGTATAGTAACAAATGAATTAGAAAAATTTGTCAGTGGTTGC TAGTACAGGAATCAAAATTTGGACTATGAACA[A/C]GACATAGTTGCTAAGGATATTCACACAAATAT TTCATGA
WI-10778	62 A G	GCAAGGGAGG AACATTTACA	TTGATGGGAGG AACATTTACA	TTGATGGGAGG AACATTTACA	TTGATGGGAGG AACATTTACA	CAGTGGCTGGCTACTGACAAAAACGTAAACATCGTGGCAGGTGGCAAGGGAGGAACATTTACAG[A/G]G TCCATCTCTGATGTACACAGCAGGGCCAGGAAGGGTTGATCTGGAG
WI-10789	21 C T GCTCTAGACC	GGGACACACT GCTCTAGACC	GGGACACACT GCTCTAGACC	GGGACACACT GCTCTAGACC	GGGACACACT GCTCTAGACC	TGGGACACACTGCTCTAGACC[C/T]TCCAGGGTCCCTCAAAGGTGGGTGTAGAGGCCCTACTGCCCT GCCCTGGGACGCAGAGGCATCAGGGCCTAGTCTCTCTGGGACAGTGAAGGGCCACACC
WI-10810	58 C T GCAGGAATT	CATCTTCATGG GCAGGAATT	CATCTTCATGG GCAGGAATT	CATCTTCATGG GCAGGAATT	CATCTTCATGG GCAGGAATT	ACAGAAAAATGCCTAGTCTTGTAGCAAGAGAGGAAGCATCTTCATGGCAGGAATTTCTTCATT CTGTGTTCTTAGGTTTGTGGCTGGCCATCAGTTCAACTCAGCCCTGTCCCTGATCCAGCAACATT TCCGTAACCTACCCCTAGAAAGTCATGCAAGAGAAATGATGA
WI-10828	23 T C ---	GCAGGAATT GCAGGAATT	GCAGGAATT GCAGGAATT	GCAGGAATT GCAGGAATT	GCAGGAATT GCAGGAATT	GGACCAACAGAAATTACTTGGCA[T/C]AGGGTTTCTTAAACTATTTCTGCAGAACATTAGTAAAGT TTAAATAAGGATCAGGCTACCGAATACAGTTAGGGAACATGTGGATGAATTTCTTTAGTAGAG GACTTCTAAAGGCTATAATTTGGATACATTAGGCTCATTTATGAATCTCAAAGGAGCATGTAGT AGGGCATATCTAA
WI-10832	91 G C AGGCTCTCC	CATTAATCTGCG AGGCTCTCC	CATTAATCTGCG AGGCTCTCC	CATTAATCTGCG AGGCTCTCC	CATTAATCTGCG AGGCTCTCC	TATGCCTTCCCAACGAGCCATCCACGCTGCTTAGCACAAAAAATAGAAATACATCATTTCTGAATG GGCACATTAACTGAGGCTCTCC[G/C]TTTCTAGTCACCTGCAGTTAGGTAGGTGCGAGACACTGTGA TACCATATAAATCTGATTTCTGAGCAGGAGGGGAGGAGATGAGAGAAGGGCTGCTCCGTGAAATAC TAGTCCGG
WI-10834	96 C T GTGTTAAT	AGAAATTAAC GTTCAAAAGT	AGAAATTAAC GTTCAAAAGT	AGAAATTAAC GTTCAAAAGT	AGAAATTAAC GTTCAAAAGT	GATTTGAGTATTATCAAAATGCCCAAAGACCATTAACAAGATTAAATAGTTAAAGCCAAAACATATA AAGAAATTAACGTTCAAAAGTGTGTTAA[T/C]TCTTAATACCAATTTTATAGGGCCACCATTAACTT CTGAAGAAAGGTGAGCATATGCAACTAAATTTCTAAAGTCCAGT
WI-2287	24 T C ---	GTGTTAAT GTGTTAAT	GTGTTAAT GTGTTAAT	GTGTTAAT GTGTTAAT	GTGTTAAT GTGTTAAT	GGATGATGTTCTGTGGTCCCTTAT[C/AA]AGGCTCTTGCAATCCCCAAATGTGTAATTTATTTATCT TGGTATTTCTCGTTACCCATAGTCACCTGTCAAGTGTTCACCCCT

WI-2296	81 A	GA	TGTTACTTTGA TTCTTTGCTCT	GCAATCACA AGCTAACTGG	TGGAGGTTAGAAATGCAGGTGGCATCCTAGAAAGGCTCAGGCTTTAGAAATAGTTGTTACTTTGA TTCTTTGCTCTGAC[A/G]CCAGTTAGCTGTGTGATTTGCAGAAAGTTACATTTGTTTGTTG
WI-2300	77 G	T	GGCACAGAAG CCAGTCATAC	GGTTGGGTCAA TTTTAAAGCA	TTTCATCATGCTGCTTCCCTCGAAATTTCCCTTTATTTGAGCGGGCAGGTGGTAGGCACAGAAAGC CAGTCATAC[G/T]GCTTTAAATTTGACCCCAACCATTAAGAAATAGCATTC
WI-2371	55 G	T	GTCTTGTTCTT CCAGCTTCT	CAAAGATTGAC AGCCACCAC	CAATGATCCCCCAACATTTCCAGGAAAGGCTGGTCTTCTTCCAGCTTCT[G/η]GTGGTGGCT GTCAATCTTTGACATTCCTTGCTTGAGCTGTATATTCCAATCCTTGCCTCCAGCTTTACATGATGT TCTCTCGTGCTG
WI-2395	122 A	C	GAACATATTT GTAGAAAAAT TACTATCCAA	TCACCTTTCTA TTTATTCTGAA TTCA	GGGGGCACAAATTTAGCTACAGTGCATATTAAAAGATAACATAGATAATCATAAATGTTGTTTAC TGAAATCTGAAATCTAGGATGAGTGAACATATTTGTAGAAAAATTTACTATCCAA[A/C]CTGAAATTC AGAAATAATAGAAAGGTGAATCATCTTATATCATTTAAAGAAAGCTAAATTTATAGTAAACAATCTTTA CATTTACACAAAACCCA
WI-2437c	192 G	A	---	---	CACAGCCACCACCTACAACTCCTCTGTTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAAATCACAACCTTTCTAAATAATAGACACCAAAAAATTTCCCAATGCTCTAA ATAGATGGACTCAACCTTCTCCTCTGCAAGAGGCAATCGACGAACATCACAGTG[G/A]GCTGTG GTGCAAGGACGCAATTAIG
WI-2437b	179 G	A	---	---	CACAGCCACCACCTACAACTCCTCTGTTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAAATCACAACCTTTCTAAATAATAGACACCAAAAAATTTCCCAATGCTCTAA ATAGATGGACTCAACCTTCTCCTCTGCAAGAGGCAATCGAC[G/A]AACATCACAGTGGGCTGTG GTGCAAGGACGCAATTAIG
WI-2437a	128 G	A	---	---	CACCAGCCACCACCTACAACTCCTCTGTTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAAATCACAACCTTTCTAAATAATAGACACCAAAAAATTTCCCAAT[G/A]CTC TAAATAGATGGACTCAACCTTCTCCTCTGCAAGAGGCAATCGACGAACATCACAGTGGGCTGTG GTGCCAAGGACGCAATTAIG
WI-2440	71 G	A	GCAACCTACT GACAAATTTAA TTTATAGTT	AACAAGTCTGC TATTGGTCTCA C	CAGTAGGAAACGGGTTCTTCTTAGACCTCCAGAAAAATAATGCAACCTACTGACAAATTTAATTTTA GTT[G/G/A]GTGAGACCAATAGCAGAGTTGTTACCTGCAGAACT
WI-1356	123 T	C	TGTTTAGGAA ATAATGACAA GAAAAA	TGGTTACAAC GTACCAAAACAT G	CTGTAACCTACACACATCCTCCTGTAACTCTAGTGTACTTTGTAATACAAACACAATGTAAATGCT ACATAAATAATGTCATACATAATTTAGGAAATATGACAAAGAAAAAGCC[T/C]GTACAT GTTTGGTACAGTTGTAACCAAGCCATTTTCCCAATATTTTCAATCCACAGTTGGTTTATCCACAG AAACCAACGAATG
WI-2886	46 C	A	CAGAGTCTGG GGGAGAAGA	TTGCCATGCTT TATCTCGTT	ACAGTTAAGAAAAAGGCTGACCGGTTGCAGAGTCTGGGGGAGAGAA[G/A]AACGAGATAAAGCATG GCAAGACCAACGCTGAAAGTATCCAGGGTGTGTATGTGCACATAGGAAGATCACTTACCTCAGCA TAGGAGGAGGGCTAGGCAAGGAAAGGTTGTCAGAAAGAAACAGAGGAGCGTT

WI-2906b	77 T A	---	---	CCTGAACACCTGGAGCATTCCCTCCCTTGGACACCTTCATTCTTGCTGGGACCTTTCCTGGAATGCTC TTTCCCTCTTGAAGCTTTGCTTGGCTTACTTTTCTTTTCCCTTAGGTTTACGCTTCAAAGTGACCT CCTTAGAGTTGGTTTGTGACCAACAAA
WI-2906a	50 A C	GACACCTTCAT TCTTCTGCTGG	AGAGCATTCCA GGCAAAAGT	CCTGAACACCTGGAGCATTCCCTCCCTTGGACACCTTCATTCTTGCTGGGACCTTTCCTGGAAT GCTCTTCCCTCTGAGCTTTGCTTGGCTTACTTTTCTTTTCCCTTAGGTTTCAGCTTCAAAGTGACCT CCTTAGAGTTGGTTTGTGACCAACAAA
WI-1736	175 C T	---	---	TACTCCTCATTCTCTCATGTCCCTAGACGTAAGTCCAGATTCCATGCCCTGAAACATTTATTCCTAAAT TAGATTTCCACCCCGGAGCACTATTACACAGAAACAGCATGGAGCAGTTGGAGCTGGCTCTTAGA GAACCTTACTTAAGGACAGTGGTTTCCATCTGTCTTCCCACTAGAGATCTAGGGTGTCTTTGGAACC ACCTTGG
WI-1851	136 G A	GCAATTGAATT AACTATAGAT GTGTTAAGTA	CACTAGCAATG TTAAACTGAAG TTG	AATACCCACCGTCTAACACCATCACACTGATCATCAATCAGGTTTAAACATATTAACTCTGGGAGG ACACAAACATTTAGACCATAGCAATTGAATTAACATAGATGTGTTAAGTAATTATTAACATGGTA CA[G/A]ACAACCTTCAGTTTAACATTGCTAGTGTCCATGTGGATACCATGTACCTTCTTACATCATG TGA
WI-3000	62 G A	CCCAAAACAC AGAGACCC	GCCACTATAGG ATTGACTAAGA CTCA	CTGATGTTTGGGAAGCACTGTCTTACATCTCTAAATGTACGACCCCAAAACACAGAGACCCCT[G/A]T GAGTCTTAGTCAATCTATAGTGGCAGTACCTGAATCAAGTGCCTGGTGCATAGTAGACACT
WI-1754	177 G A	TTTCTCCCTT CTTAAAGAGA TAGTC	AAAGTCGAATT GCTCTGG	ATGGATCTGCTCAATTATAGTCCCAGATAAACAGCCCTTCTCCCGCCACCCCGGATTATTTTACT TAAGGGTTTAGCAAAATTCACCTGACAAAGAGTTAGGTTTCAACATTGACCCCTCATAAAGTGATTTT TTCTCTTTCTGTTTGTCTTCTCCCTTCTTAAAGAGATAGT[G/A]CCAGAGGCAATTCGACTTTCTGT AGCCACAAGATT
WI-3167	37 T A	AAATTC AAC ACAGATCTAT TAGATT C	TGTGATAGTTT TGAGATGGGTG	ACAACACAGCAAAATTC AACACAGATCTATTAGATTCTT[A]CACCCATCTCAAAACTATCACATCAA AGAAGCAAGGAGACATATTACTGGTGAGGAAGCCAAATTCAA
WI-3208	140 G A	GTGGAGTGGG AGATAAAGA	TCACTCAAAC AGGCTTGG	CAAGCACACATTCAGGCAGTGGGCAGGTAGGGAAGGTGGGCAACTTGGCAGCAGAGAGGAGGAAG AAGTTCAGACCGTTGGGTAGGATAAGTGGATCCAAACCCCTTGTAGGGCAGGTGGTGAGTGGGCAG ATAAAGA[G/A]CCAAGCCCTAGTTTGAAGTGACACTGTGGGGATTCAAG
WI-1775	47 C T	CCTGCATGGT TTTCTCTG	AGTTGAGATT ATGACAATGAT GTAAA	ACTCCACCAACAGTTTTGTGAGCCAAACCCCTGCATGGTCTTTCTCTG[C/T]TTTACATCATTTGTCATA AATCTCAACTGACACATCAGTGTCTCTGCCACCCCA
WI-3402	55 G A	AGCATATTCA TTGATTTCCT ACAT	GAGGACTTAA AAGGAGCATTT G	CTGCCCTTTACATCCAAAGCCAGTTACTCGAGCATATTCAATTGATTTCCTTACAT[G/A]CAAATGCTC CTTTTAAAGTCTCAACTTTTAAAGCGGAAGTTGAGACATGCACAAATAGATTTCCCTTAGGA

WI-3416	33 C T	CCAA GTT GTA GCATT CAGAA GTC	ACGAG CACAA CTACCT CTAAG AG	TCTGGTTCCTCCAAAGTTGTAGCATTTCAGAAAGTC[CTCTCTTAGAGGTAGTTGTGCTCGTCTGTTAAAA TATGTTTTCAGAGTAGTATCTCCCTGTTGTACATTCCTCCAAACAAGTGTACCAACAGCATTGTTAAG GAAATGTGCAATGCTTGTACCTCTGACGACACAAATAATTAATCCCATTCCTTAAAGACCAGG
WI-3453	70 C T	TTCTAGGCC ATCAGAGAA	TCAATTTTCCC CATGACTTC	TCCTATTCTACAAACACAGAAATTAACAAATGAAAAATCAGCTACTCTCTTAGGCCCATCAGAG AAT[CTGAAGTCATGGGAAAAATGATGCCATGTGAATTTGGAGAAACAGACAGGCATATATGGAG AATTACAGTTTACCAGGGACACAATCCCACTTCCAGAGCCATCATCTGTAAAGAC
WI-3474b	109 G A	---	---	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAAACTTAAATCATCAAGTGTGCAACTGGTTTGA GTCAGTTTCCCTAATTTAGCACAGTATTTAATGAGGTGGTGAATGAGGAGAAAAATGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3474a	90 A G	AGTCAGTTTCC CTAATTTTAGC AC	CAACCATCAAT TTCTCCCA	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAAACTTAAATCATCAAGTGTGCAACTGGTTTGA GTCAGTTTCCCTAATTTAGCAC[AGTATTTAATGAGGTGGTGGGAGAAAAATGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3502	79 C T	CCTGGGTTTCT TGGATATAA CATCT	GGGTGACCTG TCCTCA	TTTGACCCCATACATGAGAAATAAAACCATAAAGAAATGGTGGAAAAATAAAACGGGAGAGACCTGGG TTTCTGGATGTCT[CTCTGAGGACAGGGTCAACCCAC
WI-3600b	146 G C	GGTTTCTAAC TGGATATAA CATCT	CCAGTGCAGCC TTCCAT	TCACGGCAAGTTCTGCAGCAGTCTCTGACTCCTGCTGTTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGT[GTGAGCCACCTAAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGG TAAACATCT[GTCTGAGGAGGCTGCACCTGGATGAGGTACACAA
WI-3600a	78 T G	CCATGCCCTG ATAGTTCTG	GGAAACGAGTT TAGGTGGCTC	TCACGGCAAGTTCTGCAGCAGTCTCTGACTCCTGCTGTTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGT[GTGAGCCACCTAAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGG ATATAAACATCTGATGGAAGGCTGCACCTGGATGAGGTACACAA
WI-3678	125 G T	---	---	TAAATCATGCTTATTTTACAAAGGTATCCACTCACATAGGCAATGATGATCTCTTTCTGTAA GAAAAGCTCTCATGCTCTCTCTGAACCTTCTACTTACTGTGCTGTTATGATGCACCT[GTCTCTTTTGG ATAGATGGTTGATAGGAGATGGTTGTTAAAGACACAAATTTACCTGTGTGTTTCAGGCAGAAATAG ACTCTCTGTGTAACTCACTGAATGAGTTCCAAAAGCCTTTATGCTTAC
WI-3687	67 A C	---	---	AAAGCGATGTTGAGATACCACTCCATGAAAAGTAAAAACACACACAAAAATGACATAAAA T[ACJAAAACTACTATAGTTTATGAAAATGACTTCCAAAATCAGAGAAAAAGTCACTTAAACAGG ATTCTCAATTCATCCAGAACTACTCTCTGTCATCTTAACITTAGCTGCACAG
WI-3735	72 T C	CCTCAGTTATG TATCAAAATGA AAAC	GGTCAACCAAT CATGTTTTT	TCTAAATGTGAAACCAAGAAATCTGACACGACCTAACTGCCAGTCTCAGTTATGTATCAAAATGA AAAACT[CTACACCGGTTCAATGAAAAAACAAATGATGGTGAGCCATGTCCCTTATTTAATGAAAA GATCTTGGCAATTAAGTCT



WI-1819	51	C T	---				GAAAAAGCAGGAGCCAGGAGGACAAACATTTTGAAGAGCTTTTCAGCAC[C/T]TCGTGGATCCG AATTTAGTGTGATTTGGCAGGCAATGGGGTAACATGTTCCAGTGTTCAGTGTTCACAGAAATTGC CAGATTAGCGATTGTTGACTTGTCCAATTAATGAATGTGGAAGAAAAAGGGTGGTAACCTGTT AAGCTGCTGCAATGTTAGACACAGGGTGGGGTGGGAGGTGAATACC
WI-3746	116	G A	---				GGCCTATTACATGACACTGGGCCAAGATCTTGCTTCCCTTTCTTCAATAGATAGACTAAGTAAAGAA ACTGCCCTGGCCAGGAAGATGGTTGCTTCATCATCTCTGCTCTGC[G/A]GCCCCAGGATAAAGCA GGCA
WI-3867	49	T C	CAA	ACAGTCATT AGTCTTCTGA	TAAGATAACC ATACTAGGTAC	ATCCG	AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCTTGACAA[T/C]CGGATGTACCTAGT ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTTGAACAAAGACACAGT CATTAAAGTGGAGAAGCCAGCATTTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG CATC
WI-3898	25	A C	G	TGACCAATGTC TTTAGAAGCA	TCGTGGTGTG CTCTCC		CAATGACCAATGTCCTTAGAAGCAG[A/C]GGAGAGGACACCGACGAGACACACAGGAGGAGTGAG GTGAAGATGAAGCAGTGTGACGAGCCACAAAGGTGAGGAGGAGGAGGTTGCTGGCCACT
WI-3901	114	A G	---				GGACCAATTGCTCCTCAGAAAGTACATTCAAGCCCTGACGGTGTCTCTAACACACTGTGACCTCAGGCA AGTCATGTCTGCTTCTGAACTCGGCTTCTCCTCACCTGACAAAGTG[A/G]TATCATGTGCTACACTGC AGTGTATTATAATGCTGCAT
WI-3914	99	C T	GC	TGATTCTTCTC AAGACTCACA			CTGAGGAGATTGATGCTACTTTACCTGAGGAAACATTTTATTACCTCCCTGAGTTTGTGCTTGCAA GACATTGCTGATTCTTCTCAAGACTCACAGC[C/T]ACCATCCTTCATTGCTTCTAGACCTATAACTAG ACTCAAGTCCCGCAGGAGCCCTTAAAGGTAAGGTACAAAGTGTGACCCCATGGGAGGTATGTTACGCTA CAAAAGAG
WI-4019	33	G A	A	CCAAGAGCGT CCTATGAATC	AACAGCAATA ACAGGAACAA	ATG	CCACTCCAGGCCAAGAGCGTCTCTATGAATCAT[G/A]CATTGTTCTCTGTTATTGCTGTTACAGAGT GGCAACTCTTGCAAAGGGAGGGGTACAAAGTGAATTTTATAGATGCTGCAGGAGACGAAGGGTC
WI-4091	84	A T	GTCATTGCATG	TTGAGGTCTTA GTCATTGCATG	TGAGTTCCTAT TAAGTGACAAT	ATTGTT	TAATTCACATTGCTCTGTTTGTGCAATTTATTGCTTCTCTTATGTAACACAATCACCACCATTGAGG TCCTTAGTCAATTGTCATG[A/T]TGATATAACAATATTGTCACCTAATAGGAACCAAGCATAGTTATGTT ACATTTATTGCTAACAGCAG
WI-4160	117	A G	CAACAGAA	CCTATAATTTA GCAACAATAT	TGCAGGTAGAA TTTTCTAATAT	AGCC	TCCTCTCTGTAATAGGAAGTCTGATTAGATGCCCTTTTGAGGTTAGGTTGGCTTCAAGATGGTAATT ATCTGTCCAAGTTTTTGTTCCTATAATTTAGCAACAATATCAACAGAA[A/G]GGCTATATTAGAAA ATTCTACCTGCATCCCCCTGGATCTGAACGTTCTTCATGATACT
WI-4168	32	A G	AAACA	GGTGAGAGTC AAATTGATAC	ATTGCCAAACA GATTTTCAGA		CGTTGCTGGTGAGAGTCAAAATTGATACAAACA[A/G]TCTGAAAATCTGTTTGGCAATCTATTAAAGG CAAAATATATACCAGCAGTGGTGGTCTAGCAATTTTACAGTGGGCAATACCTAACATAAATGAT

WI-4177	68 T C	TGAATAAGCA CGTATTAAATT TACCTA	AAGGCAGCA ATCATGATG	ATGCCTGCGATATACITTTCCAAATGACTAGTATGAATAAGCACGTTAAATTTACCTATTATATTT AT/CJCATCATGATTGCTGCCTCTTTCCAAATTTACTACAAATGTATTGTACATGAGGCACATG ATCCCATTAACCCAAATAG
WI-4199	51 A C	CTCCCCAAGTT AGTCAATATA AAAA	ATATGTTGATT AGGTATAACA ATATGTGTG	GCCATGAGCACAGAGGCTGAACCACCTCCCCAAGTTAGTCAATATAAAAAA[A/C]CACACATATTG TTATACCTAATCAACATATAAATGTTATAGATTAAACAGTCCACAGCAACAA
WI-5163	24 C T	CTGTCACTGGT CTGCTGT	AAAGGAACAC AGGAACAGAC C	TTCTGCTGTCACTGGTCTGCCTGTC/[G]GGTCTGTTCTGTTCTTCAATGTTCAACTGCTTGTAT CTGTGCCCACTAAGGTATCAGGTTTATATGGGCACAGGATGAGGGGCTTTGTAGACCAGAGTTTCTT GGAATTGCAACATTTGGGCAT
WI-4250b	117 A G	...	...	TAAGTGCAITTAAGTGTACAAAGTCCACAAATACCTCTTCCACCAGTGTAAAGCAGTTTAAATAACA GGTTCAATATGAGTCTTGTGAACACAGGGGTGGGAAGGATCCTGTAAAGG[A/G]TAAATATTGTTTT CCATAATATTGAAGATGTG
WI-4250a	94 G T	TCAATATGAG TCTTGTGAAC AGG	CTTTTACAGGA TCCTTCCAC	TAAGTGCAITTAAGTGTACAAAGTCCACAAATACCTCTTCCACCAGTGTAAAGCAGTTTAAATAACA GGTTCAATATGAGTCTTGTGAACACAGG[G/T]GTGGGAAGGATCCTGTAAAGGATAAATATTGTTTT CCATAATATTGAAGATGTG
WI-4255	68 G C	TGCTCCCCCAT CACCT	GGCTACTTCA AGTTGTGTAAG G	TAAATGTCTGTTGGGAGATAATAGGAAAGTCCATCCCTCTGTATACCTTGGTTGTCCTCCCATCACCT [G/C]CTTACACAACTTGAAGTAGGCCCTCATCAAAACACTGGTCAGAAAGATATACTGTGCGAC
WI-4256	57 C T	...	...	ACAGCTCTTCAATGGCACAAATCAAAAGCACCAAGTAAAGGAGAGGCAAAATCTGG[C/T]CTCAC CATTGGAAAGTCTTCTGAAGGATAAGGGAGTGAATGACTGCTAGAGAGAATGATTGGCCTT
WI-4325b	71 C T	...	...	AGTTCACCTGCCTAGATGAGTAGACCATGTTGCTTTGTTAAATGTACATGGGCAGGAC[C/T]GGAAA TGGGATGCTACTATAGATAATCTTTTTAAATGACTCTTCTGGTCTCTTCAAGATATACAGCCAC CCAGGACACTGCCATATCT
WI-4325a	58 C T	...	...	TGGCAGAAAGTCCGGTATGGCAAGTCAGGGTGGGTTAACTTGGATGCCACTTCTGCCTGTACCTTCT CTAGACTCTTGACCCCTGAGGAGGATCCCTGGCTCTGAGTTTATCATCTCCACCTCCAGCCAG GGCCCTGTATCTGTTACGGCC[C/A/G]GAATCTCAGGCTCACAACTGTGGGAGGTAGGAATGACGA G
WI-4347	158 A G	...	...	CCAGTCTAGGCTGCAAGGACTTCAATCTGGGCAAGTCTGGTGTGCTAGGGTCAGAGGCAGCG ACCTGAGGGACACACAAACAGTGGGACACCGGGGTACTTGTATCACCT[C/C]CTCCCGCAACCCCA AGCAGCACAGCTTGCAGCTCCAGGAAAGACTCTTACTTCCACTTGAGAAAGGAGAGGGGAAAGAGA AAAGAGGACTTTGACACACAACCTTGGG
WI-1936	117 T C	...	...	

WI-5204	54 C T ...			...	TAGATTTTGATTGATGACAAATAGGGAAGCCCTTTGTTAAATTTGGGTTTTGAAGAA[C/T]GAAGAAAA TGGAAAGGGAAGAAATTGACAGAAACCAAGAGAGTGTGAGGGGACAGCAATCCACAGTTTGACTGGA ATATAGAGTGATGTCAGGGTGG
WI-5215	70 A G C T C A A A A A			AGATAATTTTG TAAAGATAGTT TTGGC	TTTCCCTTATTTATTTAGGAAGCAAAJGTTTCATACAGGACCTTAATATTTAACAGACTCAAAAA TAT[G/G]CGCAAACTATCTTTACAAAATTATCTCCATAGCAAGTAGACATTTTAGCACATTTTCTCT GTAGTCAAGGTTTTAAAGGCCAAATGAAGTTGACTAAAGACAAT
WI-4448	112 T G A T A T A A			AATTAAGAA ATCTTTACATG GTTCTTT	CCCTGAAATGTGCTTTGCTTCCTCCAACTCTCTAGGGAACCTTTTCCATGTGAGGTGAAGGTTTTGA AGAGTACTTTTAATTAACCTGTATCAAGAGATGGGTATATAAT[G/G]AAAGAACCATGTAAAGATTT CTTTAATTAGTGAATTCATCAGGGCTCTCCACTGTCTATCAGTAA
WI-4456	49 C T T A T A G T T C C			AGTTGAATTA TTCAGAAAT GCATGAACCTTG	ACACATTTCTATTTGCTTTAAGTTGAATTTTCAGAAATATAGTTCC[C/T]CAAGTTTCATGCATAA CAGGAACACCAAGGTGGGCAATGATTGAATGT
WI-4461	49 A G C C T T C C			TTTGACCTTTC ACCAATTTCA	CTGAAACTAATGAGGTGCTAAATCACTGTTATTTAAAATTATCCTTCC[A/G]TGAAATTTGGTGA GGTCAAGAAATGAATTCCTCCACTTTTAGAATTTCTGGAAATTTATTTGCGATGATAATGCAATGGC CTACTGGATTTTACTTTTGTCTCAAGCCAGACACACGAAAGTATATAAGAAAAACAGTTAGTAATCTT TCACCTTT[G/A]TATTTCTCTCTACCTCAGGGAATC
WI-4465a	41 A G A C A C G A A A G T			GGTGAAGATT ACTAAGTGT TCCTT	CTACTGGATTTTACTTTGCTCAAGCCAGACACACGAAAGT[A/G]TATAAGAAAAACAGTTAGTAAT CTTTCACCTTTGATTTCTCTCTACCTCAGGGAATC
WI-1949b	160 T C T A A T C			TGAGAGGTGGG GACAAAA	GGGGTTAGGACCTCGAGATCTTTAGAAAGCACAATTCAAACCAATAATGGCAGTGCACAGGTAACCA GTGTGAGATGCTCTGAGTTCAAGGCTGCTGACATGGTCAATGCTGAATATATGTTGAAGAAATAA GGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTTGTCCCACTCTCACACCTTTCCCTGG CACA
WI-1949a	86 T G A T G C T C T G A G T			CCATGTCAGCA GCCTTG	GGGGTTAGGACCTCGAGATCTTTAGAAAGCACAATTCAAACCAATAATGGCAGTGCACAGGTAACCA GTGTGAGATGCTCTGAGTT[G/G]CAAGGCTGCTGACATGGTCAATGCTGAATATATGTTGAAGAAAT AAAGGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTTGTCCCACTCTCACACCTTTCCCTGG CACA
WI-4529	64 T C A A G A T G			TTCTAAAAATA ACACTTCCTGA AAAA	TGAGAGAGTTTTGGATTATTCCTCTGCAACACTCCAAGTAAGTCTATCATTTCTGAAGATG[C/G] GAGTCTCTTTTATATCCTATGATTATTTTTCAGGAAGTGTATTTTGAATATAAACTCCTGGGT CCATCCAGGCTAGGGTCAATGGCATCCATGGGTCTGGACAAGATGGGCCCTAGGATCATTTT

WI-4540	110 A G	GCACCATGTGG CATCC	GACAAATGCAGC CATGCA	AGCTTTTCCTTTCTTAAAAATGGTGCCATAGTACTGGCTTCTGTGTGCATCAGGAAGCAAGCCCTAT TGCTCGGTAAACAGTACTTTTGCATTAAGCACCATGTGGCATCC[AG]TGCGATGGCTGCATTTGTGCCAGTC AAATGAGACAACCTTCCTAT
WI-4582	226 T C	---	---	AGCAAGCATCTGGCAAGCCTCGGTGACGAGAACAATTAAATTCACCAACACACCACCTGCTCCAAATGT CCATGTTAATGCAATTATAGAAGACTCCAGTAGCATTTCAAGGCCAGTTTAACCTTATCCTGTACACA AATAACTTTATGGGAGACAGCATTTGTAATTCAAATCAATAAGACTCGGTTTGGCTGTACAAGCAT AAACAGAACGCTTGCAAAATATGGTTCCTCTGCTAGAAACCATTTGAT CAAAAGGTAGTTTAACCTTGGGGGCAACACAAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGCCATTGAGGAAGTGTTAAAG[G]CJAGAGAGATGACCCATCCATTCCTCTGG GCTTCTTATATGACACCATACTATTCCACACAGATGTGGAGTCAATTATTGGTTGGTGTATGACAGT CATGG
WI-1965	105 G C	GCATTGAGG AAGTGTTTAA	GAATGGATGGG TCATCTCTCT	TGTTTAAAAACCATACAGTTTGCTGCTACGTTGTAGAGCAACCCAGAAAAATTAAAAACGCCTAC CATTTTCACTGTTTTCTATTGACCGTACTTG[C]TCCTTTGCTTTTTTTCCCTCTCTCTTTTTCTG CCCTCTTTTAACTATT
WI-5248b	99 C T	CACTGTTTTCT ATTGACCGTAC TTG	AGAAAAAGAG AAGAAGGGAA AAA	TGTTTAAAAACCATACAGTTTGCTGCTACGTTGTAGAGCAACCCAGAAAAATTAAAAACGCC TACCAATTTTCACTGTTTTCTATTGACCGTACTGCTTTGCTTTTTTTCCCTCTCTCTTTTTCTG CCCTCTTTTAACTATT
WI-5248a	38 G C	AGTTTGCTG CTACGTTGT	TTTTAATTTTC TGGGGTTGCT	CATTGGTGGTCCAACTTCGGTGACATTACTCTGTTGACTTTGCTGTAAGCAGAAAAACGACGTGA C[T]A/CATTATTAGGCCCATCTCCTGCCTGAAGCCTGCCTACAGCAATTTGTAAACATATGGCATTTGGG ACATATCTCTGAGCCCATCAACTATTGTGACAAGATTCTCCTTTTTTAAACAA
WI-4596	69 T A	TGAAGCAGAA AGCACTGTGA	CAGGAGATGGG CCTAATAATG	GAATAGGGCAAAATTAAGACTTCAATAATTAAAGAGTCTGGGAAAAGGATTGTGATGATCATTTG AATCTGTTTAAATACAGAAATTAATCTGAATACCTGTGTGAATCATTTT[AC]TACCATGTACA TATTATATGAATTAACAATGTAATAATAGTATGACTAAGAAATATTGGGCCCT
WI-5252	119 A C	---	---	TGCAAAAAGGAAAATGATAACCGGACTGTTGTTCAAGCAATGCTAGAAAAATTATGCCTA[AG]C CAAGTAGACAACCTTAAGCACCTAAGGCAGAATGAAGTTTCTCTCTGTCATTAAAGTCTCTATTCA ATTACCATTTATCGGGTAATTAACACACTGGAAAGTAATGCCAGGCTAATTGTTAGATTATGATAAT TACACGCTTTGCTATGCT
WI-4606	61 A G	GCAATGCTAG AAAATTATGC	TTAGGTGCTTA AGTTGCTACT TGG	CAATGAGAAGTTACCAGATCGGGGCAAAATTAAGCATATGAAATACCAAGTGTGGCAGAGGCATG AAGCAAAAGAGG[C]A/CITTTATCTGCCCTGGTGGTTTTTCAGTAAGTGAACATGTCTTTGGCTCC CGGATGAAAAGATACCCCTTCTATGACTCAGCAATTCCTACTCTAGGTATGCACCTTAAACATGGGTG GCAAT
WI-5257	77 C A	GAGGCATGAA GCAAGAGG	COAGGGGCAGA TGAAAG	TCACCTGTTTAAAAATTTCTTCTCCTCAGTGAGACCAATCTTTCCGAATG[C]TGAATGATTTCTTGA AGTACACCTAGTACATCTATGAGCACACAATTAACAAGTACTTGTACCTGAAATTTGTATTTTTTAA AAAATCCTCCCAATATTG
WI-4649	50 C T	GAGACCATCTT TTCCGAATG	TACTTACAAGA AATCATC	TCACCTGTTTAAAAATTTCTTCTCCTCAGTGAGACCAATCTTTCCGAATG[C]TGAATGATTTCTTGA AGTACACCTAGTACATCTATGAGCACACAATTAACAAGTACTTGTACCTGAAATTTGTATTTTTTAA AAAATCCTCCCAATATTG

WI-4650	148	A	G	GCACAAAGAA AGTATAAGTT GTCTCTT	CTGAAGTGTTA AACTGGATTG G	AACGTGTGTATGTTGTTGTTGTTTCTGGAGAGTCAGTTACTCTCACTAGATCATAAAGGG GACTTGGGAACCAAAAGTATCTCAAGACATTTAATCCTAGAAGCACAAGAAAGTATAAGTTGTCTC TTATATTGCTTTTJ/A/G]CCAAATCCAGTTTAAACATTCAGTAACGTT
WI-4677	82	T	C	TCCAAAAGTG ATTAGGTGAA AAA	TTTCAACAGTG TCATTATTCAA CTT	AATTCAGATTTTGAACATACGTCGACATTTTGGAAAAAATTTGCCAAAAAGTGATTAGGTGAAAAAT GAGTTGAAATAAATGTC/JAAGTTGAAATAATGACACTGTTGAAAAATGATGAATCTGCTTTCAATTCA CATGGAAGGAGACTAGAACACAGCAGGTTTATAGGGGAATACTCAT
WI-4698	135	C	G	---	---	ATGATGCTATCATGAGGAATTCGTAGAAAAATTTTCACCTGGCAATTGATTCAAAATAAAGTTTGTC TCACCTGGGAAACTGCTTATCTTGATGTCAGTGACATTTCTTTCTTTTGACGGAAGAAAACTTCAA C/G]TCGAGAAGGCTTAGATTATATCGCTGAAGGCCATTCTG
WI-4722	88	G	A	TGCACTATGG AACACCACAC G	AATATGGAATC TGCACTCAGTT G	CTTCCCATCTGCCAGTTAGATGACTGCCTCCACCCAGCCTAGAAAAAGATGGGAGATTTATTTTC TGCACATATGGAACACCACACG/A]CAACTGAATGCAGATTCCATATTGAATACTGGGAAATCAGTGA AAG
WI-2020	145	C	A	---	---	GCCACAGTAAAGAGGAAAAATGGAGCCATGTAAACAGAGGAGAGCTTTCTGAAGATCAGTGTATTGTCA TAAAGGTCAGTAAATCAGTTTGTGTTGAGATTTTCAGAAAAACGTGAATTTAGTGAACCATGGG TCAACTATGATC/A]CCAAAAACAGCAGTGTGCTCTAAAAAATATGATAGTTTCTCTCTGTCACCC GCAATGAAAAAGGAGTT
WI-2028	176	T	C	TGTTACGTTT CCTGTCTCATC	GGTTGGAACT CAAAATTACCTA GAA	GACTACAGGCGCAGACAGAGGCAATGTGTGGCTTGCACAGGTTTGGTTTGTGTTTAAGTTAGATT TGAATCCTTTAAAGAAAGAAAGTGGCTCTTCAGTTTACTACAGACCTCATCATCTCCTGGTTCTCTTG CACCCAGTCCACTTCACCTGTTTACGTTCCCTGCTCATC/T]C]TCTAGGTAATTTGAGTTTCCAACC TGTTGG
WI-2033	183	T	C	GGTGCTAGA ACTAATCCCTC	CAGTGGTTCCA CGTTCTCC	ATGTGATGAGCTCCACATTCGCAGATTCACCAACTATGGATAGAAAAATATAGTATCCCAGATGG GCAGCCCAAGGATCAGAGGGCTAATTTTAAATTTTCCAAAGTTATACAGGACCATGTTGGAAATTT AGCATTTCTGGTTTGGCATCCATCAGGGTGCTAGAACTAATCCCTCAT/T]C]GGAGAACGTGGAACC ACTGATATACCAAT
WI-4745	131	T	C	---	---	TTATGGATACATGTTTCTGGTGAAGGACAAGAGTTGAAGCAAAAGGACAAGGAGATCAACTGGG TAGAATAACTCATCGATCCACAGGCTCCTTCCACCATCTCCATCTCTACTCTGAT/G]C AGGCAGACTTATATGAAAAAAGGGA
WI-2034	150	T	C	CCACAGTGCA CCAAGGAC	GGGTAAAGAT AGAGTGCAGGT CC	CCACGACTATGTTCTCAGAGTCCCTGTACTGACAGAGAAGGCTTTGAGGACCATGTGGCGCCAAGA CCTCCTTCTGCGTTTTCAGTGAAGACGATGAACCTTCTCATCTCTACAGCAGCTGGACTTCACCA CAGTGCACCAAGGACT/T]C]GGACCTGCACCTCTATCTTTACCCGTTCCGACACACAGATGCTGAGATGCC ACACTCTGAGTG

WI-2038	155	C T	TGTCCTTTAAA GTGTGTAAGT ATTAATTAG	ATTTCCTCTG AAAGAAACAT CA	TCAGGTGACAAGAAAAGTCACATTTCTCAATCACTCACCATTGCTGTTATTGCTCTTGCAGTGT ATCCAAGGATGTCACCTTTTGGAACTCTGTAGATCAGAAAACCTGTGCTTTAAAGTGTGTAAGTATTA ATTAGATTCTATTTTGATA[C/T]GATGTTCTTTCAAGAGGAAAATTTGTGTAAAGAGGATTCCCATTT TGCAATTCATGGC
WI-4782	113	C T	GATGCAGAAG ATAACTAGAA AATGC	GAACTCTCTG GTTATTTTCT GTTC	TCATTGACTTTTAGAGTCCCTTCAGTCTTTATGCTTATTTCTTTAGGAAAAAAGTAGGCTAGGAGAA CACAAATTCAGGTTCTCTCCAGATCGAAGAGATAACTAGAAAATGC[T/G]AACACAGAAAAATAACCA GAAGAGTTCATTATGGTTTTCAGAACGATTAC
WI-4788	65	A G	GCATAGAATC ATCTTGCTAAG TTCC	GGATAAAAT AAAATTTTGGC ATAA	AGGAGAGTTTGGCTCTTTCCGGACTCTTGGAAATTCAGTGCATAGAATCATCTTGTAAAGTTCC[A/G] JTGAAAAAAAATATGCCAAAAATTTAAATTTTATCCAACTTTAAGTCGAGATTATAATTGATATTT AAAAAACTATATTGAGTCTTTCTAAAAAGATGGCGTATCACTCTA
WI-5300	38	T C	TCCAGAGAC CACITTCATTC	CTACTCTTCT ATTCATAATC CAAAAA	CTTACTTCCAAAGTGTTTCCAGAGACCACCTTCATT[C/T]TTTGGATTATGAATAGAAAGAGT AGGTGTTATTATTCCTCTTTTACCAAGGTGAAATTTGAGGCTCAGAGACAAGGTAGATGATGAGCCCA AGGTCAGTGACAGGCCA
WI-4818b	121	G T	TGATAATGGG GCCCTGTT	CCITCCITTTA TATGTATGCCA GA	TATAATGTTTGTCCATAGTGGCCATAGACTAGGTTATGTCCACACATGAATAAACAATCTTATATA ATAATTTATTCAGAAAGGAAAAATATACATATGGGTGATAATGGGCCCTGTT[G/T]CTCTGGCATA CATATAAAGGAAAGGCTAA
WI-4818a	43	A G C	TGCCATAGAC TAGGTATGTC C	CATATGTATAT TTTCCCTCTG AATAAAT	TATAATGTTTGTCCATAGTGGCCATAGACTAGGTTATGTCC[A/G]CACATGAATAAACAATCTTAT ATAATAATTTATTCAGAAAGGAAAAATATACATATGGGTGATAATGGGCCCTGTTGCTCTGGCATA CATATAAAGGAAAGGCTAA
WI-5317	139	T C	TTCCATTCTG GTAGCAGGT	GATGCAAGA AGAAATGAGTC C	TTTTCCATTTTGTGTTGATCTTTTGTCTGAGCCCTTAGATCTCCTTTAAATTAATAGCAAGGTTAAT AATATAATAATATGATGTTATATATACAAATTTCAACTCAACAGGAATTCATTTCTGGTAGCAGGT ATA[T/C]GGACTCATTTCTCTTTCATCTATTTCTAGGTTATTTGCAGCCCGAGATCTACCCAGG
WI-4888	56	G A	GCAAGATATA AAGATTAAAG AAAGATAACA	CAATTCACCTA CCTCATTTAT CA	AAATGAGTAACCCCAAGTTACTCGGCAAGATATAAAGATTAAAGAAAAGATAACAAGA[G/A]ATGAAT AAATGAGGTAGTGGAAATGCTTGATAAATCGGAGTAGTGCCTT
WI-5328	44	A G	---	---	AACATTTTTTAACCATGCTACATTTACAAACACTGAAAAGACAG[A/G]AAAAAAGAAATATTTTG CCTCAAAAAGCTCTTAAGAGATTATGTAATAAAGAAAAAATATGAATCAGAAAAAGGAAAAAAT AGAAACACGTGATACTGGAAGAG
WI-4897	93	A G	---	---	GCCTTTTGTAGTTAAGTCTTTTGTGAGTGTCTTTTTTTTCCCCCACTAGGTAAGTCTCGGCCCAAT CCCCAAAAGAAAATAAGCGCTTGG[A/G]GATAAACACATCTTC
WI-5345	29	G A	---	---	CCCTGCTATAGGTAGTGTAAAATTCCTG[A/C]CTGCTATGTTTGTGTTGAAGCCACATCCACT GAGGTATATCTGCTGCTATTTCTATATCACTCAGCTTCAGATCCACTCCATCAACTTGACAG

WI-5370	143 T	AATAAGATGG TACCTTAACATA CATAAACAA	CAAAGTTGGTA CAGAGAATTTG AAA	TGCATGTTACTTCTTGAAATCATAAAGGGATCTGAGAGCCCTACAGTATATGGCAACATTAAACCAAT CTTTTGAATAATTTACCTGTATCCCATCATGGTTCATTTGCAAAAAATAAGATGGTACCTTAACCTA ATAAAACAAT/CJTITGAAATCTCTGTACCAACTTTGCTTTTC GATCTCCTTCATCCCTCTCCAGAAAGAGGAGAGGAAACACAAGAAACGCCCTGGTGCAGAGCC CCAATTCCTACTTTCATGGATGTGAAATGCCAGGTGAGGAGACGGCTGCTGTAGTGGGGAAGCAC TGGACCTCAACAGATTGGAATAATGTTGAGTTAGCTGTCTCGTATCCTTGAAGCTGTGCAGCAGCTT CAGTTTCTTCGCCCTGTGGAAATAATTTCCCTGATACCTCTTAAAAATTTGAATG GATCTCCTTCATCCCTCTCCAGAAAGAGGAGAGGAAACACAAGAAACGCCCTGGTGCAGAGCC CCAATTCCTACTTTCATGGATGTGAAATGCCAGGTGAGGAGACGGCTGCTGTAGTGGGGAAGCAC TGGACCTCAACAGATTGGAATAATGTTGAGTTAGCTGTCTCGTATCCTTGAAGCTGTGCAGCAGCTT CAGTTTCTTCGCCCTGTGGAAATAATTTCCCTGATACCTCTTAAAAATTTGAATG GGAGGAATTCAGGGTGAATGGACTGCTCCCGCTCTGAGTTCACTGCTACTCAGCCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCCTATTCAGCAATTCCTACTGGTATGATATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATTCCTAACTTAAATGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTTCATCCAGTGTCTACAGCATCTGATAG GGAGGAATTCAGGGTGAATGGACTGCTCCCGCTCTGAGTTCACTGCTACTCAGCCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCCTATTCAGCAATTCCTACTGGTATGATATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATTCCTAACTTAAATGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTTCATCCAGTGTCTACAGCATCTGATAG GGAGGAATTCAGGGTGAATGGACTGCTCCCGCTCTGAGTTCACTGCTACTCAGCCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCCTATTCAGCAATTCCTACTGGTATGATATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATTCCTAACTTAAATGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTTCATCCAGTGTCTACAGCATCTGATAG GGAGGAATTCAGGGTGAATGGACTGCTCCCGCTCTGAGTTCACTGCTACTCAGCCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCCTATTCAGCAATTCCTACTGGTATGATATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATTCCTAACTTAAATGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTTCATCCAGTGTCTACAGCATCTGATAG CTTTTATACTAGCTTTAAGAGGTTTTCATCCAGTGTCTACAGCATCTG TATAGTATTTAAGGAAGCCCTAGAGCAGCGGCTGTGGGTGATTTGGTCAJAGCATATCTTAGGT ATATAAATACCTTTGAAGCCATAACTTTTAACTGGAGTGGTTGATTTCTTTTTTAAATTTTATTGGGA GGGTTTGGATTTTAACTTTTTTAAATGTTGTTAAATATTAAAGTTTTGTAAAAAGGAAACCATCTCTG TGATTACCTCTCAATCTATTGT
WI-9711b	423 T	A ---	---	AGAATGGCTACTTCATAGGCGCAGAGCAGCCACTTTTGGCTAAATTTTAAACATCCAAAGCTAATAAT AATCAAGAAAGAAATAGAGAACATTAAACAAATAAATATATGTTCTATTTGGGAATACCTAATATCAG ATACTAACCAAGTACAGTGATAGAAATAAAAAAGATAATAATCACACATACCTTCTAGGTTAGTAGA AAAGC/G.TJCTTCTAGGTTAGTAGAAAAAGTT
WI-9711a	390 C	A ---	---	AGAATGGCTACTTCATAGGCGCAGAGCAGCCACTTTTGGCTAAATTTTAAACATCCAAAGCTAATAAT AATCAAGAAAGAAATAGAGAACATTAAACAAATAAATATATGTTCTATTTGGGAATACCTAATATCAG ATACTAACCAAGTACAGTGATAGAAATAAAAAAGATAATAATCACACATACCTTCTAGGTTAGTAGA AAAGC/G.TJCTTCTAGGTTAGTAGAAAAAGTT
WI-9702c	345 G	A ---	---	AGAATGGCTACTTCATAGGCGCAGAGCAGCCACTTTTGGCTAAATTTTAAACATCCAAAGCTAATAAT AATCAAGAAAGAAATAGAGAACATTAAACAAATAAATATATGTTCTATTTGGGAATACCTAATATCAG ATACTAACCAAGTACAGTGATAGAAATAAAAAAGATAATAATCACACATACCTTCTAGGTTAGTAGA AAAGC/G.TJCTTCTAGGTTAGTAGAAAAAGTT
WI-9702b	344 C	T ---	---	AGAATGGCTACTTCATAGGCGCAGAGCAGCCACTTTTGGCTAAATTTTAAACATCCAAAGCTAATAAT AATCAAGAAAGAAATAGAGAACATTAAACAAATAAATATATGTTCTATTTGGGAATACCTAATATCAG ATACTAACCAAGTACAGTGATAGAAATAAAAAAGATAATAATCACACATACCTTCTAGGTTAGTAGA AAAGC/G.TJCTTCTAGGTTAGTAGAAAAAGTT
WI-9702a	179 C	T ---	---	AGAATGGCTACTTCATAGGCGCAGAGCAGCCACTTTTGGCTAAATTTTAAACATCCAAAGCTAATAAT AATCAAGAAAGAAATAGAGAACATTAAACAAATAAATATATGTTCTATTTGGGAATACCTAATATCAG ATACTAACCAAGTACAGTGATAGAAATAAAAAAGATAATAATCACACATACCTTCTAGGTTAGTAGA AAAGC/G.TJCTTCTAGGTTAGTAGAAAAAGTT
TGR- A003N21	49 C	A ---	---	AGAATGGCTACTTCATAGGCGCAGAGCAGCCACTTTTGGCTAAATTTTAAACATCCAAAGCTAATAAT AATCAAGAAAGAAATAGAGAACATTAAACAAATAAATATATGTTCTATTTGGGAATACCTAATATCAG ATACTAACCAAGTACAGTGATAGAAATAAAAAAGATAATAATCACACATACCTTCTAGGTTAGTAGA AAAGC/G.TJCTTCTAGGTTAGTAGAAAAAGTT
TGR- A004V30	203 C	T ---	---	AGAATGGCTACTTCATAGGCGCAGAGCAGCCACTTTTGGCTAAATTTTAAACATCCAAAGCTAATAAT AATCAAGAAAGAAATAGAGAACATTAAACAAATAAATATATGTTCTATTTGGGAATACCTAATATCAG ATACTAACCAAGTACAGTGATAGAAATAAAAAAGATAATAATCACACATACCTTCTAGGTTAGTAGA AAAGC/G.TJCTTCTAGGTTAGTAGAAAAAGTT

TIGR- A004W22	232 C A ---	---	GGATAAATCAGTACATAATGTTGGGACCTTAAAACTGCTGTGATGCAGGAGTGGGGCTGGGCAGTG CCCGAGGCAGGGGAGGACAGTGGGACAGGGGATGCTCAGTGGTGGAGCCACAGCCCTGGGCTCTGGA TGGGGCATGGGAATGACCAGGTCCACATCATGCACAGCAGGGGCTGTAGCTTGAGTCCAGACAG GCCTGCCACACATTGGTGTGCTGCCCGCCCTA/C/ACTGGAGATGCTCTCTAAAA
TIGR- A005D24 b	138 C T ---	---	CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAATTCCTTTGAGATAATTGATTTCATATTG TGTGGCTTTCACCTCCATTACCTCTTGTCAATCCCAACATCTTTATAGAGAAAT/AAACCCCAATTT CTC/T/TTTCAACATTTAGTTGATTATCATCTGGATTTCACCTCAAGATGCAGCTCCTAAGATTATT GTTATGTTAAATTCATAAAGCTCTTCACTTTAATAATTAAAGGAAACAAT
TIGR- A005D24 a	123 A G ---	---	CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAATTCCTTTGAGATAATTGATTTCATATTG TGTGGCTTTCACCTCCATTACCTCTTGTCAATCCCAACATCTTTATAGAGAAAT/AAACCCCA TTTCTCTTCCACATTTAGTTGATTATCATCTGGATTTCACCTCAAGATGCAGCTCCTAAGATTATTG TTATGTTAAATTCATAAAGCTCTTCACTTTAATAATTAAAGGAAACAAT
U03735	74 C G ---	---	TGAGTCTGAGCAGGAGTTCAGCCAGGCGCAGTGGGAGGGGCTGGGCCAGTGCACCTTCGGGGCC GCATCC/C/G/TTAGTTCCACTGCTCTGTGACGTGAGGCCATCTTCACTCTTTGAAGCGAGCAG TCAGCATCTTAGTAGTGGGTTCTGTCTGTGGATGACTTTGAGATTATCTTTGTTCTCTGTTGGA GTTGTTCAATGTTCTTTAA
U39840b	42 T C ---	---	GGTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAGAAAAAT/C/CAACAGCAAAACA/CJACCACA CAACCAAAACCGTCAACAGCATATAAATCCCAACTATTTTATTCATTTTTCATGCACAACC TTGCCCCCAGTGCAAAAGACTGTTACTTTATTATTGATTCAAAATTCATTGTTGTTACTACAAA GACGGCCCCCAACCAATTTTTTCC
U39840	56 A C ---	---	GGTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAGAAAAATCAACAGCAAAACA/CJACCACA CAACCAAAACCGTCAACAGCATATAAATCCCAACTATTTTATTCATTTTTCATGCACAACC TTGCCCCCAGTGCAAAAGACTGTTACTTTATTATTGATTCAAAATTCATTGTTGTTACTACAAA GACGGCCCCCAACCAATTTTTTCC
WI-8997	41 G A OOC	---	GTGGCCATCGATCTGGACCGTCCCTGCCACTTGCTCCCG/G/ATGAGCACTGCGTACAAACATCCA AAAGTTCAACAACACACAGAACTGTGTCTCATGGT
WI-7008	180 A G ---	---	TATACCACTTCCATTTGATGGAATGCTGCTGTTTCATGACCAACTTTATGGCTAGATGGGTCAGAA AGCACCCAGTTTCATGATAGGCGATTGAGTTCATGTTGACTTTGATGACCCAGAGTCAACATTCAG TTTCCACCAAAAGCCAGTAACAGGCCAAGAGCTGCTCTCAAAAG/GAGAGATGTTATCTGCAGA AGATGGCAGGGGCTTGTCTCGAAAGCCTAGAGACCGCCACTGTGATTCACCT
WI-9005	26 C T GGGATCT	---	GGTCCACGAAATTTGCTGGGGAATCT/C/G/TTTCTTCTTAAGACTTTTGGGACATGGTTGACTCC CGAACATCAACGACGGTCTCTGTTTCTGGGTGG



WI-7593	46 G A	---	---	TTTTGTTGCTCTGGACACCCCACTGCTCCAGGATGAAAGGAGAGG/AJAATGAGATCAGTTTTGGGACCTTCTCTTGAATATAAAGATCAACAAGTTACAGTCATGTTGGGACTTCTTCTCTCCTCAA
WI-6962	78 A G	---	---	AGTGCATCTTGGGGAAGGGCTCCAGTGTTATCTGGACAGTCTCTTCACTTTTCAGGTGGGACTCTT GATCCAGAGA/GAGACAAAGCTCCTCAGTGAGCTGGTGATATCAAGACAGAGAACCCCAAGTCTCC TGACTCCTGGCCTTCTATGCCCTCTATCCTATCATAGATAACATTCTCCACAGCCTCACTTCACTCCAC CTATTCTGAGAAATATTCCCTGAGAGAGAACAGAGATTAGATAAGA
WI-7059	43 C G	AAGGCACCA GCCATC	GCTCCTCGCTG GGTCA	GCAGAAAGAGAACCATGCCAGGGGAGAGGCCACCCAGCCATC/GTGGACCCAGCGAGGAGCCAA CTATCCCAAATATACCTGGTGAAATATACCAAATCTGCATCTCCAGAGGAAAAATAGAAATAAA GATGAATTGTTGCAACTCTTAAAAAA
WI-9063	53 A C	CACCTCACTGA AAGACACCAT TT	TCTACTTTCTG OCTTGGGT	AGCAGCCATCACATGATCTGTTTTCACCACCTTCACTGAAAGACACCACTTTAT/CJACCCCAAGGG CAGAAAGTAGAACCTTACTATTCAATTAATGTTTGACACAATTGGAATTGTC
WI-7079	293 T G	---	---	AAGGGCATTGAGACTATAAAGCAGTAGACAATCCACATACCATCTGTAGAGTTGGAACCTGCATT CTTTAAAGTTTATATGCATATATTTAGGGCTGCTAGACTTACTTCTCTATTTTCTTCCATTGCT TATTCTTGAGCACAAATGATAATCAATTATACATTATACATCACCTTTTGTACTTTTCCAAAGCCC TTTTACAGCTTGGCACTTTCTCTGCCTAGGCTGTAGGTAACCTGGAT
WI-9074	38 A G	GGTAAAAGTT CTTTTGTCTCT AAAAG	GACAGATTTT GACCTAGTTCC TT	TGGATGCGGAGGTAAAAGTTCTTTTGTCTCTAAAAGAA/GIAAGGAACTAGGTCAAAAATCTGTCC GTGACCTATCAGTTATTAATTTTAAGGATGTTGCCACTGGCAATGTAACTGT
WI-7104b	249 C T	---	---	GGAGTTGCCCTTCTTAAGGGAAGGAGATCTTATCTTCTGGTGGCTTGACCACTACGTTGGGA GAAGAGAGAGAGTGCCAGGAGACCCTGAGGGCAGCCGGTCTCTACTTTGGACTGAGAGAAGGAGCC CCAGGCTGGAGCAGCATGAGGCCAGCAAGAGGGCTTGGGTTCTGAGGAAGCAGATGTTTCATGCT GTAGGCCCTTGCACCAGGTGGGGGCCACAGCACCAGCAGCATCTTTC/TJ
WI-7104	157 C A	---	---	GGAGTTGCCCTTCTTAAGGGAAGGAGATCTTATCTTCTGGTGGCTTGACCACTACGTTGGGA GAAGAGAGAGAGTGCCAGGAGACCCTGAGGGCAGCCGGTCTCTACTTTGGACTGAGAGAAGGAGCC CCAGGCTGGAGCAGCATGAGGC/CJ/CAGCAAGAGGGCTTGGTTCCTGAGGAAGCAGATGTTTCAT GCTGTAGGCCCTTGCACCAGGTGGGGGCCACAGCACCAGCAGCATCTTTCGT
WI-8974	34 C T	CCTGAGCCCTC AAGAACTCA	TGTAGGGCTGA CCTGGC	CATACAATGAGAGCCCTGAGCCCTCAAGAACTCA/CJTGCCAGCTCAGCCCTACACCAGTTTCCACC TGGAGTTTCATGCAAGGGCAAAAGGCAGTGCCATGCAAGCTGTTAA
WI-9161	61 C T	CCTAAGCATTG CCTGGC	GCTTACAGGAG AGACTAGACA GGAA	CTGTAGGGTGACGTTAGCATTACCCCAACCTCAITTTAGTTGCCTAAGCATGGCTGGC/CJ/TTC CTGTAGTCTCTCTGTAGCCCAAGAAATGAACATTCCA
WI-9014c	93 T C	---	---	CCCTGTTCCCATGCTGACCTGTGTTTCTCTCCCAAGTCACTTCTCTCCAGAGAGGTGGGCTGGAT GTCCTCATCTCIGTCAACTTAT/CJGIGCACTGAGCTGCAACTCT

WI-9014b	44 C T ---	---	---	CCCTGTTCCCATGCTGACCTGTGTTCCCTCCCCAGTCATCTTTC/TTGGTTCCAGAGAGGTGGGGCTG GATGCTCCCATCTGTCTCAACTTTATGTGCACTGAGCTGCAACTTCT
WI-7023b	206 C A ---	---	---	TCTGAGAGAAATGACTGTGGGAGACACCCCTGCAGATCCTCATGGTTTGTGACAGACCCCTGCGTGCT CAGTGCCCTTTAAGTGCATCCGCTGTGCTGACTTTGAGTGGGATCAACATCTGCTACGGGTCCCC TCCTTTTGGCCCGAGTATTCATGGCAGGTTTGTGGACACCTACTAGCTCCCTTCCCATTCACAC A/C/AJACACACATCTTCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7023a	56 A C ---	---	---	TCTGAGAGAAATGACTGTGGGAGACACCCCTGCAGATCCTCATGGTTTGTGACAG/CJCCCTGCGT GCTCAGTGCCCTTTAAGTGCATCCGCTGTGCTGACTTTGAGTGGGATCAACATCTGCTACGGGT CCCTCTTTTGGCCCGAGTATTCATGGCAGGTTTGTGGACACCTACTAGCTCCCTTCCCATTCAA CACACACACATCTTCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7093	54 C T ---	---	---	CTGAAATCCCTCTCTGCCCTGGCTGGATCCGGGGACCCCTTGGCCCTCCCT/C/TTGGCTCCAGCC CTACAGACTTGTGTGACCTCAGGCCAGTGTGCCGACCTCTCTGGGCTCAGTTTCCAGCTATG AAACAGCTATCTCAAAAGTTGTGAAGCAGAGAGAAAGCTGGAGGAGGCCGTGGGCCAAT GGGAGAGCTCTTGTATTATTATTATTGTGGCCGTGTGTGTGTGT
WI-9171	62 G A ---	---	---	ACATATCTGAATAATGTTGAAGCTAAGCCAGGAATAAAGAAAGTAGAGATAATAATCA[G/A] TTCCTTACAACCGATGTAATTAAGCTGTATTCACAAGACTTCAIGC
WI-9174	47 T C T	CTAGACCCC ATTCTCTATT ACTG	TCTAGAGGGTA TATAGGACAGG ACTG	GTGTGAGACCATCATGGTGCCAGTCTAGGACCCCATCTCCTATTAT/CJGAGTCCGTCTCTATATA CCCTCTAGAAACAGAAAGCAATTTTAGGAGCTATGGTCAAAITGAG
WI-7753	52 A G	CCATGTTCCGA GAAGAACAGA A	CAGAGGCTTG AAATACAGGG A	AAGGCCAGATGCACATCCCTGGAAGGAGATCCATGTTCCGAGAGAAACAGAT/GJATCCCTGTATT TCAAGACCTCTGTGCACATTATTATGAACCTGCCCTGCTCCACAGAACACAGCAATTCCTCAGGCTA AGCTGCCGGTCTTAAATCCATCCTGCTAAGTTAATGTTGGGTAGAA
WI-9186	76 G A	CCACTTCTCCC CGCA	AAAGGAAAG TCTGACCTAGG T	AAAGAACTACAGAGGAGCATGTCCAAACAAAAATGGCATCACCTGTCAAAAATGGAGTTCCACT TCTCCCGCA[G/A]ACCTAGGTGAGACTTCCCTTTCATCTT
WI-9193	94 G A	AGAAATTTGT CTGCCCTTAAAG CA	GGTGTGTGTGG TAGGGGG	TTGGACAAACCTAGAAATTTTCCCTTTATGTATCTCTATCGATTGTGTAGCAATTGACAGAGAAATAA CTCAGAAATATTGTCTGCCCTTAAAGCA[G/A]TACCCCTTACCACACACACCCCTGTCTC
WI-9015	48 C T ---	---	---	TTTGGATTGATATCGTGAATCTCCAGCCGAGAAATGGGCTGGATTG/C/TTGGTTGGTTATACAT CTTTCCTTAAAGAGATAAACACAAAAATCCATCCAGGTAGCTCGGCACCACTAAGAA
WI-7254	37 A G	GGTCTGAGAG AGGAGCCAC	GGAGTGGGTGT CATTAGGGA	GGAGCCAGGAGACAGCAGGGTCTGAGAGAGGAGGACAC[GJGTCCCTTAATGACACCCACTCCTAGCC CTGAGGCTCTGCCCTCAGACTGGGGAAGAGTCCAGGAAGGGAGGAGCCACTCCTCAATGC TCAATGGCTCCCTGAAATCAAGACAGG

WI-9231	32 G C	CAGGTCCCGA GATTGA CAAAATAACA ATGCAACGTT C C	CAGTGCAC ACTCAGAC GCTCTCAGAAC CAAGATTAGA AATC	GTGACCTGTGAGGTCCCGCAGATTGA/GC/GTCTGAGTGGGCAAGTGTGTCAAAAGGGGC TGCCCCCAGGAGATGAGGTGAGAGCAGGGAGTTGAGGCCGAAGATCA TTGTTGGGAAATAGAGAGTTGAGATAACACCTCTCATTCAGTAGTACTGAAAGAAACTGTGCTA GAATGATAAATGTCATGGTGGTCTATACTCCAAATAAACAATGCAACGTTCC/T/C/GATTCTTAAT CTTGGTCTGAGAGCCATTGGTTTCAGTTGAGCAATCCCATACCAGCT TCCATTCTTTGGCCCTGCAGCATGTCATGCTCCAGAAATTCAGCTTCAGCTTAAGTGACAGAT/C JGTTAAAGCTTCTGGTTAGATTGTTTTCATTTGGTGATCATGTC/TCTTTCCATGTGTACCTGTAATATT TTTCCATCATATCTCAAAGTAAAGTCA
WI-7836	120 T C	CAGCTTCAGCT TAACTGACAG C A	AAACAATCTA ACCAGAAAGCT TTAA	GTGACCTGTGAGGTCCCGCAGATTGA/GC/GTCTGAGTGGGCAAGTGTGTCAAAAGGGGC TGCCCCCAGGAGATGAGGTGAGAGCAGGGAGTTGAGGCCGAAGATCA TTGTTGGGAAATAGAGAGTTGAGATAACACCTCTCATTCAGTAGTACTGAAAGAAACTGTGCTA GAATGATAAATGTCATGGTGGTCTATACTCCAAATAAACAATGCAACGTTCC/T/C/GATTCTTAAT CTTGGTCTGAGAGCCATTGGTTTCAGTTGAGCAATCCCATACCAGCT TCCATTCTTTGGCCCTGCAGCATGTCATGCTCCAGAAATTCAGCTTCAGCTTAAGTGACAGAT/C JGTTAAAGCTTCTGGTTAGATTGTTTTCATTTGGTGATCATGTC/TCTTTCCATGTGTACCTGTAATATT TTTCCATCATATCTCAAAGTAAAGTCA
WI-7286	65 T C	CTAAGCATGT ACGTGAATTT T G TAAAT	CCCAATTTTAA TTAAAGTTTAA CATCTAT	GTGACCTGTGAGGTCCCGCAGATTGA/GC/GTCTGAGTGGGCAAGTGTGTCAAAAGGGGC TGCCCCCAGGAGATGAGGTGAGAGCAGGGAGTTGAGGCCGAAGATCA TTGTTGGGAAATAGAGAGTTGAGATAACACCTCTCATTCAGTAGTACTGAAAGAAACTGTGCTA GAATGATAAATGTCATGGTGGTCTATACTCCAAATAAACAATGCAACGTTCC/T/C/GATTCTTAAT CTTGGTCTGAGAGCCATTGGTTTCAGTTGAGCAATCCCATACCAGCT TCCATTCTTTGGCCCTGCAGCATGTCATGCTCCAGAAATTCAGCTTCAGCTTAAGTGACAGAT/C JGTTAAAGCTTCTGGTTAGATTGTTTTCATTTGGTGATCATGTC/TCTTTCCATGTGTACCTGTAATATT TTTCCATCATATCTCAAAGTAAAGTCA
WI-7858	91 T G	CTAAGCATGT ACGTGAATTT T G TAAAT	CCCAATTTTAA TTAAAGTTTAA CATCTAT	GTGACCTGTGAGGTCCCGCAGATTGA/GC/GTCTGAGTGGGCAAGTGTGTCAAAAGGGGC TGCCCCCAGGAGATGAGGTGAGAGCAGGGAGTTGAGGCCGAAGATCA TTGTTGGGAAATAGAGAGTTGAGATAACACCTCTCATTCAGTAGTACTGAAAGAAACTGTGCTA GAATGATAAATGTCATGGTGGTCTATACTCCAAATAAACAATGCAACGTTCC/T/C/GATTCTTAAT CTTGGTCTGAGAGCCATTGGTTTCAGTTGAGCAATCCCATACCAGCT TCCATTCTTTGGCCCTGCAGCATGTCATGCTCCAGAAATTCAGCTTCAGCTTAAGTGACAGAT/C JGTTAAAGCTTCTGGTTAGATTGTTTTCATTTGGTGATCATGTC/TCTTTCCATGTGTACCTGTAATATT TTTCCATCATATCTCAAAGTAAAGTCA
WI-7860	50 C G	CGTACCTCCAA ACATAATTGA TTC	GCCTGAGTGTA AGTCTGCAGA	GTGACCTGTGAGGTCCCGCAGATTGA/GC/GTCTGAGTGGGCAAGTGTGTCAAAAGGGGC TGCCCCCAGGAGATGAGGTGAGAGCAGGGAGTTGAGGCCGAAGATCA TTGTTGGGAAATAGAGAGTTGAGATAACACCTCTCATTCAGTAGTACTGAAAGAAACTGTGCTA GAATGATAAATGTCATGGTGGTCTATACTCCAAATAAACAATGCAACGTTCC/T/C/GATTCTTAAT CTTGGTCTGAGAGCCATTGGTTTCAGTTGAGCAATCCCATACCAGCT TCCATTCTTTGGCCCTGCAGCATGTCATGCTCCAGAAATTCAGCTTCAGCTTAAGTGACAGAT/C JGTTAAAGCTTCTGGTTAGATTGTTTTCATTTGGTGATCATGTC/TCTTTCCATGTGTACCTGTAATATT TTTCCATCATATCTCAAAGTAAAGTCA
WI-9064	29 A G	CGTACCTCCAA ACATAATTGA TTC	GCCTGAGTGTA AGTCTGCAGA	GTGACCTGTGAGGTCCCGCAGATTGA/GC/GTCTGAGTGGGCAAGTGTGTCAAAAGGGGC TGCCCCCAGGAGATGAGGTGAGAGCAGGGAGTTGAGGCCGAAGATCA TTGTTGGGAAATAGAGAGTTGAGATAACACCTCTCATTCAGTAGTACTGAAAGAAACTGTGCTA GAATGATAAATGTCATGGTGGTCTATACTCCAAATAAACAATGCAACGTTCC/T/C/GATTCTTAAT CTTGGTCTGAGAGCCATTGGTTTCAGTTGAGCAATCCCATACCAGCT TCCATTCTTTGGCCCTGCAGCATGTCATGCTCCAGAAATTCAGCTTCAGCTTAAGTGACAGAT/C JGTTAAAGCTTCTGGTTAGATTGTTTTCATTTGGTGATCATGTC/TCTTTCCATGTGTACCTGTAATATT TTTCCATCATATCTCAAAGTAAAGTCA
WI-7307	128 G T	GAAATGTGAC TTCACCTTGGT G	CAGGTAGAAAT TTCTGTCCATT G	GTGACCTGTGAGGTCCCGCAGATTGA/GC/GTCTGAGTGGGCAAGTGTGTCAAAAGGGGC TGCCCCCAGGAGATGAGGTGAGAGCAGGGAGTTGAGGCCGAAGATCA TTGTTGGGAAATAGAGAGTTGAGATAACACCTCTCATTCAGTAGTACTGAAAGAAACTGTGCTA GAATGATAAATGTCATGGTGGTCTATACTCCAAATAAACAATGCAACGTTCC/T/C/GATTCTTAAT CTTGGTCTGAGAGCCATTGGTTTCAGTTGAGCAATCCCATACCAGCT TCCATTCTTTGGCCCTGCAGCATGTCATGCTCCAGAAATTCAGCTTCAGCTTAAGTGACAGAT/C JGTTAAAGCTTCTGGTTAGATTGTTTTCATTTGGTGATCATGTC/TCTTTCCATGTGTACCTGTAATATT TTTCCATCATATCTCAAAGTAAAGTCA
WI-9274	25 C T	GAAATGTGAC TTCACCTTGGT G	CAGGTAGAAAT TTCTGTCCATT G	GTGACCTGTGAGGTCCCGCAGATTGA/GC/GTCTGAGTGGGCAAGTGTGTCAAAAGGGGC TGCCCCCAGGAGATGAGGTGAGAGCAGGGAGTTGAGGCCGAAGATCA TTGTTGGGAAATAGAGAGTTGAGATAACACCTCTCATTCAGTAGTACTGAAAGAAACTGTGCTA GAATGATAAATGTCATGGTGGTCTATACTCCAAATAAACAATGCAACGTTCC/T/C/GATTCTTAAT CTTGGTCTGAGAGCCATTGGTTTCAGTTGAGCAATCCCATACCAGCT TCCATTCTTTGGCCCTGCAGCATGTCATGCTCCAGAAATTCAGCTTCAGCTTAAGTGACAGAT/C JGTTAAAGCTTCTGGTTAGATTGTTTTCATTTGGTGATCATGTC/TCTTTCCATGTGTACCTGTAATATT TTTCCATCATATCTCAAAGTAAAGTCA
WI-7313e	266 T C	GAAATGTGAC TTCACCTTGGT G	CAGGTAGAAAT TTCTGTCCATT G	GTGACCTGTGAGGTCCCGCAGATTGA/GC/GTCTGAGTGGGCAAGTGTGTCAAAAGGGGC TGCCCCCAGGAGATGAGGTGAGAGCAGGGAGTTGAGGCCGAAGATCA TTGTTGGGAAATAGAGAGTTGAGATAACACCTCTCATTCAGTAGTACTGAAAGAAACTGTGCTA GAATGATAAATGTCATGGTGGTCTATACTCCAAATAAACAATGCAACGTTCC/T/C/GATTCTTAAT CTTGGTCTGAGAGCCATTGGTTTCAGTTGAGCAATCCCATACCAGCT TCCATTCTTTGGCCCTGCAGCATGTCATGCTCCAGAAATTCAGCTTCAGCTTAAGTGACAGAT/C JGTTAAAGCTTCTGGTTAGATTGTTTTCATTTGGTGATCATGTC/TCTTTCCATGTGTACCTGTAATATT TTTCCATCATATCTCAAAGTAAAGTCA
WI-7313c	256 C T	GAAATGTGAC TTCACCTTGGT G	CAGGTAGAAAT TTCTGTCCATT G	GTGACCTGTGAGGTCCCGCAGATTGA/GC/GTCTGAGTGGGCAAGTGTGTCAAAAGGGGC TGCCCCCAGGAGATGAGGTGAGAGCAGGGAGTTGAGGCCGAAGATCA TTGTTGGGAAATAGAGAGTTGAGATAACACCTCTCATTCAGTAGTACTGAAAGAAACTGTGCTA GAATGATAAATGTCATGGTGGTCTATACTCCAAATAAACAATGCAACGTTCC/T/C/GATTCTTAAT CTTGGTCTGAGAGCCATTGGTTTCAGTTGAGCAATCCCATACCAGCT TCCATTCTTTGGCCCTGCAGCATGTCATGCTCCAGAAATTCAGCTTCAGCTTAAGTGACAGAT/C JGTTAAAGCTTCTGGTTAGATTGTTTTCATTTGGTGATCATGTC/TCTTTCCATGTGTACCTGTAATATT TTTCCATCATATCTCAAAGTAAAGTCA

WI-9281	68 G A ---	GCTAACACCTTT TTAAACCCGT	--- CATTATTTTG AAAGCTATTCA GACA	ACTGGTGGGAGACTGTGAGGATCCAGGATTCAGTATTCCTGGCCAGAGGGCCTTGCTGGCTACTGG IG/ATGTTAGTTTGAGTCTGTGCTCCCTCTCTATGACTGTGTCCC
WI-7848	142 A G CTC	GTATATTACA ATGATCACCG ACTGA	CCGACAGAAC TATTGTAAAC AA	TTCTGAAATATACACGACATTGAGCTATTAAAACCTGTAAATTTTAAATTTACAAAAATATAA AATATGAAGACATAAACCCAGTGGCATCTCGTGACATAAACAATTAATGCTAACACTTTTAAAA ACCGTCTCAGTGTCTGAATAGCTTCAAAAATAAATGTGAAATGGT
WI-9304	70 G A ACTGA			TCACGTTGGTGTCTCTCAGATTCTGAGGAAATGCTTTGATTTATTAATGATCACCGACT GA/G/A/ATATGTTTACAAATAGTTCTGTGGGGCTGTTTTTGT
WI-7933b	314 C A ---		---	TTACAGAAACTTGCCTGTGCTGCCCATGCTAGGGGGGAGGGGCTTTTCCCTCTCTTTCC TACCTACCCCTTTCTCTGGCCAGGGCCTGTATCCTACCTTCCCTGCCCCGGCTGGCTGCAC AGAGGATTGCCCTTCTCTTTTTCAGAGCTGGCCCTCGATGCCAAATAGCATTTAGTATTTGCACAA AGTCTAAGGGACCATGGCTGCCTGCCCTTGGGGAGGAACCATAGCTCCCT
WI-7933	96 G ---		---	TTACAGAAACTTGCCTGTGCTGCCCATGCTAGGGGGGAGGGGCTTTTCCCTCTCTTTCC TACCTACCCCTTTCTCTGGCCAGGGGCTGTATCCTACCTTCCCTGCCCCGGCTGGCTGCAC CACAGAGGATTGCCCTTCTCTTTTTCAGAGCTGGCCCTCGATGCCAAATAGCATTTAGTATTTGCA CAAAAGTCTAAGGGACCATGGCTGCCTGCCCTTGGGGAGGAACCATAGCT
WI-7374	182 T A ---		---	CCAGATGTGCCCATCAGTTTTTCTGAGGCTTTTGTACTTTAGTAAATGCTTCCACTAAACTGAAA CCATGGTGAGAAAGTTGACTTTGTTAAATATTTGAAATGTAAATGAAAAGAGTACTGTATATTA AAAGTTGGTTTGAACCAACTTCTAGCTGCTGTGAAGAATATATTGTA/CAGAAACACAAAGGCTT GAT
WI-9343	78 C T CCTCTGCCA	CCAACAACAT CCTCTGCCA	AAATGAAACTT ACGTTTGTG TG	GGTCTGCTCCTGCTACCTTGACCCCTCCCTTCCCTGCTCTCTCCTCATCATCATCCCAACAACAT CCTCTGCCA/C/TACACAACAACAAACGTAAGTTTCATTTGGGCAAA
WI-7386b	104 T A ---		---	CTATATGTGAGAGGGGTGATCTGGATGGAAAGTGGGCTGGATGATCTCCAAAGTCGTTTCAACTCT TAAAGACATCTTAATCCTGAATGTAAACAATTGTTA/TAGTGTTTAGAAATCAGAAATTTGATTTTGA ACTTGAGTAAATTCATCCTT
WI-9357	75 A G ---		---	AAGAAGGAGCTCAGTTACGGGGTTTTTAAACCTTCATGAAAACCTGAAGAGTTCACTTTTGTTATTAT GCTCTTA/AGTGAATTACAGACTGATGCCAGACAACCTTGGGAAGA
WI-9360	79 T C TTGG	CTTTAGAAAA TCTGCTTTAAC TTGG	CCTAGGGAACA CAATTAGAGGA A	TGAAGGGGTGTGGCACTGTGTTTCTGATGCTTACTACAATATGTGAACCACTACTTTAGAAAAATCTG CTTTAACTTGGT/C/ATTCCTCTAATGTGTTCCCTAGGAAATGACGTGCCAAG
WI-7423	107 T C GTCC	TGCTGGGCTGT	GGTCCAGAAGA GCGCG	TGCTCCCTGTCCACTGAGTGGACCCAGGACCCCCCTTTGAGGAGTGGGTGAACCTGCTCCTT GGCAGGGATTGTGACACTGCATTGCTGGGCTGTGTCCT/CPGGGGCTCTCTGAGCCTTGACCCGTG GATACCAGGCCATGTGCCATGGTATTGGGCTCTGGGAGGGTGGGTGAATAAAGGCATCTGCT

WI-7424	131 T A	CAAGAGAGAG AGAGGAAAGA A AAA	TGCAAAAGAAA GAATGAAAGTT G	CCAGGAGCACTAGAGAGGGGGAAGAGAGAAAGTTAGAGAAAAAGCCACCGGAGGAAAGG AAAAAACATCGCCAACTAGAAACGTTTCATTCTGTCATTCAGAGAGAGAGGAAAGAAAA TTA/JACAACTTCATCTCTTCCTTGACGTTTCATAAACATTCTACATA
X86400	118 A C			TCCTGCAAGAAGTTCTCAAGCCTTTTGATTTTGTGCAATAAAGTACAGCTTTGCATAAGAGTGAAA TTGGGCTAGCTTAAATGGATCCATAAACCTTCTCTAAATTTTAAAGTGAGAJC/JCTTTTAAACACCT GTTAAATTTAATGTAGCAGCTGAGAAATCTAAATTAATGTACCACCTCGTTTATTTGTTTCATTCATCCA TCCCTTTCCCATGAATATTCA
WI-8053	242 T A			GTGGCCACTACATGTTATAGAAACCATCATCTTGTCACACAGCAGCTCTATGAATAAAAGGCTGAG TTATCACTAAGCAGGAGAAAAAGCATTAAGAGTGTCCCATTAAGAGGACTTTTAAATCAACCTAA TAAACTCTAATTCGTGACTTTTAAAGATCTAAGGTCTATTTAATACATGCTGAAAAAGGGTCACA ATTAATCTTTGATCTTTTACTCACTGTTAACTTATATAAT/JATTTCAGAAC
WI-6190	165 G A			TACACAATGAATTCCTTTATTTTCGGTATGCATCCACATTTTCAGCATTTAGTGGTCTCTGAACAGCAAG TGGAAGAGCGCAGCAATTTGCCAGGAGGTCAAGCCCACTTTCGGGATCTGCTGTGCACACCGG GTTCTCTTAATCCCTGCTGAGGATCTTG/JA/JAAGCAGCAGCAGCAACCAAAAGGCATGCA CGGATTCAAGGTTCTTTTTCAGTTGTCCAGTTCCAACTAGACCCCA
WI-6275	148 G C			AACAGTCACCACCAACCATGACAACTGCCAGGCAAGGCTTGTCTCCCTCCCTTGGGTCCC ATGTGCTTAGTCAGCAAGTCCGGGAGGACCGGATGTAGCTTCGCCCAAGGAGTATTACAGAGA GAGGCTTGGGAAAG/JC/JGGAAGGAAACCTGGACAGGCTTTTCAGCACTGAGAAATCACTTAAACTG ATTTGCTTTCACTGTAATGGTATGCTGAA
WI-6421	41 G T			ACCAAGAGATCAGCTGTCTAAACAGCAGCTTTTGTGTTG/JG/JGAGCTTCTGAAAGAAACCTTGC TGACAGCTTCTCACTGACCTGCAGGACGGAACCGTACCTGAGAGGGGATGGGGCTCTCTCAAAAA GAATATTTGGGAGCAACCTGGAACTGGCCACAGGAGACATCCAAATATCCCTCTCTCTCAGGG CTCACCCGACATCCTCAGCCAAATGAAGGCTCTGAA
WI-6905	215 T A			GGGTGAGACGGGTTTATGTGCATTTACACAGCTCAGCGTCTGGGCTGGCAGCGGCCATGCTC CTGTGTCGGGCTGCTCTACAAGGGCTTCACITTTCTTCCACACACTATGTACAGTCAGTCTCCAA GGTGATGGGCTACAGTGTGCTGATCAGTGTGTCGTACACACATTTTACATAAATTACACAGGACTC ATACATGAAAAAT/JA/JAGAGCCTAAGGGCTGTATTTTAAATGAGAAAAAA
WI-9420	202 G A			AACITGTTTACAAAATAGGCTTTGCAAACTTCAATCTGAATGTAAAGTCAATGACTGTGTGTTT TAAATATGTACCAAGGAAATACAAATGGATAATGATCATTTTTCATGCTCAGGAGAGAACAGCAC AGAAATAAGGATACTGCACAAGGTGCAAGGAAACCGGAACCCATTGTGTACACTGTCTTCACACAG G/JA/JGCACTTTCTCACCTTAACCTGACGCTG/GCAAGATGCCCTCAGTGTG

WI-9448	184	G A ---	---	TGGGGCTGCTTTAGACTTCATTTAGAGCAGAGCACCTAGTAGAGGAATACTGGGAGAGAGAC TGCTTGCCCATGGTGGTTAAACCTACATGAGGGGACTGAAATCTCTTTGGATGCCAGTCCAGATCCC TTTTAAGAAAATGGGCTTGGTCCAAAGGCTGAGAGCTGGCACCAC[G/A]CACTGTTTCTAAA TCTCTGGCTTGGATTTATCCAAAGGCATGTCCTAACGTGCCCCGTGAGCAG
WI-9470	204	G A ---	---	ATGTCAGAAAGAGACACAGACAGGAGTTTTCCCTTTAAATGCTAAACAGTGCCACTAATCCACA GATCTGAAAAAGTACAGCTCTCCAGGTTGATAATCAGATCCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCAGCAATATGATCTCCCTAAAGCCCCAGATTCTCTAGAGCCGCTGGGGACACTGATGAC AA[G/A]GCAATCAACTCATCTCTCAAGCTCACCAGGGCTCACCTTCCCCAAG
WI-1245b	201	G T ---	---	GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCTCATAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGCTGATGCAATCTGCTGTGAGCCATGTGCTGGCATCACAGGGTGGT TTATTAATTTCAATTTATCATCTGGACAGCCCCCTCTTATAACGTACATCCTTGCCTCTTCTGAGGC[G/ T]CTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1245a	85	T C ---	---	GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCTCATAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGCTGATGCAATCTGCTGTGAGCCATGTGCTGGCATCACAGGGT GGTTTATTAATTTCAATTTATCATCTGGACAGCCCCCTCTTATAACGTACATCCTTGCCTCTTCTGAGGC GCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1031	149	G A ---	---	TTCAAGTATAAGGACAGGCTAGAACAAAGCGTTCCCAACCCTGGCACCACATGACAGTTTGACCCAAA TAACTCTTTGTTTCAGGGGACTGTCTACACATTGTTGGGATTGTTAGCAGCCTCCGTGGCTTCTACCCCA CTAGATGCCAGCA[G/A]CACAAACACCCCTCCCAACAATCATGACAATGAAAATGTCTTTAGACATT GCCAATATACCTTTGTGGGACAAAATGGCCCTGATTGAGAACCACCTGGTT
WI-5385	110	G A ---	---	AATGAGTCAATTGTGGAGTTAGAGGAGGTTACTGAAAATGGTGACTCCAATGGTGGGATTGAAAGAGG GAAGTCTCGATAATTTAACATATGGTTTCTTGCCAGGAATCG[G/A]CAATGCTAATCTATTGCTTAA TTCCTTATCAACAGACTCTTTGAATCAATTTAGAGATACTCAGTGACCCCATGGCTAGAGTTCTCTGAC COCTGCTACGGGAACATTGAATGCA
WI-5403	199	T G ---	---	ACCAAAACCGTTGGCAAAGGCTCCCCAAGACTCACCCCAACTTTGGTGCTTACCCCTATGCCGGGTG GGATTGAAGAAATAACCATATAATTAATGCTACAAATTTCCAGTAGTACCAGGCACGACCTAT TGGAAGAAATCATAAATGTAACCTACAAATGATTGCTCTGCTGGCTTGGTGCCAGGCATAGAGTT/G JGGCTACAAACCATTTTATCATTTGAACCCCTCAGAAGCATCCAGTTGGGGCT
WI-5801b	157	G A ---	---	TGGTATTTTCTCTTCTTCTAAAATGTTATGATTAATTAGTGCTTTGTAGAATTTGAAAAAATGTAAA TCAGAGAACAGAAAGAAAATAAGTATAGTTGAAACCTCTAACAAATTTTAGATTTTAAAGGCCTAG GGAAAGAAAGAGAGCCTGGGA[G/A]AGGGGAATGAGAAAAGCACAAACAGAAAAAAGTGTGT GGCTTAAGGGAGCCCAAGGAAAGTTAAGT

WI-5801a	48 A G	---	---	---	TGGTATTTTCCCTTTCTAAATGTTATGATTAAATAGTGTCTTTGTJAGJGAAATTTGAAAAATGT AAATCAGAGAACAGAAAGAAATAAGATATAGTTGAAACCTCTAACAAATTTAGATTTTAAAGGCC TAGGGAAGAAAGAGAGCCTGGGAAGAGGAATGAGAAAGACACACCAGAAAAAAGTGTGT GGCTAAGGGAAGCAAGGAAAGTTAAGT
WI-5896	61 C A	---	---	---	TTCTATTTAAATCCTGTGCCCCATTGCAAGACTGCATTAGTCTGCATGAGCCTTAGTTTCJCAJTA AAGCCCCCTCACACCGAGGACAATGTTGAGAACTAAATGACTGCAGGTGAGCAATTCCTGTATTA TACAAACTGGGACCAAGATGACTTTATAATAGTGGCAAGAGACAATCAGGCAGACTGGGAGGACC TTATAATAGATTATAAGGCTGTGGTGAGTTTATTTAACTT
WI-7461	153 C T	---	---	---	TATTACTAGGTTCATAGAGCCCCGTTGTAATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCC AATCTAAGCCTCCTCACTCCCTTCGAACCCAGCCTCAGAGATGACACTTAGGCTGCACATTCCTG TGGCAGGGACTGTGTCTCTGTGTTCCCTGTGGGTCCCGGAACCCAGTGTGGTGGCACAGAG GAGCCCTGAGTAGCATGTGCTGCA
WI-9716	221 G A	---	---	---	AGAAGACAGGAGCACTGGGATCAAGGACTGATAAATCTGAGGCTTTAATGGTCCCTTGTCTCTAAC GCTTTGGTATACTTTCTTTCTGAAGACCACCCCTTCAAACTCTCAGAACACAGGCAAGATGCAT ATTCTGTAGTTTCAGATGTACTTCTTACATCTCGAAACTAGATGAGTTAGGCTCTCTTCATCT CAATTGAAATCTAGAAJGJAJAAACACCTAAATGGCTCATCTTGGATCA
WI-9760	49 C T	---	---	---	TTTTCGTTAAGTCTTGGAAGCCACACAGAGTGATCTACTCTTTTACJCTJAAAGTGTACTTTGCA TATATTTATGGGATGATCTATCCCTACTTAAGATTTTCTCTCTCAGGTTAAATATTCATTTCT TTGTCAGGAGTTCTTATTTGGCCTTCTTCTAAACCCCTTAACCATTCCTGCTTATCTCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
WI-9855	31 A C	---	---	---	GAAACCTCGTTGGCTCAAAGGAACTGTAGJCAJAAATCTTTTTTTTATTTTTTAACTC AAAGAGTGGAGTTTGACCTTGACCTGTGATGGCAGCTGCTCTTTGTTTGGTGTAATCCCTCTAGT GGGCATTTGCAAAAGCAATTTAGAGCAAGGTGGTGGCATGGAGTTGTGAGGTTGCTGAAAAG TAGCAATGGAAGAAAGTTAATGGA
WI-10312	41 A G	---	---	---	AAGCCCCAGTGGGAAAGCAGACAAACACTCCAAGAAATACJAGJAGATATAAACATCATCATCA GTAGAGATGGATGACCTAGGAGGTGATGCTGATGAGGCGATGTGAGCCAAAGACATTTGGGTCT TGAGGTTGAATAGGAGTTGTCTGGTGAGCTTTGCCAGTCCCATAGTAGGTTCCATAAATAAAC AGTGACTAACTGAGGTAGAGTCACAGAGAAATTTCA
WI-11152	179 C T	---	---	---	GATTCCTTGGACATGCAGAGCATACGGCAAGGCATCTTGGGCATTTGGAAGGAACGAGCCCTA ATTCATAGAAACAGACTCTACAAAGGACCAGTTAAAGGTCTCGCACCCAGGGGACTGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGACAAAGTGGGACAAAAGGCTTGTCJCTGTCTCAGAAACATTGAA AACAGCCAGTACATGCCACTGATAGA

WI-1968	167	A G	---	---	TGGTGAGGAGCTGAAGGCTGAAAGAATAGTCTCTGCTCTGGCTTTCTGTTGGAAATGGATGAGTCCT TTTACAAAATTTTCTCTTGGCCATGGGTGTTATGTTAGAAATCATGGAGTTGGAAGACTTAGATTCA ATTGGGGCTGTACAGTTTACTGGAAGTTGTJAGTGAACCTTGAGCAAGTGTCTCTTAATGTCTCTCA GCCTCAATGGCCTTCCCTGTAA
WI-4701	198	G A	---	---	GGGTTCAATTAACAGCCTTCCCACTGGGCTCAGATTGCACGGAGATGTAAAAATAGGAAGAGATAG AAAAATGGTGCCCACTATTGACTTGATAACACCTACAAAACAACACATTAAACTCTCCCCACTCTA CCGCAAAAGTCTACCTTTTGGTTCTTTTATTTCTGCTAATGACCATACTATTTCCCAATTAGA[G/A] CCATGTCAATTTTCAGAAAAGCAGTATA
WI-4823	164	C A	---	---	TTTATCTTCCAAACCATTGTGTTTCTTCACATACTTTACGTAATTTTAAATCATGTCTTTAAATTA TGCACTTACTTGTGGCTACCAGACATTGCTTCCAATTGTAATTCCTTAAACAACAGCAAGCATAACT GATGTGTCATCTTGTATTCTCTAAAA[C/A]AAAGAAAAGTGCTTTTGTGTCATCTGCCCTCTCTGT CTTCTCTGTTTCACTCTCTGATTTCCTTATTCAGCATTCATGAITTA
WI-4860	72	A G	---	---	AAAAAACAACCTTCAATTTGACATTCTAAGAAGATAAAGAAAAACAACGATCCACTGTGTGTTGCTT GATTJAGJGGAGATAAAACCTGATCTCTAAGAAAATTAACCCAAAGCAGTACACTAAAATAGCCT TTGTGTGTTGTTTTCAGGAAAGAAAGCCAAATCCAATAAGTTGCTAAGAAAAATAATGTTTCATATCA CTCTAACTTCCACATAGAGCATTAAATAGCA
WI-9705	111	C A	---	---	TGAAAGGACCAGTTTGAATGCTTACCAAGGTAAAGTAAATCGGAGGGGAGGAAAGTAGGAGTTGCTT CCGGATGTTGCATAAAATTCAGGTCTTTAAGGAGTTCCGGCTGCC[C/A]AAAAATTGTTAACACTGATGC TGCTACAACAGCACATAGAAATCGGTGTAGATTGCGGTTCTCTAGTAGCTAATGTTTAGATA TGATTGTTGAATTAATGTTGCTGTCTTGGTG
TGR- A004Z48	177	A G	---	---	CAAAATACTCTCTCTAGAAAGTTGCTCTAGGGCCATGGATTTCATGTAAGGGTGGGCAAGGTGGACTG AAGATCTGTTGGCAGGGCTCACAGAGACGGGGTGAGGGGAGAGATCGTGGTTTCATGAGATCCCAT CTTGGCAATACGGTTATCCCGTGGTCTTCATACGCCACAGAJAGTCTCCAATTTTCAGGGGCTCCC GTGGGATGGTGGAGCCAAATGAAGACCAGGTAGATGATGCCACCTAGAGATG
U17579	34	T G	---	---	GGGATTCAATGTGTCTCTCATCCAAATAGCACTJGJCATGACCTCAGCCCCATACTCTTCTTCCC TATGTTCCAGAGACAGAAATAGACCTGGCCCCCTCTCTTAGGGGATCACAATATTGGAAGGATGAG GACTCCAACAGCCAGCTCCCATGCCAAATAGAACGATGAGTGTGGGATCAATTTCTATGGGAGCC TGGGAGAGGGGATCCTTCTAGTTGA
WI-7747b	88	T G	---	---	GTGAGAGCGAGGCTGAGCCTACAGAGTAACCTCTTCTGGCCTGCTTCGTTAACTGTGTATGTACATA TATATAATTTTAAATTTGATJTGJAAAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAGTT ATTCTTGTGTTGTTGTTGGGTATCCCGCAGTGTGTTTGTAAATAAGAGATTGGAGCACTCTGA GTTTACCATTGTAAATAAGTATATAATTTTTTATGTTTGTCTGA



WI-7747a	44	T C	---	---	GTGAGAGCGAGGCTACAGATGAACCTCTTCTGGCCCTGC[T/C]TTCGTTAACTGTGTATGTAC ATATATATATTTTAAATTTGATTAAAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAGTT ATTTCTTGTGTTGTTGGTATCCTGCCAGGTGTTGTTGTTAAATAAGAGATTTGGAGCACTCTGA GTTTACCATTGTAAAGTATATAATTTTTTAAGTTTGTCTGA
WI-7189	197	T C	---	---	TCCAGAATTTCCCTTCAGCTCATTTTGTCTCTCACAATTAAGGGAGTAGGTTAAGTGAAAGGT CACATACCATTATTTCCCTTCAACAAATAATATTTTACAGAAGCAGGAGCAAAATATGGCCTTT CTTCTAAGAGATATAATGTTCACTAAATGTGGTTATTTTATATTAAAGCCTACAACATTTT[T/C]AG TTTGCAATAGAACTAATACTGGTGAAATTTACCTAAACCTTGGTTATT
WI-7850	57	G A	---	---	AGCCCCAGCTGGACTCATGGATGTGCACCCCTTGTCCCTGCTCTTCTGCCCTGG[G/A]CTCATGTA TCTGGCAGCTCTGGTACCCTCTGTGGGTGCCATCTCTACCTCTGACACAGACTGCCCTTGAAGCT GAGAAGGCACAGGCAAGGAGCCAAAGGACCACAGAGCCTCAGCCAGCCAGGATCCGTCCTCATTTT ATTGGTGATGATGAATGGGAATGAATCAGGGGGCTGTCTACTAGAGCC
WI-7907	69	G C	---	---	CTCTTCTTCATCCCATCACCCCTAAATAGGTCAGGTGAGGAGGCTGGGAAGAGGTGGGAGGAGG G[C/C]JAGAAGTGAAGGAAGATAGGAAGGATATTACCTCTTCTGTTATTTTTTAAAGAAACATTGTTT GGTGGCAGCAATCTCCCTGTCCCTATCACTGTTAGAGGCCCTAAATTTATCTATAAAATATATTA AGCAAGTCAAACTTGGATGATCAAGGTAAATTTATTGTCAAAAGTTTAAAT
WI-7919	242	T C	---	---	GAAGGCAGCTGGATCACTTCCCGCAGCTTGGGAGCGCTTGTGTGGAACACGAGAGCTCCTCCT CAGGGGCTGGCAGCTCACTTCTATTCTGTATGATGATATTGGTTAAACACTGTCAAAATAAGAGAT GTGCCAGATTTAGATTTTCTACCCCTAATCTGTTTAAATATTGTAACCTTTATCCATTGAAAGTGCA AGCCATTTCAGATAAGCTATAATCTGGTCTTTAAGGAA[T/C]ACAACCTT
WI-7928	101	T G	---	---	CTCCCTTCTATGCTCTCAGCAGCACGTTGGGCGACACTTGTTCATCTCTGACCCGTTTGTGGGCTA TTCCCTGCAGTGCAGACATCGTCAAAATTCAT/GJACAAGAGGAAATTTTCATGCAGAAAGCTGTA TGCAGGATGCTCACTGATGTTTGCACCTTAAACCTGAAATTCAACTCTTTATATAGGATTTCTTTT CTATCTCCATCTCCTCATTAAAAAATACGTACATTTCGAGGTAATGGTA
WI-7936	131	T A	---	---	TTTTGAGTCAAGACTTAAAGGGCCCAATGAATTAATATATACATACTGCATCTTGGTTATTTCTGAA GGTAGCATCTTTGGAGTTAAATGCACATATAGACACATACCCCAACACATTACACCAAC[T/A] ACTGAATGAAGAAGTATTTGGTAACAGGCCATTTTGGTGGGAATCCAAGATTGGTCTCCCATATG CAGAAATAGACAAAAAGTATATTAAACAAAGTTTCAGAGTATATTGTGAA
WI-7944	99	T C	---	---	TACAGTTCCAGCCCGTTGCCCACTCATCTGCGCGCTTGTCTTTGGTTGGGGGCGAGATTGGGTGG AATGCTTTCCATCTCCAGGAGACTTTTCATGT[C/J]AGCCCAAGTACAGCCTGGACCCCTGGTGTG TGAGCTAGTAAGATTACCCCTGAGCTGCAGCTGAGCCTGAGCCAAATGGGACAGTTACACTTGACAGA CAAAGATGGTGGAGATTGGCATGGCCATTGAAACTAAGAGCTCTCAAGTCA

WI-7805	101 A G ---	---	---	TTTCTAGGCTGACAGTCTGATGCAATGATTTTTTATAAATATTTCTACTCTTTGGAATTTGGATCTT TTTACTTTGAGCATATATTTAGAAATATGTGTA/GTGTAAAGGATCTCCACAATGTCTGCAGTGTG AAGGCAGGTTTCATTGTGGAATAGTTTAAACAGTCAGGAAGGCTAAACTGGTCAGTATTAATGTGTAGC CCTACCAAAAATAGCCAGTAGTATCTGAAAATGAAAAATAAATGAAGTAT
WI-7416	137 G T ---	---	---	GGCCAGGAGATTAGCAACAAGGATTCTGTTACTTACTTGGCCCTTTTATCTTTCCCTCTTGCCCC CAGTCCCTTCTCTCCAGCTTCATGTGAAGCTCTGCACAGACAGACACTCAGTGTCTCTTGGCAGTGCT [G/T]CTACTCCTCAGGTGCAGCATACATAACCAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACACTCAAAAATTGGCAATGTCATCAG
WI-140	252 C T ---	---	---	ATTGGAAGATTGGAGGGCTTTGCAGAGGAAATAGATTTCAATGGATCCCAAACTATAATGACA AGTTTTTAATTAGGTGATCAAGGCTTCTAAAGTGAATGCAAGTTGTACCAGTAAAGTTTATA TCTTCCATTTCAGCCAGCTCATTTGCCAGAAAATTCAGGTGAGTGGATTGGCCAGACTATCTGGCAAG GATGAAAATTTAGTTTAAAAATGTGTCATTGCTGTATTGGCAATTCCT[C/
WI-198	218 C T ---	---	---	GAGGTCTTCAGCAACATGGAAGCCCTACTGCTCAACCCGAGTCCCGGATCAAGTGTGGCACC CATGATGGAACCTCTTGCCATGGTTTGTAGTACCCTGGACCAAGTAGTATTCCTGACTTTTAAAA TTCFAAACAGCCTTTGATGGGACAACTCTGCTAAAGACTAACCACTTCCCTATCTTATCTTCAGCTA CCTGCTCCCTTTC[C/T]GTTTAAACAAAGCATAGAATATCTGAACAAC
WI-205c	146 T C ---	---	---	TTTCATGGTCCCAAGACAGATTTTAAAGAAAGAAATAAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGGCTGACTTTTCAAT GCATGAGTTTGT[C/C]CCAAAGGCTTGATGGGAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAACTGCATATGCTTTATTTTGTAGTTCCC
WI-205b	146 T C ---	---	---	TTTCATGGTCCCAAGACAGATTTTAAAGAAAGAAATAAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGGCTGACTTTTCAAT GCATGAGTTTGT[C/C]CCAAAGGCTTGATGGGAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAACTGCATATGCTTTATTTTGTAGTTCCC
WI-234	165 G C ---	---	---	GAAGACTGAGTTCCAGGAGGTTGCAGCCGTTTCTCTCGGGCCATATGGCTAATAAGGAGCTTGAGCA GGGATTCACCTGTTTGCAACCCCAAGTNCCTTCCAGAGGTCCTCAGACTACCTCCCTCCATCTCCCCCT CTCCCCCACAAACACACAAATACAGAGATT[G/C]AATTCAGGAGCCAGTTTCTAGGTGGGCTTGAGC AATCATACACAGTAATCTCTTGGTGTCTAGTTTCTCAATGGGAAATGG
WI-276b	25 A G ---	---	---	AGCTTTTGAATCCAAAAACCACAT[AG/CTTGACTCTCTTATCTCTCTCTTGTGTAACATCTATCC CTGAGGCAGAAAAACAGAACACCCCTGTGGCTGCCCTGAACGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAGCATCTCTCTGCTGAAAGACCTCTCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGTCTTATCTCTCTTGTATCCCTGCTATCCCTGATGACTGGGCAAA

WI-276	25 A G ---		AGCTTTGAAATCCAAAAACCATATGCTTGACTCTCTTATCCTCCTCTTGTGTAACTATCTATCC CTGAGGCAGAAATACAGAACACCCCTGTGGCTGCCTGAACGAGGAGGATGGGGGGGAGACAT CGGTCAATGATCAAAAGCATCTCTGCTGAAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGCTTATCCTCTGCTATCCTGATGACTGGGCAAA
WI-427	59 G A ---		TTTTCCCAATCCACAGGTAAACTAATAATGATGTATAGAAATTTAGAACTACTTCC(GA)GTTT TTTCCCTGGGGAAATATTCACAAAACATTTGGGTGCAATCAGGTTAAAAGACATAGTGTGCCA TTTGTATCAGACAGGTAGAGGCTGACTCTGGCAGGATTAGCTACCTAGCTGTGAGACTTTATGT ATCATTTATTAGAGCCAGGGCTTGTCTGTACCCAGCTTTCAGTGCAGT
WI-562c	106 T C ---		CTCTCACTCCCAACACATATGCTTACTTAATGGTTACAGATTAGCCCAAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATTTTAAIT/CJAAATGGTCTTTTATTAATAAAAAA AAAGNTATCTAAAGAGAAACCATAAATATCTCTCAGGTAATTATGGCCACAGCCAAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562b	106 T C ---		CTCTCACTCCCAACACATATGCTTACTTAATGGTTACAGATTAGCCCAAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATTTTAAIT/CJAAATAATGGTCTTTTATTAATAAAAAA AAAGNTATCTAAAGAGAAACCATAAATATCTCTCAGGTAATTATGGCCACAGCCAAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562	103 T C ---		CTCTCACTCCCAACACATATGCTTACTTAATGGTTACAGATTAGCCCAAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATTTTAAIT/CJAAATAATGGTCTTTTATTAATAAAAAA AAAGNTATCTAAAGAGAAACCATAAATATCTCTCAGGTAATTATGGCCACAGCCAAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-597c	141 A G ---		GTGTAATTTGGTGGCTTGGCACTTTTCCACAGTAACCTTTAGAAATNNAAGGTGGAAGGTAAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG/GJJAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTATAAC TTGATCTAATAATTTCTCACAACTAATACCTGAGAGAAATAGTCTATTAAAT
WI-597b	141 A G ---		GTGTAATTTGGTGGCTTGGCACTTTTCCACAGTAACCTTTAGAAATNNAAGGTGGAAGGTAAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG/GJJAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTATAAC TTGATCTAATAATTTCTCACAACTAATACCTGAGAGAAATAGTCTATTAAAT
WI-597	136 A G ---		GTGTAATTTGGTGGCTTGGCACTTTTCCACAGTAACCTTTAGAAATNNAAGGTGGAAGGTAAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GAT/GJCATGATAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTATAAC TTGATCTAATAATTTCTCACAACTAATACTCTGAGAGAAATAGTCTATTAAAT

WI-811	66 G C ---	---	TTCAAAATTAACACCATGGGTATATTAAATTTNGCTCTATCCATAGTCTAACCCCTCTCTCTG/ CJACAGTGAGACACCTGCTTCTATTGCTTGACGTATTAAAGTATTCGATCAGTCACCATCTGGA ACCAAGGTTTCATTCTGCTGACCCCTCCCTCCTCACCCCTACTTGGGCTCTGACTTCCTTCTGCTGGCT GAACCTCTCTCTGTGGCTGTCCGCTTCTCTGCTGGGCTCAATAC
WI-881b	156 A G ---	---	TGAAGCCCTCTCTATACCCCAAGTGTCTTTATCTTAAATGCTGTGGTGAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTTACAGGGGAAGCACTTTGNCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTGJTTACTATGTCACCAATTTGGGACACAGATTATATATGTCAGA CACCACGNATGTCTTTAAGATATGTCAGCAAGCAAAATCTGTCATGGTTT
WI-881	156 A G ---	---	TGAAGCCCTCTCTATACCCCAAGTGTCTTTATCTTAAATGCTGTGGTGAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTTACAGGGGAAGCACTTTGNCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTGJTTACTATGTCACCAATTTGGGACACAGATTATATATGTCAGA CACCACGNATGTCTTTAAGATATGTCAGCAAGCAAAATCTGTCATGGTTT
WI-867b	119 G A ---	---	AATCTTAACAGCCTTTTGATGCCAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCCG/GAJTTTGTGTTGGC CAAATAATATCTCCCCAGGGACGTCCTCTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTCTATGGTTTGAATGTGTCCTCCCAAGCAACACATTAGAAACTTA
WI-867	113 A G ---	---	AATCTTAACAGCCTTTTGATGCCAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCAGTCTCCGTTTGTGTTGGC CAAATAATATCTCCCCAGGGACGTCCTCTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTCTATGGTTTGAATGTGTCCTCCCAAGCAACACATTAGAAACTTA
WI-867	119 G A ---	---	AATCTTAACAGCCTTTTGATGCCAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCCG/GAJTTTGTGTTGGC CAAATAATATCTCCCCAGGGACGTCCTCTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTCTATGGTTTGAATGTGTCCTCCCAAGCAACACATTAGAAACTTA
WI-871b	123 C G ---	---	TCATCAGACCTGAGATTACGATGAATCTACCAAGGTACCAAAATGTAACTTGTCCAAAACGA ATCTCAGTTCTGCATATGTAATGGGAATGATAAGAGCACCACCTACCTCATG/GJAACGTGT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTAAATGCACCTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCAATATGNCTGTTTGTACATAA
WI-871	123 C G ---	---	TCATCAGACCTGAGATTACGATGAATCTACCAAGGTACCAAAATGTAACTTGTCCAAAACGA ATCTCAGTTCTGCATATGTAATGGGAATGATAAGAGCACCACCTACCTCATG/GJAACGTGT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTAAATGCACCTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCAATATGNCTGTTTGTACATAA

WI-884	198 T C ---	---	AGTTCTGGACTTGATGCTGGGAACAATGGGTNCTGGAGAAATTCCTATTTGAGTNTTTCACAGAT CAGTAGAGCCAAATGGAAAGGTATCCTAGTCCATCCCTTTATTAGGAACCTTCTGATCTATTGGGA ACTTCTCTCTAATAGATCAGGAAATCCACCTCATTTAATCATGGACAACNNAAGGAATATTCGJG ATCCGGCATGCAACATTTATTCAGTGAAACATGATGAAATGAACATAAT
WI-921b	205 G A ---	---	CAC TTC CAAGGGCTCTGGGGANGAGCGGTGGGAGCTGCGGGAAGCAGTTCGACACTGACTGA TGCTTTTGCTCAGGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTATCTGG CAGTGATGCCTCTCACGCCCTGGCCCCCAAGAAAGCTTNGCCAGGAAAAAGCAGCATCCATCTAC TCTGAIJGGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTCCTCCGAG
WI-921	205 G A ---	---	CAC TTC CAAGGGCTCTGGGGANGAGCGGTGGGAGCTGCGGGAAGCAGTTCGACACTGACTGA TGCTTTTGCTCAGGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTATCTGG CAGTGATGCCTCTCACGCCCTGGCCCCCAAGAAAGCTTNGCCAGGAAAAAGCAGCATCCATCTAC TCTGAIJGGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTCCTCCGAG
WI-945c	90 G C ---	---	GGCTGGGATGAGAGGTCTACTTGTGCTAGTGGAGTTTCACTGGCTTGTGCTAGAACTAGNAAGNA GAAAGACACAGNATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCCCAAGGCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAGTTCAAAACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGAATCTCTAAAGGGGAATCATGACAGATTTTCTTGGCTTTA
WI-945b	90 G C ---	---	GGCTGGGATGAGAGGTCTACTTGTGCTAGTGGAGTTTCACTGGCTTGTGCTAGAACTAGNAAGNA GAAAGACACAGNATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCCCAAGGCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAGTTCAAAACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGAATCTCTAAAGGGGAATCATGACAGATTTTCTTGGCTTTA
WI-960b	167 C T ---	---	TTGCTTCAAAGAAAGTCTTGCTCAGGAAGTTATTCATTGAGCAACCTAAAAATGTTTTTGAGTACAT ATCAAGCACAGGGTCTGAGCAATGCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTCTACCC CTGAGGAATTTATCAAAGATGTTAAGTTATCTTC/TTCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-960a	155 G A ---	---	TTGCTTCAAAGAAAGTCTTGCTCAGGAAGTTATTCATTGAGCAACCTAAAAATGTTTTTGAGTACAT ATCAAGCACAGGGTCTGAGCAATGCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTCTACCC CTGAGGAATTTATCAAAGAT[G/A]TTAAGTTATCTCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-1121	181 T C ---	---	TCCCAGTATGGCTTTCAGTAGTTTTTATTATGATGTCCTAGGTACATTTGTTTTTATTGTTCTG CGAATTGTTGATTACTTTGGGAGAAATGCTCAACTATAAATATTGCTTCTGACCCCTTTCTGTGTC CTTCTTAAAGATACAAAAATAAATGTAACATTAGACCTCTCACAATTC/TCGCTGTTTTTACTCTCCTCTG ATTTTTTTCCATTATTTTATGCTCTGGCTTCATTTTGTAATNTG

WI-1147b	204 G A ---			TTTGCCATTATTTGAAGATAACCCACACCTTGGTGCCAGGGTTTTACAGGGTATTAGTGGTCAGTCA CATAGGCATATAGTACGTGATGACTTCTATTCCAGCCACCGCAAACCTTCTCCTCCCTGGCTC CTGAGCCAAAACAGGCATTTACCAATAATCACCTTTGTTAGGATGAACCTATCTGGCCAAACTGATA C/GA/GCATGACCCACAGCCTCAGGTATATAAACACACTCTCATCAGGCAGA
WI-1158b	147 C T ---			GCATTGAGGGTTCGTTTAAATGACATTCAGTGGCCCTGCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAATACAATGTGATGGTCTCCTGAGTGTCTGAATGC/GGCCAGGTGGC TAAGTGCTGGGGC/TTTCTGGGGTCAGGCTGCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1158a	124 C G ---			GCATTGAGGGTTCGTTTAAATGACATTCAGTGGCCCTGCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAATACAATGTGATGGTCTCCTGAGTGTGAATGC/GGCCAGGT GGCTAAGTGCTGGGGCTCTGGGGTCAGGCTGCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1304	124 T C ---			AAGTTACAGAAAAAATACCAGAAAAGTGACTCAAGANTCAGCTGAGATAGAAACATATGCCCA TCATCTTCAANGTCCACAGACACTTATCCCTAGACAGCCATTTCTTTTGAATGN/T/C/GNCANT AAAAATGATTGAAATTTGGGAATAAAGCCCTCCCTCTAAATGATTGACAGTGTAGACCTTGCCTAG GGC
WI-1305d	202 C T ---			TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATATG/C /TAGGGCGGANGTAATANGTATACAGNGANTCATACAGCCCTGCCTACCA
WI-1305c	46 C T ---			TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCTTCCATT/C/TTATGTTGGTAAATATAAAG ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTC ACATCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATA TGCAGGGCGGANGTAATANGTATACAGNGANTCATACAGCCCTGCCTACCA
WI-1305b	153 T C ---			TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAAT/C/TNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATA TGCAGGGCGGANGTAATANGTATACAGNGANTCATACAGCCCTGCCTACCA
WI-1305	202 C T ---			TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATATG/C /TAGGGCGGANGTAATANGTATACAGNGANTCATACAGCCCTGCCTACCA

WI-1306b	248	A G ---	---	TTTCTGCAATTGGAATAGTTGACTTCTATGAGNNNGCAATAATAATGGACAACTTTGTGNNNNNTNG GGCTGGGTGACTGTCCCTGGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGNGAGAAAGTGCCCTNNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCCTTJAGJGC
WI-1306	240	A G ---	---	TTTCTGCAATTGGAATAGTTGACTTCTATGAGNNNGCAATAATAATGGACAACTTTGTGNNNNNTNG GGCTGGGTGACTGTCCCTGGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGNGAGAAAGTGCCCTNNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTJAGJCTTCCTAGC
WI-1307b	118	T C ---	---	GACAAGGCTGGTACTAGTTCCAAATCCAAATCTATGTACACTTTCCTCTCACTTCTCAAGTGGACA GATTTCTGCATTATACTGCTTGGGTTGGGGAGCAGTGGTAGGCAATTCJGTGAGATTGCTTTT CCTACCCCTCTTAAATGATCTTNCATTAATNATGCTAAACCCGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTGTTGTTGCTGTTGTTTCTCTCTCTGTAAGNTGTTT
WI-1307	118	T C ---	---	GACAAGGCTGGTACTAGTTCCAAATCCAAATCTATGTACACTTTCCTCTCACTTCTCAAGTGGACA GATTTCTGCATTATACTGCTTGGGTTGGGGAGCAGTGGTAGGCAATTCJGTGAGATTGCTTTT CCTACCCCTCTTAAATGATCTTNCATTAATNATGCTAAACCCGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTGTTGTTGCTGTTGTTTCTCTCTCTGTAAGNTGTTT
WI-1325b	169	T C ---	---	GAGAGTGGCCCAAGACAAGCAGAGGGAGAGAGAGCAACNCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTCTATGATAGATCAGATGACATGGAGAC ATTCAATTAGGCAACTACAATGTGCCCTTGTCTCCCTTCJACCCCTCAGAACTTCCCTGAGGGGCAGGC ATTATGATTCCTCCTTACATCAGTGGGAAATTTGGACTTGGTGAAGTTAGGTT
WI-1325	165	C T ---	---	GAGAGTGGCCCAAGACAAGCAGAGGGAGAGAGAGCAACNCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTCTATGATAGATCAGATGACATGGAGAC ATTCAATTAGGCAACTACAATGTGCCCTTGTCTCCCTTCJACCCCTCAGAACTTCCCTGAGGGGCAGGC ATTATGATTCCTCCTTACATCAGTGGGAAATTTGGACTTGGTGAAGTTAGGTT
WI-1327b	162	T C ---	---	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAGCTGTGTAGTGAAGAAAGTCTGTTATTTGTAAA ACACCAAGTGGGTTTAAATGGAATCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTTCJGAAAGTTGGGTAGCTACAGGCCCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCCTTACTGAAGAGGCAATGGTTCATCTCTAAG
WI-1327	175	C G ---	---	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAGCTGTGTAGTGAAGAAAGTCTGTTATTTGTAAA ACACCAAGTGGGTTTAAATGGAATCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTGAAGTTGGGTAGCTGATACAGGCCCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCCTTACTGAAGAGGCAATGGTTCATCTCTAAG

WI-1341b	136	GA ---	---	TATCAGCATGATTGTGGCTGTGGACACAAAGTCAATTTGTACTTTTGTGNTGNNNTCCTTTTCNTTT ACCTGATCCACTATCTCTCAAGATCANGTTCAAATTTGGCTTNCCTTTGTNAATTATACCCAAAGC [G/A]GGATTGTGATGGATCTGTTTATTTCTGTCTTGGAAACAGCAGAGTCGCTCTGNGAGTNTG GTTTCAGGATTGTCTCTGTTCCCCAGCCACCTTGCACTTAGCAAGTGT
WI-1349e	192	GC ---	---	CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAAGGCAGGTGGTAGGTCTGGCTGTGAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCACTGAAAGGATAGTCTGAATTCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTGTGAAGTACTAGATTTCAGAAAAATA
WI-1349d	264	CA ---	---	CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAAGGCAGGTGGTAGGTCTGGCTGTGAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCACTGAAAGGATAGTCTGAATTCATCTCTGA[G/C]TTCAAA ATTTGAGAAATATGATAGAAATTGTGAAGTACTAGATTTCAGAAAAATATGAT
WI-1349c	192	GC ---	---	CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAAGGCAGGTGGTAGGTCTGGCTGTGAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCACTGAAAGGATAGTCTGAATTCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTGTGAAGTACTAGATTTCAGAAAAATA
WI-1349b	264	CA ---	---	CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAAGGCAGGTGGTAGGTCTGGCTGTGAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCACTGAAAGGATAGTCTGAATTCATCTCTGA[G/C]TTCAAA ATTTGAGAAATATGATAGAAATTGTGAAGTACTAGATTTCAGAAAAATATGAT
WI-1349	264	CA ---	---	CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAAGGCAGGTGGTAGGTCTGGCTGTGAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCACTGAAAGGATAGTCTGAATTCATCTCTGA[G/C]TTCAAA ATTTGAGAAATATGATAGAAATTGTGAAGTACTAGATTTCAGAAAAATATGAT
WI-1403b	57	CT ---	---	TGGTATTTGGGAATGGGTTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/TT]TCGAAAT GCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACGT AAAGTTTACATCAACATAAATCTTGGCCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGCTCCTCA TAATCCCCAAAGTGCCAAAAAGGGTTGTATCTGATTGT
WI-1403	58	T C ---	---	TGGTATTTGGGAATGGGTTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/TT]TCGAA TGCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACG TAAAGTTTACATCAACATAAATCTTGGCCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGCTCCTC ATAATCCCCAAAGTGCCAAAAAGGGTTGTATCTGATTGT



WI-1417c	31 C T ---	---		CAGCCGGAAGAGATTACGTGGAGAGATGTC/TTTGGCCAGGGCGGGAGAGATGTGAGCCACCGGG GGTGACAGCATGCGCTGCTGGCATTGGAGGGCCCCAGAGGAATCCAGTGGCCCTCTCAATGACTTGG GGGTCTCGACTCGGAAGTTAAGGGGCTCGGCTTCAAAAAGCTGGTCCGGTTTGGAGCGGTTGC AGGCGAGGCCCTTAGGTCGGTATTTAATGTTTGGCTTTGTAGAAAAAGTCGC
WI-1417b	31 C T ---	---		CAGCCGGAAGAGATTACGTGGAGAGATGTC/TTTGGCCAGGGCGGGAGAGATGTGAGCCACCGGG GGTGACAGCATGCGCTGCTGGCATTGGAGGGCCCCAGAGGAATCCAGTGGCCCTCTCAATGACTTGG GGGTCTCGACTCGGAAGTTAAGGGGCTCGGCTTCAAAAAGCTGGTCCGGTTTGGAGCGGTTGC AGGCGAGGCCCTTAGGTCGGTATTTAATGTTTGGCTTTGTAGAAAAAGTCGC
WI-1729	172 A ---	---		CCATGAGCAAAAGCATGTTTCTACTCTGTGATGTATGTTAGGGGCATGTATCTATCTGATTTCTT TTTTATTCTCCAAAAGAAATTTCAATTGCAAAACATTCAGGCCAATCGAGCTCGTAATAAAGA TGTTGGAGAACTGAAAAGAGAGACTTACATGCACCCCAATAGCAAAACTCTCCACACATTTCCAGCA GATGTATGTGCTTCCGTGGTNACTTCTCTCCACCACATCACCTGTGTTTT
WI-1732b	122 T C ---	---		TGCCTTACTTCTTTGTTTCATTCGCCACCATTACATTTTGTAAATTTGGAATCTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAGGGGACATATTCAGAGGAGTNTCCCTGGGTCAACCCCTTTC/ATTCAGTCT CTGCCACATGCTAGTAACTGTGAGTGATGGGTGCATCAGTATACTCTGAGCCTCCCAAGGTACAGC CTTTCACACTATTTCATCATATTGGCTAAGGTATTTCATCATATTGGCTAAG
WI-1732	114 C T ---	---		TGCCTTACTTCTTTGTTTCATTCGCCACCATTACATTTTGTAAATTTGGAATCTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAGGGGACATATTCAGAGGAGTNTCCCTGGGTCAACCCCTTTC/ATTCAGTCT CTGCCACATGCTAGTAACTGTGAGTGATGGGTGCATCAGTATACTCTGAGCCTCCCAAGGTACAGC CTTTCACACTATTTCATCATATTGGCTAAGGTATTTCATCATATTGGCTAAG
WI-1750	97 A G ---	---		GCGAATTTAATGACTCCAAAAGGTAGTAAATTCCTTTCCCCCAAAAAGGTTTTAAATCTGTGTGGGA -CATAATGTTTGAATTTGCAGTTCACCTTGG/AGTTAAGGTGTGCTGTTTTCTGGCAAGAGTCAG TGGGAGTGTCCGGGAAAAGGGCTAAAGTCTTTGTAGTCAGACAAACCGGCTTGCAGTCTGACTGAG CTACATTACCTTATGATCTCCAGCAGGTTCTTCCA
WI-1780	31 A G ---	---		GGTACACAAAGAAATGCTTCTGGAAATCTAC/AGTAGCGCCTTAACATTTTGGCTGAGTATTATC TGTACATGTGTAATGTGAACCCCATGAAGCTGGGCAAGAAACAAATTCCTAGGAAAGTACAATTAAC TGGGAAACTGTAGAACAAATAATCTCATAGTTTACACATAGCTGGGAATCACTCATGTTCOCATCA ACTGGAGAGACCTTGTGTAGTACAGAGGACATTCAGAATAATCATAAAAAT
WI-1803c	77 A G ---	---		CCACTCAGTAATAATAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTTTTCAGGCAGAA CCATTATGAT/AGJAGTAGGTAGAGCATCACACTTGGGAGGACATATCTGGAGTNAGATATCCTG GGTGCTAAATTTCAAATATATCTACTAAAGCATGACTTCTAGAAAATTACTTATTACTCTTGTCTCTCAA GGAATGGGAATACCTATAATACAGTCTTATTGAGGAAAAATAAAGTGAATCA

WI-1803b	77 A G ---	---	---	CCACTCAGTAATAAGTGTGGAGATAAGTATATGGTAGGCACATAATAATATTTTCAGGCAGAA CCATTATGATAGTAGGGTAGAGCATCACACTTGGGAGGACATATCTGGAGTNAGATATCCTG GGTGCTAATTTCAAATATACTACTAAGCATGACTTCTAGAAAATTACTTATCTCTTGCTCTCAA GGAATGGGAATACCTATAATACAGCTTATTGAGGAAAATAACTGGAATCA
WI-1837b	112 C T ---	---	---	TTTACTGGGATTTTCATAGCTGATCATAATTTACCATTTGATAATTCACCTCTTTTCCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAAATAGACCCGTTTATAC[CTGCTGCCAGTTTATTTT AAGTTTTCATTCACCTGATGCCAAAACAAACCTCAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACITGGGAAGTCTGGGAACGTTTAGCTTCTGCTGGCT
WI-1837	112 C T ---	---	---	TTTACTGGGATTTTCATAGCTGATCATAATTTACCATTTGATAATTCACCTCTTTTCCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAAATAGACCCGTTTATAC[CTGCTGCCAGTTTATTTT AAGTTTTCATTCACCTGATGCCAAAACAAACCTCAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACITGGGAAGTCTGGGAACGTTTAGCTTCTGCTGGCT
WI-1840b	79 G T ---	---	---	TCACCTAGGGAGGTCGCTAAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACT[CTGAGAAATCTGAATATTCAGCACATACAAAGTGTGACAAACCTTGTTAGTAT ATTTATCTCCAGAGTGTGTTGAAATTTACTAAAAGTTCTAAAGAGCCATGAAGAATTATAAGACT ATCGCA
WI-1840	79 G T ---	---	---	TCACCTAGGGAGGTCGCTAAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACT[CTGAGAAATCTGAATATTCAGCACATACAAAGTGTGACAAACCTTGTTAGTAT ATTTATCTCCAGAGTGTGTTGAAATTTACTAAAAGTTCTAAAGAGCCATGAAGAATTATAAGACT ATCGCA
WI-1879b	110 C T ---	---	---	GGGCTCAGTTTCATCAGAGCACATATCACGTGATAGTCTGTTTCTCTTTTCATAACTACTCCCCG CACTGTAGGNTTTCTTTGAGGTAAAGGACCTGCCNTTTTAC[CTGCTGCNAAATAAACTCCCAAAA AAGTGGTTAGTCCACAGGGTTTAAATAGTCTGTTGAATGAATTTCTGTGCGACCCCTGTGCCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1879	110 C T ---	---	---	GGGCTCAGTTTCATCAGAGCACATATCACGTGATAGTCTGTTTCTCTTTTCATAACTACTCCCCG CACTGTAGGNTTTCTTTGAGGTAAAGGACCTGCCNTTTTAC[CTGCTGCNAAATAAACTCCCAAAA AAGTGGTTAGTCCACAGGGTTTAAATAGTCTGTTGAATGAATTTCTGTGCGACCCCTGTGCCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1900b	119 C T ---	---	---	TGTTCTCTGGTCCAGGCACCGGGCTAAGTCTTGCTGCATAATGGAATAATCAACTGGACAACCCGNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAGAGG[CTGCTCTGAGAGGT AAAGTGCCTGCCCAACGCGCACAACTAGAGAGCAGCAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGCTTAAGTCCCATGAGAAACCACTTTTCTTTGCTCC

WI-1900	119	C T	---	---	---	TGTTCTCTGGTCCAGGCACCGGGCTAAGTCTTGCTGCAATAATGGAATAAACAAGTGGACAAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAGAGGG[C]TGCTCTGAGAGGT AAAGTCCCTGCCCAACGCGCACAACTAGAGAGAGCCAAAGAGGTGTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTCTTAAGTCCCATGAGAAACCACTTTCTTGTCTCC
WI-1943c	165	C T	---	---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAATGGGTAGGGAAGACCAAGCC[C]TCTCTGAANCTGGTCCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCAGATGACTCCAAAGCCCGGCTGGAGTAT
WI-1943b	165	C T	---	---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAATGGGTAGGGAAGACCAAGCC[C]TCTCTGAANCTGGTCCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCAGATGACTCCAAAGCCCGGCTGGAGTAT
WI-1943	164	C T	---	---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAATGGGTAGGGAAGACCAAGCC[C]TCTCTGAANCTGGTCCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCAGATGACTCCAAAGCCCGGCTGGAGTAT
WI-1960c	270	A T	---	---	---	CCAGGTGAGGCTGAAAGAGGAGGAGGCAATTGCTGTTGGAGTGGGATCTGGAGAAAGCACCCCT GCAGAGCTTCATCTGTTTTCAAAAGTGGCCATGCANGGCTGCTGGGTTGTGAGCTCATNGCTGAG TTATCAGAGCTCCTGATGACAGATCATGAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACITAAAATGCACCTCCCAACTTT
WI-1960b	270	A T	---	---	---	CCAGGTGAGGCTGAAAGAGGAGGAGGCAATTGCTGTTGGAGTGGGATCTGGAGAAAGCACCCCT GCAGAGCTTCATCTGTTTTCAAAAGTGGCCATGCANGGCTGCTGGGTTGTGAGCTCATNGCTGAG TTATCAGAGCTCCTGATGACAGATCATGAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACITAAAATGCACCTCCCAACTTT
WI-1977	203	T C	---	---	---	CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTGGATCTGGTAAGTAGGAGTCA TTCTGGGCATTTCTCATAGAGTNTGTTTTTAGTCTGTAATAATACTGTTGCCCTAGGAAGGTTGTT TTTCTACTGCGTCTGTGAAAGCCCTTCCCCATCGAGTGATACAGTACTTCCAGTTATGGAGATTTT /C]TAACATCAACACTGGCTGAGGCTGTTGG
WI-2012	102	T C	---	---	---	AAATCTAGAAGCCAGAGTCAAGTCAAGCTACGATTTATAAGTTGAAGTAAATGCATTTAGTTTCATGT TTTCTCTTAATCTGCACAAAAGTCTAGCTAAAATC]T/C]TTTAAATCAGTTACCAGAGGCAATACCT GGGTTAATGTAGCACTCAAAAGTTATGTAGAGTAGCTGTCTCTGAGTCACTTTTTTCTACTCTCATTT GGCTTCACCAATGCTTCCACTGGATC

WI-2013	127 C T ---	---	CTTTTAGAGGGTGGTCATTTCGGTTCCTCTGGAAAGTGATTCGTGTTAAGAAAAATAGATGCAACG TTGCTAAGTACACCTAACATTTAAACAGTCTCCAGACAGATAAATGCTGATAGTACACTC/TCTCA CCAGAAAAAGAGAAATACCATCATGAGGAAGAGAAATGACTTTTGTCAGTTATGCTCCCGGGTCC CCTTTCAGTGGAGGGATATCTCAGCTTTCTGAGCCCCGTGGTTACTGCAATCC
WI-2032c	166 GA ---	---	ACCAGACATCCCATCAGGAGTAGTCCCTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAAACC TCAATTTTTCTTNACTTACTCATATAATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATACCCCAACTGGTTTTCTAGATGTACACG/AJGTGGGACCTCTGTCTCAACCTCCGACTTTCAC AGATCAITGGTTAGGCTACCTTCCTGTAATTGCTTCTGTTTTTCAAAGGG
WI-2032b	219 C G ---	---	ACCAGACATCCCATCAGGAGTAGTCCCTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAAACC TCAATTTTTCTTNACTTACTCATATAATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATACCCCAACTGGTTTTCTAGATGTACACGTGTGGGACCTCTGTCTCAACCTCCGACTTTCACAGA TCAITGGTTAGGCTCA/C/GCTTCTCTGTAATTGCTTCTGTTTTTCAAAGGG
WI-2032	219 C G ---	---	ACCAGACATCCCATCAGGAGTAGTCCCTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAAACC TCAATTTTTCTTNACTTACTCATATAATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATACCCCAACTGGTTTTCTAGATGTACACGTGTGGGACCTCTGTCTCAACCTCCGACTTTCACAGA TCAITGGTTAGGCTCA/C/GCTTCTCTGTAATTGCTTCTGTTTTTCAAAGGG
WI-2054b	188 C T ---	---	CGTTTTCTCTACATCTGGGNACATAAAGANGAAAGAGNAGCTGCTTTTTGTGGTAGTTTTGCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAAATACCTTACAGACTTAGGATTTGGA TTTTCATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTTTC/JCTGCTGCCAC CAGCCCTATCTCTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGCTTT
WI-2054	183 T C ---	---	CGTTTTCTCTACATCTGGGNACATAAAGANGAAAGAGNAGCTGCTTTTTGTGGTAGTTTTGCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAAATACCTTACAGACTTAGGATTTGGA TTTTCATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTTTC/JCTGCTGCCAC CAGCCCTATCTCTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGCTTT
WI-2573d	129 T C ---	---	TGGGATTAACCCCTGTTTTCTCTCCAGTTCAGTGTGCCCTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTTTAAATGCACCTTGCCGTTCAAGGTTTCCGTCGCTTTC/JTGA TATCATCTGATCTCCCAACCAGGGCTTATTTATGCCTAGGTAGGGGTAAAGCAACAGAGGCTGTGT GAAGTGAATGATTTGCTTGACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573c	165 A C ---	---	TGGGATTAACCCCTGTTTTCTCTCCAGTTCAGTGTGCCCTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTTTAAATGCACCTTGCCGTTCAAGGTTTCCGTCGCTTTCGAT CATCTGATCTTCCCAACCAGGGCTTATTT/JCTGCTAGGTAGGGGTAAAGCAACAGAGGCTGTG TGAAGTGAATGATTTGCTTGACAAGGTCATATGGCTGGGCTTGGACGAG

WI-2573d	129 T C ---			TGGGATTAAACCCTGTTTCTTCTCCAGTTCAGTGTGCCCTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTGCCGTTTACAAAGGTGTTTCCGTCCTTTC/JTGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCTAGGTAGGGGTAAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTATATGGCTGGGCTTGGACGAG
WI-2573c	165 A C ---			TGGGATTAAACCCTGTTTCTTCTCCAGTTCAGTGTGCCCTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTGCCGTTTACAAAGGTGTTTCCGTCCTTTC/JTGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCTAGGTAGGGGTAAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTATATGGCTGGGCTTGGACGAG
WI-2573b	165 A C ---			TGGGATTAAACCCTGTTTCTTCTCCAGTTCAGTGTGCCCTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTGCCGTTTACAAAGGTGTTTCCGTCCTTTC/JTGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCTAGGTAGGGGTAAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTATATGGCTGGGCTTGGACGAG
WI-2573a	129 T C ---			TGGGATTAAACCCTGTTTCTTCTCCAGTTCAGTGTGCCCTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTGCCGTTTACAAAGGTGTTTCCGTCCTTTC/JTGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCTAGGTAGGGGTAAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTATATGGCTGGGCTTGGACGAG
WI-2868b	60 A G ---			GAC TTCATGCTCATGAACAAGCATTTGCTTAAATTTACAGACATTTAAGAACAAAGCTTTC/JGJCTC CCACTTCCTCCCTCCACTATCACCTCAACCTCTTCATCCACTTTAAAGAGGTTTCTTAGGTCCTCTGCAT ATCATGGAAGCCCAACTACTCTATTAAACGCTTTCCCAATGATGCAGCCCCAGTTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACACAGCTGAAAAATGAAATATCGATATAC
WI-2868	60 A G ---			GAC TTCATGCTCATGAACAAGCATTTGCTTAAATTTACAGACATTTAAGAACAAAGCTTTC/JGJCTC CCACTTCCTCCCTCCACTATCACCTCAACCTCTTCATCCACTTTAAAGAGGTTTCTTAGGTCCTCTGCAT ATCATGGAAGCCCAACTACTCTATTAAACGCTTTCCCAATGATGCAGCCCCAGTTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACACAGCTGAAAAATGAAATATCGATATAC
WI-2870b	131 T C ---			CATGCTGTGTAACCTCTGTGCTGCTGCTGCTGCGGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGATTC/J AGAAATGAATAGAGCCCCATTTAAATTTATATACAGAGCTTTATGTCCACTTCCTGTTCTCCTGCCATCAG TGGGCTTTTACAAAGGAGGGCTTT
WI-2870	131 T C ---			CATGCTGTGTAACCTCTGTGCTGCTGCTGCTGCGGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGATTC/J AGAAATGAATAGAGCCCCATTTAAATTTATATACAGAGCTTTATGTCCACTTCCTGTTCTCCTGCCATCAG TGGGCTTTTACAAAGGAGGGCTTT

WI-2954c	49	T A ---			TTAGCACATATCTGTTGGGACTTAAGTGGACAAAGGCATATAAAATTAAGCAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2954b	41	A G ---			TTAGCACATATCTGTTGGGACTTAAGTGGACAAAGGCATATAAAATTAAGCAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2954a	38	G T ---			TTAGCACATATCTGTTGGGACTTAAGTGGACAAAGGCATATAAAATTAAGCAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2971b	62	T C ---			ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTACCCAGCATTTCTAAGAATC/G CTGCCAGCACCAATAAGCTTTCTTCAAAACAATTTGTGAACCTCCTCCTTCTTAATAAACCTAAC ATTTCCCTTTGTTCCCTGACATCTGAAGGCCACGCTGGTCTAGATGTATGCCAGATTGCAATCCT AGTCTTTAATGTTATTCTGAAGAAACCTTTTACTAGGATTGTCT
WI-2971	62	T C ---			ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTACCCAGCATTTCTAAGAATC/G CTGCCAGCACCAATAAGCTTTCTTCAAAACAATTTGTGAACCTCCTCCTTCTTAATAAACCTAAC ATTTCCCTTTGTTCCCTGACATCTGAAGGCCACGCTGGTCTAGATGTATGCCAGATTGCAATCCT AGTCTTTAATGTTATTCTGAAGAAACCTTTTACTAGGATTGTCT
WI-2995d	133	A T ---			TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTINATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA /AAATCTTTCTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995c	151	G C ---			TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTINATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTJA /AAATCTTTCTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133	A T ---			TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTINATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTJA /AAATCTTTCTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGTT

WI-2995c	151	G C ---			TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGAGCTGGANTTTTTTTNA AATCTTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133	A T ---			TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGAGCTGGANTTTTTTTNA /AAATCTTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAG GAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995e	151	G C ---			TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGAGCTGGANTTTTTTTNA AATCTTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995b	151	G C ---			TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGAGCTGGANTTTTTTTNA AATCTTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995a	133	A T ---			TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGAGCTGGANTTTTTTTNA /AAATCTTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAG GAATGAGACAGAACTAGCAGAAAGTGTT
WI-3147	85	C T ---			GTGGTGCAGTTTCATCTCTGGAGCTCCCTGTGAGATCAGACTGGAGCCAGTCTCCAGCTTGAGACCCAG ATCTCACTTAGCTCCTT[C/TT]CCTGCCATATCCTGTTTCTTACTCTATCTCCTGAGACTTCTCCT GAATGAATTACATGCACCTCAATCCCTGCCCTCAGTCTCTGCTTINAGGGAACCTTGACCTAAGACAGAA ATCTTAGTACCAATACTTTGCAAGG
WI-3234b	68	T C ---			ATTCTGTAATGTTTTCAGTCTTCCAGTAAATCTTTATTGAGGTCCATGTCCATTACCTCTACTTA[ T/C]GACAAAGCAAGAACACACAGAAAGCCCTGTTTGCAATCTGGCCTCTTATAAATAGTTTCTG TATATTTAAACAAGTACTGTAGAGTATGAATCATTACATCCTTAAATAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGGAGCAATGGAATGTACTTATTTTATATCTTAT
WI-3234	68	T C ---			ATTCTGTAATGTTTTCAGTCTTCCAGTAAATCTTTATTGAGGTCCATGTCCATTACCTCTACTTA[ T/C]GACAAAGCAAGAACACACAGAAAGCCCTGTTTGCAATCTGGCCTCTTATAAATAGTTTCTG TATATTTAAACAAGTACTGTAGAGTATGAATCATTACATCCTTAAATAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGGAGCAATGGAATGTACTTATTTTATATCTTAT

WI-3292b	106	G A ---	---	---	GTTTGTGCTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACCTCATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCT[G/A]TGGTATGGATGGGATGGATTACTT GCCATGAATATTTCCATTGTTCTCATTAAATGATTAAATTAAGTAAATATTTATTTNCCATGA GACACAATGGAAAAATGGAAACATTTCATGGAAAAAACCCCATTTCAATC
WI-3292	106	G A ---	---	---	GTTTGTGCTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACCTCATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCT[G/A]TGGTATGGATGGGATGGATTACTT GCCATGAATATTTCCATTGTTCTCATTAAATGATTAAATTAAGTAAATATTTATTTNCCATGA GACACAATGGAAAAATGGAAACATTTCATGGAAAAAACCCCATTTCAATC
WI-3355	19	G C ---	---	---	CCATGAACCATGGGCTACA[G/C]ATATTCTCTAACTTCAGAGTCCCTCTTACTGGAGAGGGATCCA CTTTTAAAATATGATTTCTTGAAGTGGCTGCATACCTATTCCTCCAGCACTTAAACCTCATCAGAA AAAAAATCATCAAAAAGTCGAAGTTAGTTTNNATTTACCTCACCTTTTCAATGGAAACCTTTTATAA ACTGTGGATCAATTTATATTACTTTTGGATCAGTTTAGATGACTTTNAGTTG
WI-3408	194	G A ---	---	---	CCATGAAGAATGAGTTCCTCCCTCCCTGGGTACGTC TAAGAATAGCACACCTTGAGAAATTNACT TAGCACGTGGCATTGTAATGGCTGGATTTCCTCCGCTCTAAGACACACCTTTATGCTTTTCAAGCTTT CTGGAATTGGGATGAATCTNACATTCAATGTGCACCTTCGTGTGGGATCAGTCTCTCC[G/A]TGCCTCC ATCTCTGNAGAAGCCACTGGGAAGTCGAAGGAGTGACTTCAAAATCAGG
WI-3505b	131	G A ---	---	---	TAACTTATGCCTCATCTGGCTTACTGCTTAGTTCCTTAGTTCCTCATCAGTGCACCTTAAAAATTTATTT GAAAAATTGCCATTTTAAATATCTTTGGAACCTTCTTAACACACATTACCTATTTTNAACCAAAC[G/A] AGGTGATTCCTTATGGGAAAAATATATACAGCAAGAAAAAANANGGAAAAATGTTGATGATACCT GTTTAAATTGGGAAATATGTTTGCATAT
WI-3505	131	G A ---	---	---	TAACTTATGCCTCATCTGGCTTACTGCTTAGTTCCTTAGTTCCTCATCAGTGCACCTTAAAAATTTATTT GAAAAATTGCCATTTTAAATATCTTTGGAACCTTCTTAACACACATTACCTATTTTNAACCAAAC[G/A] AGGTGATTCCTTATGGGAAAAATATATACAGCAAGAAAAAANANGGAAAAATGTTGATGATACCT GTTTAAATTGGGAAATATGTTTGCATAT
WI-3564b	177	C T ---	---	---	GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGAGTCACTAAATGTTTGGAGAAATAAAAGT GAAATCAATGTGCTTCCAGTGTATTACATGGCAGAGTGTACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACGTGGTTGACTAACGTTAACATGCATGTCTGTTC[CT]AACAAAGTGTGTGTGGTGTGCATC AGTGTACACATGCTACCTTCTTCCACAAAAACAAA
WI-3564	177	C T ---	---	---	GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGAGTCACTAAATGTTTGGAGAAATAAAAGT GAAATCAATGTGCTTCCAGTGTATTACATGGCAGAGTGTACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACGTGGTTGACTAACGTTAACATGCATGTCTGTTC[CT]AACAAAGTGTGTGTGGTGTGCATC AGTGTACACATGCTACCTTCTTCCACAAAAACAAA



WI-3649	64 A G ---				AATGTCCATGCTGTGACTGACCTGTCTAACACCTTTCCCTAGTATTCCTTTAGTGAAGATTTCAC[AG] AGACCAGTTTGCCTTCACTTAGTAGGGCCAAATGATAGACTTTTTAGGTGCTACCACAAGGGTACCTGCG ACAGCCACATCAATGTACAGTATGGTTGCAAGGACCTGCTAGACTCTTTCTGCCTGCCTTGGTC TTCTGTTTTACCATTAATGATGACATGCAAAACCTCAGAGCCTTTTA
WI-3674b	133 G C ---				ACAGTACACATGGCCCCATTATGGAACAATCATCTGACTTATGTTACCTGAGAAAGTTCCCTCTCTAA ATTTAACTACCAGGGGAGTCTTTTATAGTAATTAATAATGTTTATTTAGAAAATAACAAAAT[G /CJAAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAAAATTGTAACCTGGTCAAATGATTGTT AATCTTAATTAATTGTTTATGTTTATGTTTATGTTTACTGCCAATCACAGCCAAG
WI-3674	133 G C ---				ACAGTACACATGGCCCCATTATGGAACAATCATCTGACTTATGTTACCTGAGAAAGTTCCCTCTCTAA ATTTAACTACCAGGGGAGTCTTTTATAGTAATTAATAATGTTTATTTAGAAAATAACAAAAT[G /CJAAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAAAATTGTAACCTGGTCAAATGATTGTT AATCTTAATTAATTGTTTATGTTTATGTTTATGTTTACTGCCAATCACAGCCAAG
WI-3682	137 G A ---				CAATATAGACCAATGACTGCCACAAGAGAAATTAGTGGATCTACATTTAGAAACCACATGTTTT ATTGGCTTCTCTCTCTCTCTCTTTTAAATGCTCTCCAACACCAATTCACTTTATCTTTTCAA T[G/A]AGCAATTTGTCCAATTTAAAGTCAATGAAAAATAATGTACATTTTTCAACAAGTATACATTAA GCCTGCAAAAGTCTTATATGCTAT
WI-3854b	194 G A ---				GGTATGTTGAGGTCAGCTAATGGTCAGTGGTTGGAGTGAATCTAAATGGATTTTTGGCCCTTGA CAAAAGACCAAGGACAACTGTAGGACTTCTGCATGGTCTACCTCACTTAGGCTTCTTGATTAAATACTC TGGTTCAGGAAGGCAAGGGCAGTTATGACCACCTTACAACTGAGGAAATCAAAGCAAC[G/A]AGAA GTTAAATGGCCTGTCCCACTCCACAGAAATGGTTATAACAGATCAGAGCCA
WI-3854	194 G A ---				GGTATGTTGAGGTCAGCTAATGGTCAGTGGTTGGAGTGAATCTAAATGGATTTTTGGCCCTTGA CAAAAGACCAAGGACAACTGTAGGACTTCTGCATGGTCTACCTCACTTAGGCTTCTTGATTAAATACTC TGGTTCAGGAAGGCAAGGGCAGTTATGACCACCTTACAACTGAGGAAATCAAAGCAAC[G/A]AGAA GTTAAATGGCCTGTCCCACTCCACAGAAATGGTTATAACAGATCAGAGCCA
WI-4039	210 G A ---				AGCCAGCCACATCATGTTGAGTCTGCTCATCTTCCATCTTATTTCTCTACTGCGCTTCACTT CCATTAAACAAAGAACTCTTGTGATTACATTTGATGTTTGGTTACACTACAGAAATCCAAGATGACCTC CCCATCTCAAGGTCAACTAAATTAACACCTTAATCTCTATTGCAATCTTTGTCAATTACCATATTT CATGG[G/A]TCTGGGATAAGGGGTAGACATTTTATGGAGGCATTA
WI-4110b	130 T C ---				GAAAAATGATGTTTTGATTTCCCTTCCCTATCTTCAGATTATGGAGTGTCATTAGAAAACTGATAGT AACCTTTTATTGATGAAACTCTGCTATAATTAACCTTCCCTCTCTCTCTTTTATTTTGGCTTC/JACA GTTTAGGTAATAAAGATGCCAAGAAATTCAGTATTCAGGTACAGTAAAAAGTAGCAACCATGGG GTAGGACAAGTNCAGAAAAAGGGAGGAGGTNGGGGGGTTTTCTCGGGAAGA

WI-4110	130	T C ---			GAAAAATGATGTTTTGATTTCCCTCCTATCTTCAGATTATGGAGTGTCAATAGAAAACTGATAGT AACCTTTTATTTGATGAAACTCTGTCTATAATTAACCTTCCTCTCTCCGCTTTATTTGCGTTC/JACA GTTTAGGTAATAAAGATGCCCAAGAAATTCAGTATTCAGTACAGTAAAGTAGCAACCATGGG GTAGGACAAAGTNCAGAAAAAGGAGAGGTTGGGGGTTTCTGGGAAGA
WI-4119b	168	G A ---			ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGCTTGGGTGGGAAAAAGTAATAATAG AATGGAAGGATAAATAAGGTAACTACGGGGAAGAACAGGACAAGAACAGACAGAAAGGGGTT AGAGGAAGGAATCAGTTGTGCGCAATCAAAAGTTAA[G/A]CAAGGTACCAAAATTTGTTTCTTTCA TGAGACCGTCTGCAATCTTTGTTTTTAAAGGCTCTGTGATCATCATCTCA
WI-4119	168	G A ---			ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGCTTGGGTGGGAAAAAGTAATAATAG AATGGAAGGATAAATAAGGTAACTACGGGGAAGAACAGGACAAGAACAGACAGAAAGGGGTT AGAGGAAGGAATCAGTTGTGCGCAATCAAAAGTTAA[G/A]CAAGGTACCAAAATTTGTTTCTTTCA TGAGACCGTCTGCAATCTTTGTTTTTAAAGGCTCTGTGATCATCATCTCA
WI-4123b	51	T G ---			CAAAGTCAGATTTTGATTATTCAGGATAACAATTTTGAATAAGAAAGTG[G/J]TTAAACTATTT CAAATAAAACAATAAAGAAAAACATGATGAAATCTTCGTACATAATTGTATAGAATTTAGTGGG TTCTCCATGACATGGCTTGTCTTCTCAACAGTGGGTGGTTGGATGTTTCCATGCTTTCTC AGGCACAAACACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTG
WI-4123	51	T G ---			CAAAGTCAGATTTTGATTATTCAGGATAACAATTTTGAATAAGAAAGTG[G/J]TTAAACTATTT CAAATAAAACAATAAAGAAAAACATGATGAAATCTTCGTACATAATTGTATAGAATTTAGTGGG TTCTCCATGACATGGCTTGTCTTCTCAACAGTGGGTGGTTGGATGTTTCCATGCTTTCTC AGGCACAAACACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTG
WI-4149b	145	G C ---			TTGTACATGTTTCATTCATCCCTCCCATTTCTTTCTGCTTATAAGAAACCTCGCTTCTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTTTATTTCCATCAAGCTTCTCAGCATCTTCTATATACT GTGCTG[G/C]CTTGTGAAGAGCCAGAGCCGAGCATACCAACATGATCTTTGCTTGAACGTAGT AGGAGAGACAAGACAGATGTGGGGTCCCCATGATATAAGGTAATTG
WI-4149a	137	T C ---			TTGTACATGTTTCATTCATCCCTCCCATTTCTTTCTGCTTATAAGAAACCTCGCTTCTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTTTATTTCCATCAAGCTTCTCAGCATCTTCTATATACT T/CJGTGCTGCTTGTGAAGAGCCAGAGCCGAGCATACCAACATGATCTTTGCTTGAACGTAG TAGGAGAGACAAGACAGATGTGGGGTCCCCATGATATAAGGTAATTG
WI-4182	188	G A ---			TAACACACTTTTCATTTGGTTTCTTATTAAGGAGTAAAGGAGGACCATCCATTATTAACAATCCCTC AGTTCTATGCTTTAGAGTNCATATAGGACTACTGTAAATTTTCAGAGGGAATTAATCTCTGGAGTA GGGGAATGAGTTAAATAATCTACCACATGCCAATTCAGGAGTGTGGTTAA[G/A]ATGTCCTCTCT TGCCCCCTTCCCAAGTCTTAAATTCCTAG

WI-4230	93 T	---	---	---	AGAGACGTTGAATGGGGACATCTTTCTATTTCGATTTTAGTTTAACATTTGATAAGAATTGATGAAA GTTTGTCACATCCAGATTTATCTTTATAGCAGCAGAAAGTCTGGCAATATAACAGCACACTGACT TTTCCATGGTAAAGAGATTAGAGAAAAACAGCCTATTTTCTTAATGTTAAATGTAATCTGAAAT ACATTTAAATGGAGGAGAAATAGTGACCTTTGAAATTTTGAATTTATGG
WI-4241	118 C	---	---	---	GAAATTCATTTGAAGTTTGGACCTTGAACCTGATCTCATTAATCTTTNCCTGTAGTGGTTGATTT CATTTTGACAACAGAACAGACGAAAAATTTCCACTTAAATTTAAATCTC[CT]AAGTATCTATGAT TTAGCACTGTTAGCACCCAGAAACTGTGAAATTAATCTCCTAGATATCTTCAGAACTAGGATGGAAG AA
WI-4271b	151 A	---	---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGGAGCCCCAACCCCTCCCTCTCTCAGG CTCTTAGAAGGTCCAGTCAGGGGC
WI-4271	151 A	---	---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGGAGCCCCAACCCCTCCCTCTCTCAGG CTCTTAGAAGGTCCAGTCAGGGGC
WI-4389b	156 GA	---	---	---	AATCGAAACATTTGATTTTGTAAAGGAACCATTTATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAGAAAGGATATTATTGCATAACCTTTGGA AGGTAAGATGTGAACCTATACA[G/A]JINGCAAGGAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4389	156 GA	---	---	---	AATCGAAACATTTGATTTTGTAAAGGAACCATTTATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAGAAAGGATATTATTGCATAACCTTTGGA AGGTAAGATGTGAACCTATACA[G/A]JINGCAAGGAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4488	31 A	---	---	---	GATGACAAATTTATGTGATTGGCATTTTAAAG[G/G]TACCATTCCATTTCTCTGGCTTTCGTGTGTT TGTTGTTGAGAAGTCAGGGGTAGTCGTATTGCTCTTTCTAGTTCTCTCAGTAGGAAGACTGATC CTAAACAACTTAATTACCCATGCCAAAGTACGTCCAAACTGATCTTTAAAGAACATAAATCAAAATTG TATTATCCTATGCTTAAATGCTCAG
WI-4491	145 GC	---	---	---	ACCATCAATGTATCACCTTCTAAAAATTTATAGATGATTAACCTGGCTCTGTTAAAAAATAAAAAACCT GTCTTGGACATTTGAAAAATAAAACATTAATTTGGTCATTTTCTGCTACTTACAAAGGTACTGCACTA AACAAAGTTAAG[G/C]GTTTTTGGAGGGGAAAAATCATAAAAATGCATAAAAAATTTCTACCACCTGTC TTTCTTGTCCCATAAATAAAATTTTACATGCCT

WI-4584	144	A G	---		TTGGTTGGCATTAGCCCTCATAACAACATATTTACAATCATAAATTTGTTACTCTTATTTTACAAAACAG AAAATGAGGCTTAACATCACACTTCTGCTTAGTCGAGAGCCAGATTTGAACCCAGGAATCCATT CACCGGTACAGTGGCTACCTGGGTAAAAATGTTTAAATTAATAATCTATGGCATTAGATTTCAAAGA GTCTTAATGTGGTTTGAATAAGGTGGCTTTAAATTTTATCAGTATGC
WI-4639	185	C T	---		TTTCTGCATTGAATGTATGTGTCAGACTTCAGAGAACCCAGGAATCTCATTTATTCAGTACAATA TGGTGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACTTTCCAAATCCACCATTTAC TGACCATATGACTTGGGAACATTATCTCACCTATCTGAGTCTGTATCQCTCATCTTTAAATTTGTA AATTTTAAAGACACCTATCATAGTAATTTGTGAGGATAAAATGAAATAA
WI-5327	63	A	---		AAATGAATCCGCTTTAGAGCAAATACCAGTAAGGGCTGGTGCAGGATGGTGGTGGCTGAGAGA/- JGATTACTCATAAAGCATATTAATTTTAAATATGGAATAATTAAC TAGATAATTAATTAATGTGAAT TGAGTTTGAAGGTGCATGAGAGTAGGGAGGAGGTAGTTTCTACTTATAGGGTTTATATAAGTNTGCT TCAATAGATGGCTCTTCGGATGACATGATGAACCTGTTCTAAGCAGACAG
WI-5390	87	C T	---		GCCTTGAGAAATGAAAGGGAGCCTGGACCATTGCAGGGCTTCTCATCTCTGATTATTTTGTGTAT TTATTGTTCACTTATTTATCTGCTGCTCCCTCTGGTATGCTGTGCATGAAACAAATGAATTC CCAGTGCCTGGCCGATCTGGCTCCTAGAGGTGTCAGAAAAAGTTTCGGTGAATAGAAATG ACGAATGGTTCAGAAATGAACTGTGAATCTATGGAAGACAAACGAAT
WI-5404b	87	G A	---		CCCTGCCTGCTTATGCATAATGAGAAATAGAGTTGACTCTCTGCAAGAAATCAATTTAAGCAGT GCAACATATTTTAAATTTGAAAGAACTTTGTTCTGAAACTTTGTACTCTTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTGGTGAATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTATAGAGTTCAACAA
WI-5404	87	G A	---		CCTTGCCTGCTTATGCATAATGAGAAATAGAGTTGACTCTCTGCAAGAAATCAATTTAAGCAGT GCAACATATTTTAAATTTGAAAGAACTTTGTTCTGAAACTTTGTACTCTTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTGGTGAATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTATAGAGTTCAACAA
WI-5545b	77	A C	---		TAGGAAAGGGGATGGTATGGCTCTGAGACATTTAAATCTATCTTCCACACTCACACTGCCGCCA TATCTCTCTG/CJCCAACACCTCTGTTTCTGACAGCCAAAGTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACTCCAAAAAGANTC GAGATACCCATGAATTTTATTTTCAATTTCA
WI-5545	77	A C	---		TAGGAAAGGGGATGGTATGGCTCTGAGACATTTAAATCTATCTTCCACACTCACACTGCCGCCA TATCTCTCTG/CJCCAACACCTCTGTTTCTGACAGCCAAAGTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACTCCAAAAAGANTC GAGATACCCATGAATTTTATTTTCAATTTCA

WI-5860b	134	A G	---	---	ACTCAAGTTTGGGGATAAAATCAGAAGTTTCTATGTACAACTTAAATTTTCTAAGATTTTATTGT TTCTTTTATATAAATTATGGATTGTTTACITTCCTTAACCAACCTTCTAAGTGAAGAACTACIA/ GJTATACTGGAATCATGTGAAGACATCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTCCAAATCATCAACTTCTGTAT
WI-5860	134	A G	---	---	ACTCAAGTTTGGGGATAAAATCAGAAGTTTCTATGTACAACTTAAATTTTCTAAGATTTTATTGT TTCTTTTATATAAATTATGGATTGTTTACITTCCTTAACCAACCTTCTAAGTGAAGAACTACIA/ GJTATACTGGAATCATGTGAAGACATCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTCCAAATCATCAACTTCTGTAT
WI-6106	208	C G	---	---	GCAACAACCTATTATACCTGATCCAACCCAGGTCTACTAACATTAATCAACCCCTAACCAATAC TATATATTGCTCTGTTCTGAATTAATTTCAITTAGAATCTGATGAGATTTAGCATGGGATAAGTGCAG TGCAGAGATAGTAACACTGCTCTTTTGTCTCCAGGAGTCTCAATGTGAAGTATAATTTCTACAGAG TAATTTC/GJATAGTAGGTGACCAACAAAGTCTATATTGTATGTGAAGGAAAG
WI-6109d	129	T C	---	---	AAGTAGACAAACATATGCCAGACCAACAAACACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTTC/ AAACCTATATTNCTGCTTGTGCTACTTTAAATGTATAATGTGGGAGAGAAAGAAATTTTGATGT GNAAAATTATCCCTGAAAAATTTTATACCA
WI-6109c	147	T C	---	---	AAGTAGACAAACATATGCCAGACCAACAAACACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTAA ACCCTATATTNCTGTC/CJCTGTGCTACTTTAAATGTATAATGTGGGAGAGAAAGAAATTTTGATG TGNAAAATTATCCCTGAAAAATTTTATACCA
WI-6109b	147	T C	---	---	AAGTAGACAAACATATGCCAGACCAACAAACACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTTC/ AAACCTATATTNCTGCTTGTGCTACTTTAAATGTATAATGTGGGAGAGAAAGAAATTTTGATGT GNAAAATTATCCCTGAAAAATTTTATACCA
WI-6109a	129	T C	---	---	AATGCCTATCACCTTCCATCATGCTGCATAACTGATTGATTCATAATGCTTATTGTTAGCACCTGTC TTCCACACATGCTGTTTTGTTCAATGATTC/GCATATCCCAAGTGCCTTAGACAATGCCCTCCCATAC AGTGAACAGTATTGACTAAACACATACCTTGTAAATCAATAAATAATCAACTTGGCATATGCAGG GAAC
WI-6112	96	T C	---	---	

WI-6244	103	T C	---	---	TAATTGCACAACCTTACATATCAGGGTTCTGATTGAAAGGAAGAGAATATTCCTTTCTTTAGTGATT GCTTAATATTAATTCATAATAAGTGCACCCTCTCTTCGCTCCTTATAAATGTGTTTGAAGAAGG AAATTGAGTGTGGGAATTAGCAACAGGAGACATTTTATATACTCTACAGTGGGGGAAGACTT CCTATTTCTTCCCAAGGATGGATACATTCTAC
WI-6268	124	C T	---	---	CTGGCCTTATAATCCAAGTTTAGGATTAATCTACCCCACTTAATAGACTTCAGACAGTTCGACGTT GTCTACAAGATTTCTCTAGTAGGGCTTTGGGTGTGGCACCCTTTGGCTCATTCCTCTCTCTCCCT GGGTCTTATGACTTTCAGGGAGCCTAGAAGAGCTGGACAAAACCTGCTCTTTGCGAGAAAGAGTCG GGGTCCCAAGATTCGTTACGATTTTGA
WI-6336b	234	C T	---	---	AGGTGCCATTAAATCCATTCAAAATTTGGAAGCTACATCTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATCCCCCTTTACATGTTTCTTATAAGACATACAGTTTAATCAATTAAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCCAAGTGCATTATGTCCTGGTAGAGCCCTTTGAGGACACTGACAGT
WI-6336	234	C T	---	---	AGGTGCCATTAAATCCATTCAAAATTTGGAAGCTACATCTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATCCCCCTTTACATGTTTCTTATAAGACATACAGTTTAATCAATTAAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCCAAGTGCATTATGTCCTGGTAGAGCCCTTTGAGGACACTGACAGT
WI-6381	92	C A	---	---	TTGGATACAAAAATTCAGTTACACAATCAGTAGCATTCAAAATTTAGTTATGATGATTATACAATTA CAAAAATGGNTTCATGTTTAAACA[C/A]GTATTTTAAAGCTCAAACTTTTAAACAGGCACAAT ATTCTAANGGCATATGCATTCACCATGGGCTTTTGAATGTCTCACTCCCAACTTCACAATCAAAATC TACAGANGGGCAAAAGATCAGAGTTTCAAG
WI-6436	198	C G	---	---	GGTTGAGGCATTGGGAAAGGCAAAATTTGAGGCAGTAGAAAATGGACATTTTAGGAAAAGAGAAGT TCAGAGGCAAGTGCATGACAGACAGGAAATACAAAGGCTTAGGAAGACAGTAGTCTGTGGTTGAA ATTTGGTGTCAATAAAGAAGTTAGACTTTGGGTGTAGTAGTTGTAGTAGGAGGAGCGTT[C/
WI-6449	186	C T	---	---	GTATGGCTAGTGTGTTCTGATTGGTGGTGCCTCACACTGCCAGATGTTAAATATTTTGAATAATC GTATCTGGTCTATTTCATCTGCACTCTGATCTTATGTCGGCTCTATT[C/TA]TCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTTCCTTAATTTTCTGTGGGTGATTTATA
WI-6449	186	C T	---	---	GAGGCCTCTTGTCTTTCCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTCTGATTGGTGGTGCCTCACACTGCCAGATGTTAAATATTTTGAATAATC GTATCTGGTCTATTTCATCTGCACTCTGATCTTATGTCGGCTCTATT[C/TA]TCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTTCCTTAATTTTCTGTGGGTGATTTATA

-127-

WI-6463	72 T C ---	---		GCTGGAGAGAAAGACCTCCAAAAGAGAAACTAAATCAGAGTCTCTTGAGCAAGAGGAATTGAAAGAACAT/CJTGAATAAAATTAAGGTAGAACTCAAGAGAGCCAAAAGTCCCCAAATTGTGTCATTATAAGAAATATTTTGAATGGAATCTTAAGAATGATTTTATTGATCAGTTAAATGTTCTTCCTCCTCCTCAGTCCCATTTATATGACATTCGCATCGCTG
WI-6474b	76 C T ---	---		AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGGTAATGTTATAGAAACTTTCAGAGGANACAGAGGCAA/CJTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCCAGAAAAAGTAGGATTTGAAAGGCACAGAGAAAAGGGGTGTAAGAGGAACTATGTAAAGCAGAGGTATAGAGGAACATAAGTATAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6474	76 C T ---	---		AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGGTAATGTTATAGAAACTTTCAGAGGANACAGAGGCAA/CJTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCCAGAAAAAGTAGGATTTGAAAGGCACAGAGAAAAGGGGTGTAAGAGGAACTATGTAAAGCAGAGGTATAGAGGAACATAAGTATAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6478b	175 T A ---	---		GAACTCAATTAACCTTTCACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTGAGATTGGAGCCTTGGTATCCAAATGGGGAATGCCAGCTTCGAGGCCGTGCTATATGCTTTATTTTGTGACACTGTCTATTTACCTCCCAATAGTGGAGAAATCAGAGT/AJGCTCCTTGTCAGTGTGCTACAGAGAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6478	175 T A ---	---		GAACTCAATTAACCTTTCACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTGAGATTGGAGCCTTGGTATCCAAATGGGGAATGCCAGCTTCGAGGCCGTGCTATATGCTTTATTTTGTGACACTGTCTATTTACCTCCCAATAGTGGAGAAATCAGAGT/AJGCTCCTTGTCAGTGTGCTACAGAGAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6559	149 G A ---	---		CACATTTGAATGCAACTGAGAAANTGGTTTNTAGGCCTACCTTTTATTTAAGAGTACATCTGGCTCCAATGTTACCCCAACATGCAAAACATAAGGCAACAATCTGATCATTTTATAGGNTCCCAAGCCCCATAGCAATATCTTA/GAJTCAAAATTTTAAAGAGAGAACAGGAAATAAGGAAGGCCCTAACAGAGGAGTTAAATAATTGTGCAAAACTTATCAGTCTCTC
WI-6564b	54 G A ---	---		TTCTTTATTTGGTCTACCAATGTGACTCTTTACCCAGGCCACTGTTCCTATGC/GAJCACTGGCTTTGTAGGCATTCACATCATATGCTGTGCTGCTGAAATCTCAATTAATTTCTCCTNCCTATTCCTTTTCCATGCTCTGCCCTCATTTNCTCAGAAATGAAGGCATTTGATTATNATTTTTTTGTTGGGCTGTGTAAAGGTTCTTTGGCAGGAGAACATGCATATGACTTTTAAATAAGACCAACA
WI-6564	54 G A ---	---		TTCTTTATTTGGTCTACCAATGTGACTCTTTACCCAGGCCACTGTTCCTATGC/GAJCACTGGCTTTGTAGGCATTCACATCATATGCTGTGCTGCTGAAATCTCAATTAATTTCTCCTNCCTATTCCTTTTCCATGCTCTGCCCTCATTTNCTCAGAAATGAAGGCATTTGATTATNATTTTTTTGTTGGGCTGTGTAAAGGTTCTTTGGCAGGAGAACATGCATATGACTTTTAAATAAGACCAACA

WI-6608b	46 C ---	---	---	CTAATCACAGTAGCACGTAACATGGCTCTAGTGAGTGGGCGCTCAGT[C/- JAGTTCAGGCAGCTAAAGGGAGGGGATTCCTCTAGTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGTATTTTCTAGAGGAAAAAGAACTCCAGCACTAG GTAAACTGCAAAAGAAAAACACCTGTGCCAGGCACCTAGCTACAAGGCCACACAGAAAAAGGAA AGC
WI-6608	46 C ---	---	---	CTAATCACAGTAGCACGTAACATGGCTCTAGTGAGTGGGCGCTCAGT[C/- JAGTTCAGGCAGCTAAAGGGAGGGGATTCCTCTAGTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGTATTTTCTAGAGGAAAAAGAACTCCAGCACTAG GTAAACTGCAAAAGAAAAACACCTGTGCCAGGCACCTAGCTACAAGGCCACACAGAAAAAGGAA AGC
WI-6666	68 C A ---	---	---	GTTAGACAGTATCCAGCAAAAAAGGTTATTTTATACCTCTACCTTTCCAAAACGAGGAAACCTCCCC A[C/A]AAATCCCATCAACACACAGTCATGCTGGAAGGCATTCTGCTTACTCTGTTGGTTTCATGTAA ATGTTGGGGTGACTCATTCGCCCTCTCTNTTCTCAAGTTCAGGCTCTTGGGTAGACCAAAACTA ATACACAATGTTAGAGCACACAAGAGA
WI-6670b	120 A G ---	---	---	AGATTAAACATAATTACTGGGGCCATTGTAGGGTTNGGAGGAGTGTTTTCTATCTGCAGCCAAA CAGAAATACGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTTAGCCA GCATTGCCATTTCAGGGCCGGAGTCAGGGTTTGTGGGCCAGAAAGTTAGACAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAAATTGTAACACAGACACAGAAATCTTAGAAGGGAT
WI-6670	120 A G ---	---	---	AGATTAAACATAATTACTGGGGCCATTGTAGGGTTNGGAGGAGTGTTTTCTATCTGCAGCCAAA CAGAAATACGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTTAGCCA GCATTGCCATTTCAGGGCCGGAGTCAGGGTTTGTGGGCCAGAAAGTTAGACAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAAATTGTAACACAGACACAGAAATCTTAGAAGGGAT
WI-6704c	33 T C ---	---	---	TTTGAATAATAATTTCATGCACCAATGTTTTAACT[C/C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAACGTTTACAAATAAGTTTTTCATGACACACCGNCA CTATTGCTCTTTAAATATGTTGTACATGTCATCATTAATCGATTTCATTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAGATAGGCAGACATG
WI-6704b	33 T C ---	---	---	TTTGAATAATAATTTCATGCACCAATGTTTTAACT[C/C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAACGTTTACAAATAAGTTTTTCATGACACACCGNCA CTATTGCTCTTTAAATATGTTGTACATGTCATCATTAATCGATTTCATTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAGATAGGCAGACATG
WI-6704	28 T C ---	---	---	TTTGAATAATAATTTCATGCACCAATGTTTTAACT[C/C]AACATACATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAACGTTTACAAATAAGTTTTTCATGACACACCGNCA CTATTGCTCTTTAAATATGTTGTACATGTCATCATTAATCGATTTCATTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAGATAGGCAGACATG



WI-6710	106	G A ---	---	COATGGACAGTTTAATTAGGAAGCTTCGACTTGTTAGAATAACAGAGGAAGTCCAGTTATCTACCT ATTCTTTAAACACACATTTTGTGAGGCTGGAATGATCC[G]ATAGTAAACCTCAACATCCACACCT GCATAAACATCGCTCCCAAGTGACTATTTACTGAGTCGACACAGGATGCCACGAGTGAGCCTC ATCTCCAGTCCAATGGAGAGTTGACTAGACCTTCCTTGGACAGGAAGGGTC
WI-6766b	148	G C ---	---	AAAACAAATGGTGCATTGCATAATATTTGTGGTCACAGTATAAAACAATACAAATTAGTTCATATAAC ATTGGATATGGACAAAAATACACANGATCCTTCTTGTCTACGGAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G]CJAAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAAACAGTGGAGNGAACITACCCAAATCCCGATCCCTCTTC
WI-6766	148	G C ---	---	AAAACAAATGGTGCATTGCATAATATTTGTGGTCACAGTATAAAACAATACAAATTAGTTCATATAAC ATTGGATATGGACAAAAATACACANGATCCTTCTTGTCTACGGAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G]CJAAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAAACAGTGGAGNGAACITACCCAAATCCCGATCCCTCTTC
WI-6787b	97	A G ---	---	ACAGATAAAAGTCTTTATCCCTGTATGTTACATAAGAAAGTCTTTACAGACTTTTTTTTATACA ATACCTGTGCAGCAATGTTCAAATTCAC[G]ATTTTACTGCATAAGATATCTTCATGTACAACCTGT ATGCTTTGTCTCTTGGGAAGGACGCGTTAAAGACCTATGATAAACACACATCCACATGACAAAAGGA GAGTCAATAGGCGACAGTAGANTACTCACAGGAAAGAGTAAATTCCAGTT
WI-6793	105	C G ---	---	GAACCCACCAGGTCCTGTTATTTTAAAGGAGCATTTACATTATGATAGCAAGTTTCAACACATTCA TCAACAAGGCGGCTTCAATCAATCAATCAGTCAACCCCG[G]GAGTTAGAAGTAGAGTCATGAGGAA GAGCTGCTGGCTGTAGGAAGTAGGTTAATGCCCTCTAATCCCGTAAATCCCGGAAAGGGCAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACAGTTTCTCATCACAGGTAAAAAGGCAAC
WI-6810b	37	T C ---	---	CACAATAATAAATCACTCCCTACCTTGAACCTTTAT/CJAGAAGCATTTTAAATTTTACAACACA AAGCTCAACGNACCTACAATAAGTCTAGTAGTCTGTTACGNGCCAGGATAAGGCTGAACAATA AATTAAACCTTTAAATGTCTATGNACAAGTACAATTTCTTTTGGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
WI-6810	37	T C ---	---	CACAATAATAAATCACTCCCTACCTTGAACCTTTAT/CJAGAAGCATTTTAAATTTTACAACACA AAGCTCAACGNACCTACAATAAGTCTAGTAGTCTGTTACGNGCCAGGATAAGGCTGAACAATA AATTAAACCTTTAAATGTCTATGNACAAGTACAATTTCTTTTGGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
WI-6817b	145	C A ---	---	GCATGATTAAACCAGTGCAGAAAAATACCAAGTACATTTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGTCTTTTGTAAATCCAGTTAAGACCATCAGCATATACAACATCACTCACTCAACAATGTAGCT GCAGGTAAC[C]ATJGTGGATACCTGTGTGCTCTACTNGCCTCCAAAGGCAATCAGGGGATCATCA AAGATGTTGGACACCTTGTTCAATCTTGTTTCAGGTCGGGCTGTGCAG

WI-6817	145	C A ---	---	GCATGATTAACACAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACATCATCATCACTCACTCAACAATGTAGCT GCAGGGTAACG/AJGTGGATACCGTGTGCTCTACTNGCCTCCAAAGGCATTCAGGGGATCATCA AAGATGTTGGACACCTTGTTCAAATCTTGTTACAGTGGCGCTGTGCAG
WI-6819b	221	C ---	---	GATGGAAGCCATTTATTTTCTCTAAATTTTAAATAGAGACTTTAATGGAAACATTTTAGTAC CATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCGCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGTGCTTCAACAGTTTTCATATACAAAATTTTCTGCTATTTG CTTAGCAAAACAGCAATAACTTTTGTTTCTTATATGACACCTAATATCCAG
WI-6819a	175	G T ---	---	GATGGAAGCCATTTATTTTCTCTAAATTTTAAATAGAGACTTTAATGGAAACATTTTAGTAC CATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCGCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGTGCTTCAACAGTTTTCATATACAAAATTTTCTGCTATTT TTGCTTTAGCAAAACAGCAATAACTTTTGTTTCTTATATGACACCTAATAT
WI-6826b	154	A G ---	---	GCAAAAAGCTTTATGGCTCCAACAAATATCCCTTTTAAAACTCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTTTCAGATTTGCAGTTTATAGCATTTTTCCTAAGAACCATATAAATAC ATGCAAAACCTTTGTACAT/AJGAGCTTAAATATATCAAAATGCAAAATATAGATTGGTGCACGTG TAAGCTGAATTGCAAATATGGCAACACACACTGGACTGGGTATACGTTG
WI-6826	154	A G ---	---	GCAAAAAGCTTTATGGCTCCAACAAATATCCCTTTTAAAACTCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTTTCAGATTTGCAGTTTATAGCATTTTTCCTAAGAACCATATAAATAC ATGCAAAACCTTTGTACAT/AJGAGCTTAAATATATCAAAATGCAAAATATAGATTGGTGCACGTG TAAGCTGAATTGCAAATATGGCAACACACACTGGACTGGGTATACGTTG
WI-6857a	122	T C ---	---	AGTGCAAACTATTTGAACAAAAGTAACTATGAGTCACAGCATTCAGCAAGACATCAGACACGGA AGAGTGAACAATATTCACATAAGTAAATACAGCAGATGAGATGCTCTCACATGTAT/CJATTTAAT TATTCATGCTTTTCAATAGTCTTGTAGTCAACTTTCAGTAAATTTCCACAAATATATAGCAGCTCA AACACAAATGCAGGAGCACAAATGGCAAAGTTTGGCACTGTTTGGGCTAAT
WI-6865	153	G A ---	---	TTATAGAATACTTATGGGCATACNGTAAATGAACGTCAACCTTAAATCTAAACAACAGCTTG TTTGTTGTTCTGCTGAAATCCCTGCTCAAAAACAGCAGCTACTNGGTTTCTTAAAGACGTA ATTTGCAAGGCAAACTTCG/AJTAGAGCCATTCGTGCAAGAAAGGGAAGGAGAGCTGTTTGT TTACCTGTAGTATGAAGATATCTTTGCGCTGTGTAGAACTGAGCTCATTA
WI-6909	73	C T ---	---	ATTGAAAACCTGGTTAGCAACAGATAAATTTACAATAGAGCTGGATATAAAAATGAGAGAAGATGC AGACTTA/CJTAGCTTATAGAGAAAGTCAAAAAGGAGCAAGTTTGTGAATCAGATTTTATGATAC GGAAAAAAATTTCTTTTGGCAACAGGATTTATTCGAATAAATCTGCCAGTGCCCAATCAG AAACACCATTTCCACAATATTTGCATGCCCTAGTTGCTTATTTATACATATC



WI-6996b	242	G T	---	AC TCTAGTGCCTCTGTTACCAACACCTCTAATGCCTCTGGTCGCCGCACTCTGATGTCGTAGGCCT TAAATCTGCCTGGCGTCCCTCCCTCTGCTTTCAGCACCCAGAGAGGAGAGAGCCGGCAGTTCCCTG CAGGAGAGAGAGGGGCTGCTGGACCCAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCCTGACT CTCTCCTGATGGTGGCCCTCTGTGCTCTCTCTCTCCGCTGCTGCGGATC
WI-6996	228	T G	---	AC TCTAGTGCCTCTGTTACCAACACCTCTAATGCCTCTGGTCGCCGCACTCTGATGTCGTAGGCCT TAAATCTGCCTGGCGTCCCTCCCTCTGCTTTCAGCACCCAGAGAGGAGAGAGCCGGCAGTTCCCTG CAGGAGAGAGAGGGGCTGCTGGACCCAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCCTGACT CTCTCCTGATGGTGGCCCTCTGTGCTCTCTCTCTCCGGTCCGATC
WI-7021b	112	G A	---	TGGGGAGGACAGGGAGATGCTGCAGTTCCAAAGAGAGGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGCTGAAGCCACAGACAATATGGTCCCAAATG/AJCCGACTGCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTCCGTTCCACATCCACACGCCAATCCAATTAATCAAACC ACTGTTATTACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7021	108	A G	---	TGGGGAGGACAGGGAGATGCTGCAGTTCCAAAGAGAGGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGCTGAAGCCACAGACAATATGGTCCCAAATG/AJCCGACTGCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTCCGTTCCACATCCACACGCCAATCCAATTAATCAAACC ACTGTTATTACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7056c	118	CT	---	GGCAGTAGACACCAAGTGTGGGTTCTGCTGGACCTTGGAGAGCCTGCATCCAGGATGCGGGTGG CCCTGCAGCCTCTCCACCTCACCTCCATGACAGCGCTAAACGTTGGTGA/CJGGTTGGAGCCTCT GGGGCTGTGAAGTCACCTTGTGTGTTCCAAAGTTTCCAAACAACAGAAAGTCATTCCTCTTTTAA ATGGTCTTAAGTTCACAGAGATGCCACATAAGGGGTTTGCCATTGATA
WI-7056b	118	CT	---	GGCAGTAGACACCAAGTGTGGGTTCTGCTGGACCTTGGAGAGCCTGCATCCAGGATGCGGGTGG CCCTGCAGCCTCTCCACCTCACCTCCATGACAGCGCTAAACGTTGGTGA/CJGGTTGGAGCCTCT GGGGCTGTGAAGTCACCTTGTGTGTTCCAAAGTTTCCAAACAACAGAAAGTCATTCCTCTTTTAA ATGGTCTTAAGTTCACAGAGATGCCACATAAGGGGTTTGCCATTGATA
WI-7091b	153	A C	---	AAATCGCTGAAAAGGAACCTACCTATCCCTTACATTTACACCTACTAATGTCTCTTAACATCTTAGAG GTCCATGGAGAGGCATATGGAGAACATGTTTATACCTGCTATAAATAGTATTCACATCACTGTG CTTAATTTAAATAGCATT/AJCTTATCATTTATCAGCCTTTTATGTTATTTCCAAAGTAAATATTA ACATATTATTCATTGGTCTCTCTTTTATCTGTTCTATATGAATGCTAT
WI-7091	153	A C	---	AAATCGCTGAAAAGGAACCTACCTATCCCTTACATTTACACCTACTAATGTCTCTTAACATCTTAGAG GTCCATGGAGAGGCATATGGAGAACATGTTTATACCTGCTATAAATAGTATTCACATCACTGTG CTTAATTTAAATAGCATT/AJCTTATCATTTATCAGCCTTTTATGTTATTTCCAAAGTAAATATTA ACATATTATTCATTGGTCTCTCTTTTATCTGTTCTATATGAATGCTAT

WI-7136	58 T C	---	TGTGAAGCCACATTTTCCAACATGAGCCTCATGAAGCCAACTAAGTGTATTGAAGCTGT/CJAATTC TCTCAATAACTCAGTGTAGCACITTTAAAGCTGAAGGACAGCAACATGAAAAGAGCATATCAATGTG GTGGAGAAAGGGAAGGGTTGGCTTTTAAATTTATTTTCTCATCTTTATAACAAGAAAGNNNN NNNGTAGCTTCTTATATATG
WI-7146c	210 A G	---	GGGAGCCCTGTTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTCCATTTTCGTTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTGCTCTCCTTGTGGCCCCAAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGGCTGTGGATGGAGGGGTCCCAACATGGATGTGTGGCCCTCTCTCGCATGCC AACGC/GJGTTCAATGTACAAGGCCCTCTGCAACTGGAGAGAAAATTA
WI-7146b	210 A G	---	GGGAGCCCTGTTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTCCATTTTCGTTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTGCTCTCCTTGTGGCCCCAAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGGCTGTGGATGGAGGGGTCCCAACATGGATGTGTGGCCCTCTCTCGCATGCC AACGC/GJGTTCAATGTACAAGGCCCTCTGCAACTGGAGAGAAAATTA
WI-7146	202 G A	---	GGGAGCCCTGTTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTCCATTTTCGTTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTGCTCTCCTTGTGGCCCCAAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGGCTGTGGATGGAGGGGTCCCAACATGGATGTGTGGCCCTCTCTCGCATGJA JCCAACGCAGTTCAATGTACAAGGCCCTCTGCAACTGGAGAGAAAATTA
WI-7153	161 A T	---	ATATTACAACTTGCTTTTAGCTGATCTCCATCCTCAAAATGACTCTTTTCTTTATATGTTAAACATA TATAAAATGGCAACTGATAGTCAATTTTGATTTTATTTCAGGAACATATCTGAAATCTGCTCAGAGCT ATGTGCATAGATGAAACNNNNNNNN/JTAAAAAAGTTATTTAACAGTAATCTATTTACTAATTAT AGTACCTATCTTTAAAGTATAGTACATTTACATATGTAATGGTAIGTTT
WI-7155	156 T G	---	TAGAAATAGATGCGGTCATATCTCTTTGGCTTCGTGTTCTCCAGCCCTCATGGTGGCATCACATAT GCCTGCATGCCATTAACACAGCTGGCCCTACCCCTATAATGATCTGTGCTCTGCTCTAAATTAATACAC CAGTGGTTCTCTCTCCCTGTGT/JTAAAAAGACTAATGCTCAGATGCTGTTTACGGGATATTTATATCTAG TCTCACTCTCTTGCCACCCCTCTCTCTCTCCCATCCCAACTCCAG
WI-7169b	161 A G	---	AGCTCCACACAGATGCAGATTTGTGTTTGTGTTTCTGTTATCACTGTCCACAGCTTAACATGTAT GCTTTTCAGAAATACAGTTGTCTAGCCAAAGCCATCAAGTGTCTGAAATCAATATGGTTTATGCAAA ACAGCAAACTTTTATTAAGTAGAT/JGJGGAGAAATATGTTTAAAAATTAAGGAATCCTAGACCATA TTTTCAAGTCACTTAGCAGCTAGGATTTCTCAAATGGGAAGTGTATATA
WI-7175b	194 C T	---	CTCCTAGACTAGTGCCTTACCCTTTTAAATGAAGTGTGACAGGAAGCCCAAGGCAGTGTCTCTACCA ATAACTTCAGAGAAGTCAGTTGGAGAAAAATGAAGAAAAAGGCTGGCTGAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAAAATATAAATGGTTTACTGCTGTCAATGTCCATGCCTA/CJTJAGAT AATTTATTTGATTTTGAATAAAAAACATTTGTACATTCCTGTACTGGG

[illegible]

WI-7216c	237	T C	---				TGACACTAACACTCTAAATTCAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGCTCTTCTCCCT AAGGACAAAATGTAGAAAGATGTAGATAACTTACTCAAGATTCCCTCCAGAAAATACGTATGT TTAAAACCCCTTCTGCTATACATAGGAAAAGACACACATCCACCTAAATTTGACTGTACTGTTAA CTGTCAATTCTCTGAGGCTAAACACAGTTGTTTTCCTTGTAAACACTT
WI-7216b	237	T C	---				TGACACTAACACTCTAAATTCAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGCTCTTCTCCCT AAGGACAAAATGTAGAAAGATGTAGATAACTTACTCAAGATTCCCTCCAGAAAATACGTATGT TTAAAACCCCTTCTGCTATACATAGGAAAAGACACACATCCACCTAAATTTGACTGTACTGTTAA CTGTCAATTCTCTGAGGCTAAACACAGTTGTTTTCCTTGTAAACACTT
WI-7220b	147	A T	---				AGGATGATGCTCCAAAAGGGGACCTTGAACCTATTACCATTTATTTGTCTCTTTAAGCTGGCAACCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAAATATCTTGGCACAGTGAATGACCTATCTCTGCAACATCTAATGGATCTCTA AAGGTAACAAACCCCTATAAAATCTGGCTTACTGCACATATTAGTGTTT
WI-7220	140	A T	---				AGGATGATGCTCCAAAAGGGGACCTTGAACCTATTACCATTTATTTGTCTCTTTAAGCTGGCAACCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAAATCTTGGCACAGTGAATGACCTATCTCTGCAACATCTAATGGATCTCTA AAGGTAACAAACCCCTATAAAATCTGGCTTACTGCACATATTAGTGTTT
WI-7226	232	C	---				GATCGAATTTTCAGATGATTCGGAATTTTCATTCAGGTTATTTGTAATAGTGACATATATATGATATA TACATATCACCTCTCTTCTTAAATTTTGTAAATGTTAACTGGCAGTAGTCTTTTTTGTATCATTT CCCTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTGTCAGTGAATAA TTACCCACAAATGCCACCAGTAACCTAACGATCTTCACTCTTGGGTTT
WI-7228b	254	G A	---				ATAGCTTCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAAGTAATGGCTCCCAATTCATAA TATGTTCCAGGAGATTACAAATTTTGTCTCTTCTTGTCTTTGTAACTATTTAGTTGATTTTAAATTA CTTTCTGAATAACGGAAGGGATCAGAAATATCTTTGTGCTAGATTGCAAAATCTCCAATCCACA CATATTGTTTAAATAAGAAATGTTATCCAATTAAGATATCTCAATGTT
WI-7228a	163	G A	---				ATAGCTTCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAAGTAATGGCTCCCAATTCATAA TATGTTCCAGGAGATTACAAATTTTGTCTCTTCTTGTCTTTGTAACTATTTAGTTGATTTTAAATTA CTTTCTGAATAACGGAAGGGATCAGAAATATCTTTGTGCTAGATTGCAAAATCTCCAATCC ACACATATTGTTTAAATAAGAAATGTTATCCAATTAAGATATCTCAATGTT
WI-7233c	213	C T	---				CGATCGTACTGCCAGTAGCATGTGCTGTGCGGGCTTGTGTACATCCATTTTCAATTTGTTACA GATGTGAACCTTATTCCTTGTCACTAATTATATTTAAATTTATTTCTAGGAAGTCAAAAAATATAA TAAAGGTTGAGCCCTCTACTTCTTCTGCGCCACTTTTGTGGCAATATTAAAGGAAGTCTGCTAATA GTGTAAGTATCTTGTGACAAAACCACTGCGAGATAACCAAGGGGCTG

WI-7233b	213 C T	---	---	CGATCGTACTGCCAGTAGCATTTGCTGTCTGTCGGGCTGTTGTGTACATTCATTTCAATTGTTACA GATGTGAACCTTTATTCCTTGCTACTAATATATTTAAATTAATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTCTCTTGCCACCCTTTTGGCAATATTAAGTGAAGTCTGCTAATA GTGTAAAGTATCTGTGCACAAAACCACTGCCAGATAACCCAGAGGGGCTG
WI-7233	211 T C	---	---	CGATCGTACTGCCAGTAGCATTTGCTGTCTGTCGGGCTGTTGTGTACATTCATTTCAATTGTTACA GATGTGAACCTTTATTCCTTGCTACTAATATATTTAAATTAATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTCTCTTGCCACCCTTTTGGCAATATTAAGTGAAGTCTGCTAATA GTGTAAAGTATCTGTGCACAAAACCACTGCCAGATAACCCAGAGGGGCTG
WI-7238	128 T C	---	---	GGCTACAGACAGCTCACCATTTTGTCTGTATCTGTAAACACTTTTGTCTTAGCTCTTTCTTG TAAATTTGATGTTCTTTAAATCGTTAATGATAACAGGGCTATGTTTCAGTTTGTCTTCTGCGTT CTGTTTAAACAGAAATAAAGGAGTGAAGCTCCTTTCTCATTTCAAAGTTGCTACCAGTGTAT GCAGTAATTAGAACAAGAAGAAACATTCAGTAGAACATTTTATTCCTA
WI-7252f	520 T C	---	---	CCACAGGATCCAGCCCAAGCGGCCCTCCCGCCCTCCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCGGGGGCGCCAGCCCGGCCCTGGCTCGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGTGGAACTCAGTCAATTAGACTCCTCCTCCA
WI-7252e	552 T C	---	---	CCACAGGATCCAGCCCAAGCGGCCCTCCCGCCCTCCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCGGGGGCGCCAGCCCGGCCCTGGCTCGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGTGGAACTCAGTCAATTAGACTCCTCCTCCA
WI-7252d	540 T C	---	---	CCACAGGATCCAGCCCAAGCGGCCCTCCCGCCCTCCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCGGGGGCGCCAGCCCGGCCCTGGCTCGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGTGGAACTCAGTCAATTAGACTCCTCCTCCA
WI-7252c	552 T C	---	---	CCACAGGATCCAGCCCAAGCGGCCCTCCCGCCCTCCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCGGGGGCGCCAGCCCGGCCCTGGCTCGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGTGGAACTCAGTCAATTAGACTCCTCCTCCA
WI-7252b	540 T C	---	---	CCACAGGATCCAGCCCAAGCGGCCCTCCCGCCCTCCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCGGGGGCGCCAGCCCGGCCCTGGCTCGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGTGGAACTCAGTCAATTAGACTCCTCCTCCA



WI-7252a	520 T C ---			CCACGAGATCCAGCCCAAGCGGCCCTCCGCCCTTCCACTCGCAGCAGCGCCGGGACAGAG GCCTGCCGGGCGCGCAGCCCGGCGCTGGCTCGGAGGCTGCCCGGCGCCCTGGTCTCTGGTCCG GACTCCTAGAGAACGCGCCTAGAGCCTGCCTGGAGGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAAGTGAACCTCAGTCACTTAGACCTCCTCCA
WI-7265m	252 T A ---			AACTTGGTTATGTCAGTTCCTGTGTGACAGTAAGGAAAAAAGGCATGCTATGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCAATTTACCCATTCTGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCAATAGTGAATTTGTTTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCCTT[ ]
WI-7265l	231 T A ---			AACTTGGTTATGTCAGTTCCTGTGTGACAGTAAGGAAAAAAGGCATGCTATGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCAATTTACCCATTCTGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCAATAGTGAATTTGTTTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCCT
WI-7265k	121 T G ---			AACTTGGTTATGTCAGTTCCTGTGTGACAGTAAGGAAAAAAGGCATGCTATGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCAATTTACCCATTCTGTGGTTCAATTGTA GTTTAAAGGAAACCAAGCATATAGATGCAATAGTGAATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCCT
WI-7265j	174 T A ---			AACTTGGTTATGTCAGTTCCTGTGTGACAGTAAGGAAAAAAGGCATGCTATGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCAATTTACCCATTCTGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCAATAGTGAATTTGTTTATATATGTAATAATAACGATCTCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCCT
WI-7265i	227 T C ---			AACTTGGTTATGTCAGTTCCTGTGTGACAGTAAGGAAAAAAGGCATGCTATGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCAATTTACCCATTCTGTGGTTCAATTGTA GTTTAAAGGAAACCAAGCATATAGATGCAATAGTGAATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCCT
WI-7265h	80 T A ---			AACTTGGTTATGTCAGTTCCTGTGTGACAGTAAGGAAAAAAGGCATGCTATGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCAATTTACCCATTCTGTGGTTCAATTGTA GTTTAAAGGAAACCAAGCATATAGATGCAATAGTGAATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCCT
WI-7265g	170 T G ---			AACTTGGTTATGTCAGTTCCTGTGTGACAGTAAGGAAAAAAGGCATGCTATGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCAATTTACCCATTCTGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCAATAGTGAATTTGTTTATATATGTAATAATAACGATCTCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCCT

WI-7265f	231 T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATTAGTGATTTTGTATATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTT/AJ/AAGGAGTAAAGATTGCGCT
WI-7265e	227 T C ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATTAGTGATTTTGTATATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265d	174 T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATTAGTGATTTTGTATATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265c	170 T G ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATTAGTGATTTTGTATATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265b	121 T G ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTCACCCATTCTGTGGTTCATTGTGTA GTTTAAGGAAACCAAGCATATAGATGCAATTAGTGATTTTGTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265a	80 T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTCACCCATTCTGTGGTTCATTGTGTA GTTTAAGGAAACCAAGCATATAGATGCAATTAGTGATTTTGTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7281b	183 C ---	---	GATCACCCAGCCACAAAGCCCTTCGAGGGCCCTATACCATGGCCCACTTGGAGCAGAGAGCCAAAGC ATCTTCCCTGGGAAGTCTTCTGGCCAAAGTCTGGCCAGCTGGCCCTGCAAGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTCTTGGCAAAAAACGGAGTCGCGAGGCCGAG GTGTTGTAAGACCACTCGTTCGTGGTGGGTCTGCAAGAGGCCTCCTC
WI-7281	171 C A ---	---	GATCACCCAGCCACAAAGCCCTTCGAGGGCCCTATACCATGGCCCACTTGGAGCAGAGAGCCAAAGC ATCTTCCCTGGGAAGTCTTCTGGCCAAAGTCTGGCCAGCTGGCCCTGCAAGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTCTCAGACTCTC/AJTTGGCAAAAAACGGAGTCGCGAGGCCG CAGGTGTTGTAAGACCACTCGTTCGTGGTGGGTCTGCAAGAGGCCTC

WI-7282b	159	G C ---				TGTCACCTGGCACATTCATTTCTCAGTTGAAGAAGAGAAAATTTGAAAATGTCCTTATGCTTTTAGA GTTGCAACTTAAGTATATTTGGTAGGGTAGTGTTCACACTCAAAATATGTCAACTTNNNNNNNT AGGCCCTTTCATAAAAACCAAACTG/CJTAGCAAGATGCAATGCATGGCAATCTGTCGGTCTCCA GTTGGTTATCTGAATAGTGTACCAATTCACACCAAGACAGTGTGAGATTGG
WI-7292	92	T C ---				CTTGATTACTTCCACTGAGGTGGGAGCATCTCCAGTGTCCCAATATATCTCCCCCACTCCACTAC TCTCTTCTCCACTTCATTTTCC/CJTGTGCTTCTCTCTAATCAGTGTTTTGGAGGCTGACTTG GGGACAACGTATTATTGATATTATGCTGTTTCTCTTCTCCCAATAGAAATAAGTCATGGAGCC TGAAGGGTGCTAGTTGACTTACTGACAAAAGGCTCTAGTTGGGCTGA
WI-7301f	133	A G ---				AACTATGGCAGTGGTCTGTTATAGTAGAGGCGGGTATGGTGGTGGTGGACAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTGGAGGATATGATGGTTACAAATGAAGGAGGAAATTTG A/GJCGGTAGTAACATATGGTGGTGGTGGAACTATAATGATTTTGGAAATACAGTGGACAACAGCA ATCAAAATTATGGACACATGAAAGGGGGCAGTTTGGTGGAAAGAGCTCGGGCAG
WI-7301e	94	T G ---				AACTATGGCAGTGGTCTGTTATAGTAGAGGCGGGTATGGTGGTGGTGGACAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA TGACGGTAGTAACATATGGTGGTGGTGGAACTATAATGATTTTGGAAATACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAAGGGGGCAGTTTGGTGGAAAGAGCTCGGGCAG
WI-7301d	138	A G ---				AACTATGGCAGTGGTCTGTTATAGTAGAGGCGGGTATGGTGGTGGTGGACAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACTATGGTGGTGGTGGAACTATAATGATTTTGGAAATACAGTGGACAACAGCAATCA TCAAAATTATGGACACATGAAAGGGGGCAGTTTGGTGGAAAGAGCTCGGGCAG
WI-7301c	211	A C ---				AACTATGGCAGTGGTCTGTTATAGTAGAGGCGGGTATGGTGGTGGTGGACAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACTATGGTGGTGGTGGAACTATAATGATTTTGGAAATACAGTGGACAACAGCAATCA AATTATGGAC/CJCATGAAAGGGGGCAGTTTGGTGGAAAGAGCTCGGGCAG
WI-7301b	182	C T ---				AACTATGGCAGTGGTCTGTTATAGTAGAGGCGGGTATGGTGGTGGTGGACAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACTATGGTGGTGGTGGAACTATAATGATTTTGGAAATACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAAGGGGGCAGTTTGGTGGAAAGAGCTCGGGCAG
WI-7301	88	G T ---				AACTATGGCAGTGGTCTGTTATAGTAGAGGCGGGTATGGTGGTGGTGGACAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTT TGACGGTAGTAACATATGGTGGTGGTGGAACTATAATGATTTTGGAAATACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAAGGGGGCAGTTTGGTGGAAAGAGCTCGGGCAG

WI-7301	205 A C	---	---	---	AACATATGGCAGTGGTCTGGTTATAGTAGTAGAGGGGGGTATGGTGGTGACAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGTTACAAATGAAGGAGGAAATTTTGA CGGTAGTAACATATGGTGGTGGTGGAACTATAATGATTTTGGAAATTTACAGTGGACAAACAGCAATCA AATTACITGGACACATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7314c	49 G A	---	---	---	CTCTCCTTTTCTTCAGATCTGCTCTGGTTTTAATTTGGGAGGTCA[G/A]TTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTTCTTTTCAGCAGTGTAAATAAGTCAATTAATAAACTTCCCAGG ATTCTTTGGACCCAGGAACAGCCATGTGGTCTTTCTGTGCACTATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAAACAAAACCTTGTTTTT
WI-7314b	49 G A	---	---	---	CTCTCCTTTTCTTCAGATCTGCTCTGGTTTTAATTTGGGAGGTCA[G/A]TTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTTCTTTTCAGCAGTGTAAATAAGTCAATTAATAAACTTCCCAGG ATTCTTTGGACCCAGGAACAGCCATGTGGTCTTTCTGTGCACTATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAAACAAAACCTTGTTTTT
WI-7314	36 A G	---	---	---	CTCTCCTTTTCTTCAGATCTGCTCTGGTTTTA[G/G]TTGGGAGGTCA[G/A]TTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTTCTTTTCAGCAGTGTAAATAAGTCAATTAATAAACTTCCCAGG ATTCTTTGGACCCAGGAACAGCCATGTGGTCTTTCTGTGCACTATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAAACAAAACCTTGTTTTT
WI-7321b	199 C T	---	---	---	ACTCAGGAAGGGATGCCCATTAAGTGACAAAAGGGTGGGTGGGCACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGGAGTCTTTGGCATCCAGGGCCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGGTGGCACACCCCATC[C TGGTTGCTGGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7321	199 C T	---	---	---	ACTCAGGAAGGGATGCCCATTAAGTGACAAAAGGGTGGGTGGGCACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGGAGTCTTTGGCATCCAGGGCCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGGTGGCACACCCCATC[C TGGTTGCTGGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7336b	248 A C	---	---	---	AGACATTCGCTTCCTGAAAGACTGAAGAAAGTGTAGTGCAATGGGACCCACGAACTGCCCTGGC TCCAGTGAACCTGGGCACATGCTCAGGCTACTATAGGTCCAGAACTCTTATGTTAAGCCCTGGCAG GCAGGTGTTTATTAAATTCGAATTTGGGATTTTCAAAAGATAATTTTACATACACTGTATGT TATAGAACTTCATGGATCAGATCTGGGGCAGCAACCTATAAATCA[A/C]CA
WI-7336c	221 A G	---	---	---	CTCTTTCTCAGCACATTTGATGGCAACTAGAAATTTACAGCAGTTTCAAACTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGTGGCAAGAAATATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTCAGAGAAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTGTTCTCTTTACACAC[A/G]TATACACAGACATCAGAAAATCTGTT



WI-7388	94 T A ---	---	---	TGAAATCCTGGGCTCTGGCCCTGCTAGCTGGTTATTTTACITTTGCCCCCTGCCACITTTT TGAGATCCATCCTTTATCAAGAAGT/AJCTGAAGCGACTATAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAAGCATTCACAAGGTTACCTCTATTTGCCACAAGCGTCTCGGATTTGTGTTGA CTTGCTGCTGCCAAGAACTTTCCCCCAAGATGTGTATAGTTATGG
WI-7438	64 A G ---	---	---	TTAGATTTTAAATGGCAACCAGCACTCACTGCCACCATTCACACTGCAGATCTNCTATTCCTGG[AG] GTTGATATGACAAGGAACCCCTATTGGAACCAAGTCTTCAGATGTGNCATGTGCAGACAGGCTCCT TGTCTGTAGGTGTAGTAGCATGTACACTGTACTGTTCACCTGTACATAGTTTGTNCTGGTATTTGTTA TTGGAAATGAATATCGCTTCCACTGACITTTTACCA
WI-7454b	152 T C ---	---	---	CCATGATCCCTCCTCTTGCCAAATGGAGAGCGCTGTGGATGGTACCACAACAAAGCCCCAACCC CAGTACAACTGAGAAATGAGAGAACCTGTATAGCACTGTCTGAATGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTTCTT/CJTGTGTTTAAAGTTATTTAGCCACCACAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCATTTGTCTACTTCTCAAAATGTTTTGACA
WI-7454	152 T C ---	---	---	CCATGATCCCTCCTCTTGCCAAATGGAGAGCGCTGTGGATGGTACCACAACAAAGCCCCAACCC CAGTACAACTGAGAAATGAGAGAACCTGTATAGCACTGTCTGAATGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTTCTT/CJTGTGTTTAAAGTTATTTAGCCACCACAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCATTTGTCTACTTCTCAAAATGTTTTGACA
WI-7464c	177 G C ---	---	---	AATTTGAAATCTGAAAAAGTGCATAAGCAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACAAATGCATAAATTAATTAATTTCCCTATGTA CAACAGAGCCACAGCACAAAGAGGGTGGGCATAAGCAGTTGCCA[G/C]CCAGAAGAGCTTTCACAT GAAAGAAAGCCCTACAAATAGGCCAGGAGAGCAACGTTCCACCAACAATTAT
WI-7464b	168 C A ---	---	---	AATTTGAAATCTGAAAAAGTGCATAAGCAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACAAATGCATAAATTAATTAATTTCCCTATGTA CAACAGAGCCACAGCACAAAGAGGGTGGGCATAAGCAGTTGCCAGCCAGAGAGCTTTCACAT GAAAGAAAGCCCTACAAATAGGCCAGGAGAGCAACGTTCCACCAACAATTAT
WI-7464a	103 C A ---	---	---	AATTTGAAATCTGAAAAAGTGCATAAGCAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACAAATGCATAAATTAATTAATTTCCCTAT GTCAACAGAGCCACAGCACAAAGAGGGTGGGCATAAGCAGTTGCCAGCCAGAGAGCTTTCACAT GAAAGAAAGCCCTACAAATAGGCCAGGAGAGCAACGTTCCACCAACAATTAT
WI-7499b	134 T G ---	---	---	CAATTCCTCAATCCAACTAGTCTGTNTGCTTAAACCATCCAGACAACTTCCACTTCGAAGGTTTTA AATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCAGTCTTTTGAATGCTTCAIT /GJTATAGTCCCTTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTAGGA ACTCTGTACAAAAATCCCTTTGAAAAATAAAATTTGGAAATGAGTGATGA

WI-7499a	33	A G	---	---	CAATCTCAATCCAACCTAGTCTGNTGCCTAAAGJCCATCCAGACAAACTCCACTTCGAAGGTT TTAATGCATAAGTCAGATAGCAATCCTCAGTGGCCAGAGGCACATCAGTCTTTTGAATGCTTC ATTATAGTCTCTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTAGGAA CTCTGTACAAAATCCCTTTGAAAATATAAAATTTGGAAATGAGTGATGA
WI-7506b	118	A C	---	---	TGGGAATAGTAAGAGAAAGATGGGAAAGGTGACCAAAACAATATAGAGGCAGAGGCCAAAGTGAAT GCATCCAGCAGCAGACCACTTNAAGTAGTCTCTGGTCTGATTGCTAGC[AC]GGAGAGTTGAG TGCCACAGGTAAAGATGAGTGAAGAGGAAAAATCATGATGTCATGATGCAAGTAATTAATGATCA GAAGAAAATATTTTAAAAATTTGGACCACTCTTGTCTACCATCCCTACCCACT
WI-7506	118	A C	---	---	TGGGAATAGTAAGAGAAAGATGGGAAAGGTGACCAAAACAATATAGAGGCAGAGGCCAAAGTGAAT GCATCCAGCAGCAGACCACTTNAAGTAGTCTCTGGTCTGATTGCTAGC[AC]GGAGAGTTGAG TGCCACAGGTAAAGATGAGTGAAGAGGAAAAATCATGATGTCATGATGCAAGTAATTAATGATCA GAAGAAAATATTTTAAAAATTTGGACCACTCTTGTCTACCATCCCTACCCACT
WI-7534b	143	C T	---	---	TGTGAATCTTAGCTCTGGAAGGTGTTATGCCCTTGGGGTTCCTGATGTTGCGAGTGTACCCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGGAAACACATCCCGGTGATAGAAATGCT AAATTGTC/TTGTAATAGGTTAGAAATTTTCTTAAATATGTTTCTTATTCGTGAAAAATTCGG AGAGTGTCTGCTAAAAATGGATTGGTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7534	135	T C	---	---	TGTGAATCTTAGCTCTGGAAGGTGTTATGCCCTTGGGGTTCCTGATGTTGCGAGTGTACCCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGGAAACACATCCCGGTGATAGAAATGCT /CJAAATTTGTCGTGAAATAGGTTAGAAATTTTCTTAAATATGTTTCTTATTCGTGAAAAATTCGG AGAGTGTCTGCTAAAAATGGATTGGTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7543b	162	G A	---	---	GGGAAAGAATAAAATAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCTCTGTTGCAGGGAAGCCCACTTGAGGAAGAAGTCTAAGAGTGAAGTAGGTGACTTGAAC TAGATTGCATGCTTCTCTCTTCTCTTGAAGAGACCACTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTCTCTGGCTCTCTGGATGTAGTCAGTTA
WI-7543	162	G A	---	---	GGGAAAGAATAAAATAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCTCTGTTGCAGGGAAGCCCACTTGAGGAAGAAGTCTAAGAGTGAAGTAGGTGACTTGAAC TAGATTGCATGCTTCTCTCTTCTCTTGAAGAGACCACTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTCTCTGGCTCTCTGGATGTAGTCAGTTA
WI-7555c	60	T C	---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTC/CTTA AAAAGAAAGTGGTATGTTGTGATGATCAGCACTAAGTCTGCTGATCTTAAAGCCACTTGGGTC ATAAGAGGGGAAGTAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTCATTTTGAATTCAG

WI-7555b	60 T C ---	---	GGTGATCAAGATCTGTCCACAGGGCTAATGCCACCACTCCCTCAAAAATTTGTAGAGGT/CJCTA AAAAAAGTGGTATGTTGTGATGATCAGCACTAAGTCTGCATTCCTGTTAAAGCCACTTGGGTC ATAAGAAGGGAAGTAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGIGATATAGTTTTCATTGATGTGCATTTTGAATTCAG
WI-7555	60 T C ---	---	GGTGATCAAGATCTGTCCACAGGGCTAATGCCACCACTCCCTCAAAAATTTGTAGAGGT/CJCTA AAAAAAGTGGTATGTTGTGATGATCAGCACTAAGTCTGCATTCCTGTTAAAGCCACTTGGGTC ATAAGAAGGGAAGTAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGIGATATAGTTTTCATTGATGTGCATTTTGAATTCAG
WI-7567b	290 G T ---	---	TGAGCCATCTACTAGAAAGAAAGCCCATTTTCAACTGCTTTGAAACTTGCCTGGGGTCTGAGCATGAT GGGAATAGGGAGACAGGGTAGGAAGGGCGCCTACTCTTCAGGGCTAAAGATCAAGTGGGCTTGG ATCGCTAAGCTGGCTCTGTTTGATGCTATTTATGCAAGTTAGGGTCTATGATTTAGGATGCGCTAC TCTCAGGGTCTAAAGATCAAGTGGGCTTGGATCGCTAAGCTGGCTCTGTT
WI-7569b	63 T C ---	---	AATGATCCCCCTTCGGTCCAACAACAGGAACCTGACTGGGCACTGAAGGAAGGATGGCA[7C] AGCGTTATGTAAAAAACAAGTATCTGTATGACAACCCGGGATCGTTTGCAGTAACTGAATCCAT TGCACATTGTGAAGGCTTAAATGAGTTTAGATGGGAAATAGCGTTGTTATCGCCTTGGGTTTAAATT ATTGATGAGTTCCTACTGTATCATGGCTACCCAGGAGAAGAGGAGTTG
WI-7574c	216 A G ---	---	GCCACAGCAGATGGAGCGGTGTGAGGAAGGTCCCTTTTCCCTGTTTGTGTTGCCAAGGCCAAAC TCCCACTCTCGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCTCACTGAAATCATTTTG TACCACTTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTCTTG ATAGCCCCAGGGC[A/G]TCTGCTGGGCTGACCACGTTACTATCCCCGTTA
WI-7574b	216 A G ---	---	GCCACAGCAGATGGAGCGGTGTGAGGAAGGTCCCTTTTCCCTGTTTGTGTTGCCAAGGCCAAAC TCCCACTCTCGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCTCACTGAAATCATTTTG TACCACTTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTCTTG ATAGCCCCAGGGC[A/G]TCTGCTGGGCTGACCACGTTACTATCCCCGTTA
WI-7574	216 A G ---	---	GCCACAGCAGATGGAGCGGTGTGAGGAAGGTCCCTTTTCCCTGTTTGTGTTGCCAAGGCCAAAC TCCCACTCTCGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCTCACTGAAATCATTTTG TACCACTTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTCTTG ATAGCCCCAGGGC[A/G]TCTGCTGGGCTGACCACGTTACTATCCCCGTTA
WI-7576c	168 A T ---	---	AATGATGATGATATGATGATGACGACGACAACGATGATGCTTGTAAACAAGAAACATAAGAGAGC CTTGGTTTCATCAGTGTAAAAATTTTGAAGGCGGTACTAGTTCAGACACTTTTGGAGTTTGTGT TCTGTTTGTAAAACTGGCATCTGACACAAAAA[A/T]GTTGAAGGCTTATTCTACATTTCACTAC TTTGTAGTGAGAGACAGAAGCAAGCAANNNNNNNNNNAAGAAAAAATAAAC



WI-7576b	168 A T ---	---	AATGATGATGATAATGATGATGACGACGACACGATGATGCTTGTAACAAGAAACATAAAGAGAGCCTGGTTCATCAGTGTAAATAATTTTGAAGGGGCTAGTCTCAGACACTTTGGAAAGTTGTGTCTGTTTAAACTGGCATCTGACACAAAAA[A/J]GTGAAGGCCCTTATCTACATTTCACTTCACTTTGTAAGTGAGAGACAGAAGCAAAANNNNNNNAAAGAAAAAATAAAC
WI-7577q	77 T C ---	---	AACCATGTTCCCTTCTTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAAATAATGCAT/CJCAAAATCGTCTCTCACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAATAAGAAAGTTCAATTTGGTTACAGTAGGAAGAAGAGAGCATCAAAAGTGGAGATATGTTAACTATGTATAATGTGGCCTGTTATACATGACACTCTCTGAATTGACTGTAATTC
WI-7577p	50 G C ---	---	AACCATGTTCCCTTCTTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTTAAATAATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAATAAGAAAGTTCAATTTGGTTACAGTAGGAAGAAGAGAGCATCAAAAGTGGAGATATGTTAACTATGTATAATGTGGCCTGTTATACATGACACTCTCTGAATTGACTGTAATTC
WI-7577o	157 G A ---	---	AACCATGTTCCCTTCTTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAAATAATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAATAAGAAAGTTCAATTTGGTTACAGTAGGAAGAAGAGAGCATCAAAAGTGGAGATATGTTAACTATGTATAATGTGGCCTGTTATACATGACACTCTCTGAATTGACTGTAATTC
WI-7577n	48 A G ---	---	AACCATGTTCCCTTCTTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTTAAATAATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAATAAGAAAGTTCAATTTGGTTACAGTAGGAAGAAGAGAGCATCAAAAGTGGAGATATGTTAACTATGTATAATGTGGCCTGTTATACATGACACTCTCTGAATTGACTGTAATTC
WI-7577m	84 G A ---	---	AACCATGTTCCCTTCTTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAAATAATGCATCAAAATCGA/JTCTCTCACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAATAAGAAAGTTCAATTTGGTTACAGTAGGAAGAAGAGAGCATCAAAAGTGGAGATATGTTAACTATGTATAATGTGGCCTGTTATACATGACACTCTCTGAATTGACTGTAATTC
WI-7577l	93 T C ---	---	AACCATGTTCCCTTCTTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAAATAATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAATAAGAAAGTTCAATTTGGTTACAGTAGGAAGAAGAGAGCATCAAAAGTGGAGATATGTTAACTATGTATAATGTGGCCTGTTATACATGACACTCTCTGAATTGACTGTAATTC
WI-7577k	154 C A ---	---	AACCATGTTCCCTTCTTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAAATAATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAATAAGAAAGTTCAATTTGGTTA/CJACGTAGGAAGAAGAGAGCATCAAAAGTGGAGATATGTTAACTATGTATAATGTGGCCTGTTATACATGACACTCTCTGAATTGACTGTAATTC

WI-7577j	117	A G ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTCTCTGAGGGTTTAGTA/GJACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAAITGACTGTATTTC
WI-7577i	77	T C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAAITGACTGTATTTC
WI-7577h	50	G C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA TAAATATGCATCAAAATCGTCTCTCATTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAAITGACTGTATTTC
WI-7577g	157	G A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTACAC/G/ATAGGAAGAGAGAGAGCATCAAGTGGAGATATGTTAACT ATTGATAATGTGGCCTGTTATACATGACACTCTCTGAAITGACTGTATTTC
WI-7577f	48	A G ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA TAAATATGCATCAAAATCGTCTCTCATTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAAITGACTGTATTTC
WI-7577e	84	G A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCG/ATCTCTCATTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAAITGACTGTATTTC
WI-7577d	93	T C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAAITGACTGTATTTC
WI-7577c	154	C A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTA/C/JACGTAGGAAGAGAGAGAGCATCAAGTGGAGATATGTTAACT ATTGATAATGTGGCCTGTTATACATGACACTCTCTGAAITGACTGTATTTC

WI-7577b	117	A G ---			AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTCCCTTTAA AAATATGCATCAAAATCGTCTCTATTACTTTTCTCTGAGGGTTTTAGTA/GJACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAAAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577	107	GA ---			AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTCCCTTTAA AAATATGCATCAAAATCGTCTCTATTACTTTTCTCTGAG/GJTTTTAGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAAAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7619a	106	C G ---			ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCAAGAC AGAGAAAGGGCCAAATGGGGTCATCCCTCCCTAACGAGACTG/GJCTGTGCTGGGGTGTCTAATTAC ATGGCAGGAAGATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCT CTCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619b	150	T C ---			ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCAAGAC AGAGAAAGGGCCAAATGGGGTCATCCCTCCCTAACGAGACTCTGTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619c	228	A G ---			ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCAAGAC AGAGAAAGGGCCAAATGGGGTCATCCCTCCCTAACGAGACTCTGTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619d	237	G C ---			ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCAAGAC AGAGAAAGGGCCAAATGGGGTCATCCCTCCCTAACGAGACTCTGTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619e	99	C T ---			ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCAAGAC AGAGAAAGGGCCAAATGGGGTCATCCCTCCCTAACGAGACTCTGTGTGCTGGGGTGTCTAATTACATGG TGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCT TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619f	189	T A ---			ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCAAGAC AGAGAAAGGGCCAAATGGGGTCATCCCTCCCTAACGAGACTCTGTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619k	90 C G	---	---	---	ACAAGGGGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCG/C/G/C/TCCCTAACGAGACTCTGTGCTGGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT CTCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619j	206 T G	---	---	---	ACAAGGGGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT CGCT/G/G/TCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619i	106 C G	---	---	---	ACAAGGGGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT CTCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619h	150 T C	---	---	---	ACAAGGGGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619g	228 A G	---	---	---	ACAAGGGGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT CGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619f	237 G C	---	---	---	ACAAGGGGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT CGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619e	99 C T	---	---	---	ACAAGGGGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGGTGCTAATTACATGG TGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619d	189 T A	---	---	---	ACAAGGGGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619c	90	C G	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAGAC AGAGAAGGGCCCAATGGGGTCATCC[C/G]CTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCT CTCTCGCTTTCTTTCTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619b	206	T G	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT CGC[T/G]TTCTTTCTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619	189	T A	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT TCTCGCTTTCTTTCTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7626d	105	A G	---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGCTTGGC[A/G]TTAAACCAACATCATGGACCAATGTG CCATACATAATGATGAGCATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAITTTTCCCTTGGACTGTTCA
WI-7626c	155	C T	---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGCTTGGCATTAAACCAACATCATGGACCAATGTGCA TACTAATGATGAGCATTTAG[C/T]ACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAITTTTCCCTTGGACTGTTCA
WI-7626b	28	T A	---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGCTTGGCATTAAACCAACATCATGGACCAATGTGCA CCATACATAATGATGAGCATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAITTTTCCCTTGGACTGTTCA
WI-7626	144	T C	---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGCTTGGCATTAAACCAACATCATGGACCAATGTGCA TACTAATGAT[C/G]GAGCATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAITTTTCCCTTGGACTGTTCA
WI-7689c	134	A G	---	---	TCCATAACCGCTGATTCTCAGGCTCTCTGCTGCCGCCACCCAGATGGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTTCTCTAA[A /G]TAAGGGCAGAGTACACTGGGGCAGCTGATACAAATTTGCAGACTGTGTAAAAAGAGAGCTTAAT GATAATATTGTGGTGGCCACAAATAAAATGGATTATTAGAAATTCATATGAC

WI-7689b	134 A G ---				TCCATAACCGCTGATTCTCAGGGTCTCTGCTGCCGCCCCACCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTCTCTAAAJA JGJTAAGGGCAGAGTCACACTGGGCAGCTGATACAAATTCAGACTGTGTAAAGAGAGCTTAAT GATAATATTGGTGCCACAAATAAATGGATTATTAGAAATTCATATGAC
WI-7689	121 G A ---				TCCATAACCGCTGATTCTCAGGGTCTCTGCTGCCGCCCCACCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAJGJGTGTCTCTAA AATAAGGGCAGAGTCACACTGGGCAGCTGATACAAATTCAGACTGTGTAAAGAGAGCTTAAT GATAATATTGGTGCCACAAATAAATGGATTATTAGAAATTCATATGAC
WI-7690	45 G A ---				TGGAGAACATTCAATCTGCCGTCACTATTCAATCAATGAAGATTAGJACATGAGATCCAGAGAGG CTGGATGACTTGCTCAAGTTCCACGAGCATGGTAGTGGCAAAAGAGAGTCCAGAGTCTGCCCTTGAT GCCAGCTCAGTGCACAAAGCTCAGTAGGAGGATGTTCCAGTGATGAGGGCCACCAGGAAGCAC AGGTCAAGGCTGGTCCACACTTATCAGCAGCAACAACCTGTCAGTTTCATCC
WI-7703b	164 T C ---				ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTCACATTTGGAACAAGTCAGTCATTCAGATGATTCAAA TGCTATAAACCAAACTGATGTAAAGTAAATTCJGGTCTCTCACTTGTTTTTAACTCTAAATTCCT TTCATTTTAGGGTAGCATTTGTGTTGAAGAGTTTAAAGCTTCCATTGT
WI-7703	156 T C ---				ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTCACATTTGGAACAAGTCAGTCATTCAGATGATTCAAA TGCTATAAACCAAACTGATGTAAAGTAAATTCJGGTCTCTCACTTGTTTTTAACTCTAAATTCCT TTCATTTTAGGGTAGCATTTGTGTTGAAGAGTTTAAAGCTTCCATTGT
WI-7743e	106 C A ---				TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATTCGTACCTCAGTGGGTCTCTGGGGCTCGAGGCTCATCCGAGGCGAGGTCAGGA GAGGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCAGCCAGCTCTCAGCC
WI-7743d	275 C T ---				TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTACCTCAGTGGGTCTCTGGGGCTCGAGGCTCATCCGAGGCGAGGTCAGGAGAG GGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCAGCTCTCAGCCAAACG
WI-7743e	106 C A ---				TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATTCGTACCTCAGTGGGTCTCTGGGGCTCGAGGCTCATCCGAGGCGAGGTCAGGA GAGGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCAGCCAGCTCTCAGCC

WI-7743d	275 C T	---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCGACACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG TACAGAACTTCTGTACCTACTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743e	106 C A	---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCGACACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAACTTCTGTACCTACTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743d	275 C T	---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCGACACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG TACAGAACTTCTGTACCTACTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743c	106 C A	---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCGACACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAACTTCTGTACCTACTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743b	275 C T	---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCGACACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG TACAGAACTTCTGTACCTACTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743	106 C A	---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCGACACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAACTTCTGTACCTACTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743	275 C T	---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCGACACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAACTTCTGTACCTACTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743	275 C T	---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCGACACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAACTTCTGTACCTACTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7758	144 A G	---	---	---	TGACATTATTCAAAGTTAAAGCAACACTTACAGAAATTATGAAGAGGTATCTGTTTAAACATTTCC TCAGTCAAGTTCAGAGTCTTCAGAGACTTCGTAATTAAAGGAACAGAGTGAGACATCATCAAGTG GAGAGAAATC(A/G)TAGTTTAAACTGCATTATAAATTTTATAACAGAAATTAAGTAGATTTTAAAA GATAAAATGTGAATTTTGTATTATTTTCCCATTTGGACTGTAACTGACTGCC

WI-7765b	126	G C ---	---	ACAGGGCCTTTGGCAGGTGCAGCCGCCACTGCCTTTGACCTGCCTCCCTTCATGCATGGAATTCCT TCATCTGGAACCATCAGAAACACCTCACACTGGGACTTGCAAAAGGGTCAGTATGGG(C)TTAGG GAAACATTCATCCTTTGAGTCAAAAATCTCAATCTCCCTATCTTTGCCACCTCATGCTGTGTG ACTCAACCAAATCACTGAACCTTTGCTGAGCCTGTAATAAAAGGTCGGA
WI-7773b	237	C G ---	---	TTAATTTACTGATTCAGCAAGACCAATCATTTGATCATAGATTATTTAAGTTTATCCGTAGTTTT GATAAAGATTTTCTATTCTCTGGTTCTGTCAGAGAACCTAATAAGTGTACTTTGCCATTAAAGCA GACTAGGGTTCATGCTTTTACCCCTTTNNNNNNNTTGTAAAGTGTAGTTACCTACTTTTCTTT GATTTTCGACGTTTACTAGCCATCTCAAGCAAC(G)TTTCGACGTTTGA
WI-7774b	170	T C ---	---	TGCAACCTCTTTTCGTGATGGCAGCCTGCTGGTCAGCACTCCAGTAGCGAGACGGCACCCAGAAT CAGATCCCGAGCTTCGGCATTTGATCAGACCAACAGTGTGTTCCGGGAGGAAACACTTTTTTAA TTACCCCTTTGCAAGGCACCACTTTAATCTGTTT/CJATACCTTGTCTTATTAATGAGCGACTTAA ATGATTGAAATAATGCTGCTCTTTAGTAGCAAGTAAATGTGCTTGCT
WI-7785c	165	G ---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATTCGTAAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATCTGTAATGCATTGGAATAAACTGTCTCCCTCATTTGCTCTATGAACTGC ACATTTGGTCATTGTGAATANNNNNNNNNGCCAAAGGCTAATCCAATTATTATCATCATTTACCA TAATTTATTTGTCCATTGATGATTTATTTTGTAAATGATCTTGGTCTGC
WI-7785b	165	G ---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATTCGTAAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATCTGTAATGCATTGGAATAAACTGTCTCCCTCATTTGCTCTATGAACTGC ACATTTGGTCATTGTGAATANNNNNNNNNGCCAAAGGCTAATCCAATTATTATCATCATTTACCA TAATTTATTTGTCCATTGATGATTTATTTTGTAAATGATCTTGGTCTGC
WI-7785	156	T ---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATTCGTAAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATCTGTAATGCATTGGAATAAACTGTCTCCCTCATTTGCTCTATGAACTGC ACATTTGGTCATTGTGAATANNNNNNNNNGCCAAAGGCTAATCCAATTATTATCATCATTTACCA TAATTTATTTGTCCATTGATGATTTATTTTGTAAATGATCTTGGTCTGC
WI-7789c	84	G A ---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATTCGTAAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATCTGTAATGCATTGGAATAAACTGTCTCCCTCATTTGCTCTATGAACTGC ACATTTGGTCATTGTGAATANNNNNNNNNGCCAAAGGCTAATCCAATTATTATCATCATTTACCA TAATTTATTTGTCCATTGATGATTTATTTTGTAAATGATCTTGGTCTGC
WI-7789b	84	G A ---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATTCGTAAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATCTGTAATGCATTGGAATAAACTGTCTCCCTCATTTGCTCTATGAACTGC ACATTTGGTCATTGTGAATANNNNNNNNNGCCAAAGGCTAATCCAATTATTATCATCATTTACCA TAATTTATTTGTCCATTGATGATTTATTTTGTAAATGATCTTGGTCTGC



WI-7789	73 GA ---			TGTCCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGACCACATCTTACAGAGACTCTCCC TGACCG/GA/TTGAAATTTAAGTTTAGGGTCCCTAAAGCATTTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTAGTGAAGCTCCCTTACGGCCCGCTGACCTAGGATAT GCGCTCTGTGACTCGGGGCTGTCTAGACGACTAGCCAGACCCATCT
WI-7790b	190 CT ---			AATTGTCAGTCACTCTTCAAAACCTTACAGTCCCTTCTAAGGTTACTTTCATGAGATTATCCATT TACTAATACTGTAATTTTGGTGGACTAGGCTTGCCCTATGTGCTTATGTGAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAGTTGTGTTCTATTTCTTGAACCTC/TTTCTATACITTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACITTTAAG
WI-7790	190 CT ---			AATTGTCAGTCACTCTTCAAAACCTTACAGTCCCTTCTAAGGTTACTTTCATGAGATTATCCATT TACTAATACTGTAATTTTGGTGGACTAGGCTTGCCCTATGTGCTTATGTGAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAGTTGTGTTCTATTTCTTGAACCTC/TTTCTATACITTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACITTTAAG
WI-7795b	81 CA ---			CAGATGTTCTGGTAACTGATTGCTGGCAACAACAGATTCTCTGGCTCATATTTCTTTCTTCAT CTTGATGATGATC/GA/TTGTCATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCACATATAAATGATCTTTTCTCCAGAAAAATTCCTTGAGGAAAAATGTCCAAAA TAAGATGAATCACTTAATACCGTATCTTCTAAATTTGAAATATAATCTG
WI-7795	81 CA ---			CAGATGTTCTGGTAACTGATTGCTGGCAACAACAGATTCTCTGGCTCATATTTCTTTCTTCAT CTTGATGATGATC/GA/TTGTCATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCACATATAAATGATCTTTTCTCCAGAAAAATTCCTTGAGGAAAAATGTCCAAAA TAAGATGAATCACTTAATACCGTATCTTCTAAATTTGAAATATAATCTG
WI-7814c	41 GA ---			TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCG/GA/TTTCAATTTAGTCATGTGACCACCTC TGCTTTGTGTTTCCACAGCCTGCAAGTTGAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGATCTTTAGAGAAGTATACATAAGTTTAGGATAAAATAATGGGATTTTC TTTCTTTCTCTGGTAATTTGACTTGATATTTTAAAGAAATAACAGAA
WI-7814b	41 GA ---			TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCG/GA/TTTCAATTTAGTCATGTGACCACCTC TGCTTTGTGTTTCCACAGCCTGCAAGTTGAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGATCTTTAGAGAAGTATACATAAGTTTAGGATAAAATAATGGGATTTTC TTTCTTTCTCTGGTAATTTGACTTGATATTTTAAAGAAATAACAGAA
WI-7814	28 GA ---			TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCGTTTCAATTTAGTCATGTGACCACCTC TGCTTTGTGTTTCCACAGCCTGCAAGTTGAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGATCTTTAGAGAAGTATACATAAGTTTAGGATAAAATAATGGGATTTTC TTTCTTTCTCTGGTAATTTGACTTGATATTTTAAAGAAATAACAGAA

WI-7830d	150 C T ---				GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAGAGAGAGTCTGTCTGTGATGA TGGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAACG ATCCATAACTTTAGT[C/T]TTAATGTACACATTCGATTTTGATAAAATTAATTTTGTGTTCCCTTTG AGGTTGATCGTTGTGTTGTTTGTGTCACATTTTACTTTTTTGGGTGGGA
WI-7830c	54 G A ---				GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAGAGAGAGTCTGTGATGATGA TGATGGATAGGGGCAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCGATTTTGATAAAATTAATTTTGTGTTCCCTTTG AGGTTGATCGTTGTGTTGTTTGTGTCACATTTTACTTTTTTGGGTGGGA
WI-7830b	134 G A ---				GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAGAGAGAGTCTGTGATGATGA TGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC G/AJATCCATAACTTTAGTCTTAATGTACACATTCGATTTTGATAAAATTAATTTTGTGTTCCCTTTG AGGTTGATCGTTGTGTTGTTTGTGTCACATTTTACTTTTTTGGGTGGGA
WI-7830	44 A G ---				GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAGAGAGAGTCTGTGATGATGA TGATGGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCGATTTTGATAAAATTAATTTTGTGTTCCCTTTG AGGTTGATCGTTGTGTTGTTTGTGTCACATTTTACTTTTTTGGGTGGGA
WI-7865e	25 C T ---				CCACTTCCTATCTGATTTTCCAG[C/T]AAATGAGGAGGCAATTCAGTCTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCTATCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTTTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGTATTCACCCAGTAAACCCAAA
WI-7865d	191 C T ---				CCACTTCCTATCTGATTTTCCAG[C/T]AAATGAGGAGGCAATTCAGTCTCCACAAACATCTA ATCTAAATGGAGAGATGAATCTATCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGG ATGCTACTCATAAGATTTTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGT[C/T]GAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGTATTCACCCAGTAAACCCAAA
WI-7865c	25 C T ---				CCACTTCCTATCTGATTTTCCAG[C/T]AAATGAGGAGGCAATTCAGTCTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCTATCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTTTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGTATTCACCCAGTAAACCCAAA
WI-7865b	191 C T ---				CCACTTCCTATCTGATTTTCCAGCAAATGAGGAGGCAATTCAGTCTCCACAAACATCTAGCC ATCTAAATGGAGAGATGAATCTATCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAAGATTTTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGT[C/T]GAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGTATTCACCCAGTAAACCCAAA

WI-7865	25 C T ---			CCACTTCCTATCTGATTTTCCAG[C/TAATGAGGCGAGCAATTCCTAGTCTTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTATAAGATTTGAGGGTGTCTTCCAACCTGAATCTCAATGTTCTCAGTACGAAAAAC CTGAATCACATGCTATGTAAGGAAAGTGCTATTACCCCGAGTAAACCCAAA
WI-7865	191 C T ---			CCACTTCCTATCTGATTTTCCAGCAATGAGGCGAGCAATTCCTAGTCTTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAAGATTTGAGGGTGTCTTCCAACCTGAATCTCAATGTTCTCAGTAC[C/TAAGAAAAC CTGAATCACATGCTATGTAAGGAAAGTGCTATTACCCCGAGTAAACCCAAA
WI-7867c	92 A C ---			TTCAAACACCTGTCTTCCACCTCCACCATCTGTGCAATCACTTCACCTTCAGCCTCACTAGTCCCC CTAACAAATACCTGTCAAGAGG[C/AGAGTCAGCTCAGGTGGATTTAATGTGGTTAATATGGC CTGTTGAGTTAATGTTAATGTTGATTTCTTTAAGTAACCATTTCTGTTCTGCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7867b	92 A C ---			TTCAAACACCTGTCTTCCACCTCCACCATCTGTGCAATCACTTCACCTTCAGCCTCACTAGTCCCC CTAACAAATACCTGTCAAGAGG[C/AGAGTCAGCTCAGGTGGATTTAATGTGGTTAATATGGC CTGTTGAGTTAATGTTAATGTTGATTTCTTTAAGTAACCATTTCTGTTCTGCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7868c	173 C T ---			TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGCTTT CACCAACCTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCAGTCTCCATCTCAGTACACAAT CAITTAATATTTCCCTGCTTACCCCTATTCAAGCAA[C/TTAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTTGACTCAGGTTCAGTAGTTCATTTCTAATGCCTAGAT
WI-7868b	173 C T ---			TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGCTTT CACCAACCTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCAGTCTCCATCTCAGTACACAAT CAITTAATATTTCCCTGCTTACCCCTATTCAAGCAA[C/TTAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTTGACTCAGGTTCAGTAGTTCATTTCTAATGCCTAGAT
WI-7868	66 T C ---			TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGCTTT C/TTACCCCAACCTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCAGTCTCCATCTCAGTACAC AATCAITTAATATTTCCCTGCTTACCCCTATTCAAGCAA[C/TTAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTTGACTCAGGTTCAGTAGTTCATTTCTAATGCCTAGAT
WI-7870b	85 T C ---			ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTCTGCAGTATTAGAAGGG GTGGGTGGCGGGAATCC[C/ATTTATCAGACTCTGTAATGAATATAAATGTTTACTCAGAGGA GCTGCAAAATTCCTGCAAAAATGAAATCCAATGAGCACTAGAAATTTTAAACATCATTTACTGCCAT CTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTG

WI-7870	76 C T ---	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTACTCTGCAGTGATTAGAAGGG GTGGGTGGIC/TJGGGAATCCTATTATCAGACTCTGTAATGAATATAAATGTTTTACTCAGAGGAG CTGCAATTGCCTGCAAAATGAAATCCAATGAGCACTAGATAATTTAAACATCATTTACTGCCATC TTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG
WI-7889c	54 C ---	---	---	TTAGTCTCATGCCCACTCCCAAGAGCAGCTGGCACTGACAGCCTGGGGGGCCGCTCTCCCCCTG CAGCCGTGCAGGACTCTAGCTCATGAGTGGAAGTCACTACAGGACTGGCCGGCCCGGCGCTCT GGCTTCCCTGCCCAATCCTCCTGGAGAAAGGACATGGGAATGAATGAAATGGGGCGCTGGACACC TACAGCAGCACGCATGTCCTCCCAAGGCTGCTTCTCCAGAGCACAAAG
WI-7889b	54 C ---	---	---	TTAGTCTCATGCCCACTCCCAAGAGCAGCTGGCACTGACAGCCTGGGGGGCCGCTCTCCCCCTG CAGCCGTGCAGGACTCTAGCTCATGAGTGGAAGTCACTACAGGACTGGCCGGCCCGGCGCTCT GGCTTCCCTGCCCAATCCTCCTGGAGAAAGGACATGGGAATGAATGAAATGGGGCGCTGGACACC TACAGCAGCACGCATGTCCTCCCAAGGCTGCTTCTCCAGAGCACAAAG
WI-7894c	142 A G ---	---	---	AGCCACCCCAATATAACTGTTATCCAGAAGCTGTTATGTCCTGTTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGTCCTATTGTTTGTAATTTATTTGCGTATAC ATTATC/A/GJTATGTAATAATTTGCAATTTTATTGAAATTTATGTTTCTGAGATTTATCCACATTG AACATGGAGCTCAATCGTTAATTTTAAACCGCTATAGAGTATCCATA
WI-7894b	142 A G ---	---	---	AGCCACCCCAATATAACTGTTATCCAGAAGCTGTTATGTCCTGTTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGTCCTATTGTTTGTAATTTATTTGCGTATAC ATTATC/A/GJTATGTAATAATTTGCAATTTTATTGAAATTTATGTTTCTGAGATTTATCCACATTG AACATGGAGCTCAATCGTTAATTTTAAACCGCTATAGAGTATCCATA
WI-7900e	84 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCTJCTGCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGA/C/TACA AAATGCAATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAGAAATC
WI-7900d	128 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCTJCTGCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGA/C/TACA AAATGCAATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAGAAATC
WI-7900e	84 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCTJCTGCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGA/C/TACA AAATGCAATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAGAAATC



WI-7901	33 C T	---	---	AGACTTAGGTACAAATTGCTCCCTTTTATATACJTAGACACACACAGGACACATATATTAACACAG ATTGTTTCATCTGCAATGTCATATTTCCATATAGTCATCAAGAGACCAATTTTATAAACATGGTAAGAC CCTTTTAAACAACATCCAGCCCTGGTTGCGGTGCTGGTTATGGGCAGCGCCGCTGGTGGTGGT CACTCAGTCGCTCGCATGCTCTGTCATACAGACAGGTAACCTAGTCT
WI-7901	271 T G	---	---	AGACTTAGGTACAAATTGCTCCCTTTTATATACAGACACACAGGACACATATATTAACACAGATT GTTTCATCTGTCATATTTCCATATAGTCATCAAGAGACCAATTTTATAAACATGGTAAGACCGT TTTTAAACAACATCCAGCCCTGGTTGCGGTGCTGGTTATGGGCAGCGCCGCTGGTGGTGGT TCAGTCGCTCGCATGCTCTGTCATACAGACAGGTAACCTAGTCTGCTG
WI-7926c	150 C A	---	---	CATTCCGCATCTGTCAACGAGGACAAAGCATGGACAAGGATGAGCTTTACAAAGATGATGCAC TTGGAGATCAGAAAATTCATATTAAGCAAGATGATACAAACACAGATGATTTGGGAATGCCCTTCATT TACAATGCAATACCTTAC/AJATTTTAACTCTTTGAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTGCAACCTATATCAGAGAAATACACTGTGGGAA
WI-7926b	28 A T	---	---	CATTCCGCATCTGTCAACGAGGACAAAGCATGGACAAGGATGAGCTTTACAAAGATGATGCAC ACTTTGGAGATCAGAAAATTCATATTAAGCAAGTGTACAAACACAGATGATTTGGGAATGCCCTTC ATTTACAATGCAATACCTTACATTTTAACTCTTTGAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTGCAACCTATATCAGAGAAATACACTGTGGGAA
WI-7926	150 C A	---	---	CATTCCGCATCTGTCAACGAGGACAAAGCATGGACAAGGATGAGCTTTACAAAGATGATGCAC TTGGAGATCAGAAAATTCATATTAAGCAAGTGTACAAACACAGATGATTTGGGAATGCCCTTCATT TACAATGCAATACCTTAC/AJATTTTAACTCTTTGAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTGCAACCTATATCAGAGAAATACACTGTGGGAA
WI-7947b	203 G T	---	---	AAGAGCCAGCAGGTCAAAAAGGCCAACACACACCATAGCAGCCAGACCCACAGGCCAGGTCCTGT GCTATCAGAGGGTCACCTCTTTACAGTTAGAAACACCAGCGAGGCCACAGAAATCCCATCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTTGCTCAATTCAATCCATAGATTTTCGAAGCCACA GA/GTJCTCTCCCTGGAGCAGCAGACTATGGGCAGCCAGTCTGCCACCTG
WI-7947	203 G T	---	---	AAGAGCCAGCAGGTCAAAAAGGCCAACACACACCATAGCAGCCAGACCCACAGGCCAGGTCCTGT GCTATCAGAGGGTCACCTCTTTACAGTTAGAAACACCAGCGAGGCCACAGAAATCCCATCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTTGCTCAATTCAATCCATAGATTTTCGAAGCCACA GA/GTJCTCTCCCTGGAGCAGCAGACTATGGGCAGCCAGTCTGCCACCTG
WI-7963b	145 T C	---	---	CATGTGCTGCATGAAGACTAATTTAAAAAGCAAGTAAGACTAATTTTAAAAATAAAATGCC ACAAATTCATTTCTCCTCTAAGTATTACAAATGGAGTTTATCTTCGCTAAAAAGTGAAGAAAT TGAGTGAATGA/TGJAATTTTGTAATTTAGGATAAGATCCAAAGTATTTTCCCCAACTCTTTGTTCCC CCATAAAGTTAGCATGAGGAGGAGCACTATTAAAGGCAGAAAGACGGAAAA



WI-8021b	57	C T	---	---	ACAACTCTCAGAAGGACTGTGCAAGTCAATGAGTCGGCTTGTAATCTCTATCTGGAA[C/T]GATCCC ACGTCCTAGAACCTTCACCACAAGGAGTTTCTTGTAGTGATCTCAAAGTCTTGGTAGGCAATTCGA ACTGGTCCCTTTCACCTTGAGATCTTTCTTTGCGCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTAAGGGTGATTCGAATTCGGTGAATTGCCA
WI-8021	57	C T	---	---	ACAACTCTCAGAAGGACTGTGCAAGTCAATGAGTCGGCTTGTAATCTCTATCTGGAA[C/T]GATCCC ACGTCCTAGAACCTTCACCACAAGGAGTTTCTTGTAGTGATCTCAAAGTCTTGGTAGGCAATTCGA ACTGGTCCCTTTCACCTTGAGATCTTTCTTTGCGCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTAAGGGTGATTCGAATTCGGTGAATTGCCA
WI-8024c	206	A G	---	---	CTGAAAATTTACTATGCTCTCCACAACAGAGCTCCCATTTCCACAGACACAGTCAATGTCAGTCA GCTTGATTCAGGAGGACAGGGCAGAGGATCCCACTGGCAGTCCCATTCCCATGGGAAGACAGAAGAGT GGGCCCAGAGATGGAAGGACCCCACTGTCATACCAAAACACCAATTTAGCCGCTCTAGCCTCTAA TTCCC[A/G]CTCTAGAACAGCTGGCCCTGGTCTGTCAGTACACAAAGGAAAGAGC
WI-8024b	206	A G	---	---	CTGAAAATTTACTATGCTCTCCACAACAGAGCTCCCATTTCCACAGACACAGTCAATGTCAGTCA GCTTGATTCAGGAGGACAGGGCAGAGGATCCCACTGGCAGTCCCATTCCCATGGGAAGACAGAAGAGT GGGCCCAGAGATGGAAGGACCCCACTGTCATACCAAAACACCAATTTAGCCGCTCTAGCCTCTAA TTCCC[A/G]CTCTAGAACAGCTGGCCCTGGTCTGTCAGTACACAAAGGAAAGAGC
WI-8077	167	A G	---	---	GAATGAGCCTTCTAGCGCGAGGACCTGCTGCTGTTGTTGGCCTGCACATGCAATCTATGGAATGC TTTTGGCCAAAGCGGGGCACTGAGGACTAAGCTCTGANNNNNNNNATCTGCCCAAACTCCTTTCT AAGGAGTCTGGGCTGTCATGCCCTTACAAACC[A/G]TAAATTCATCATCAGATGGATTTTATTTAACGTT GTGATTGTGACTTACITTTCAATCTGACTCTGGCATAACAAGGGAAGAAA
WI-8118f	114	G C	---	---	TCTAGGTTTAAATCAAAGCAATTTGCANITTTGGATTTTGGAAATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGAATGTAGCTTGT[G/C]TTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCCT AAAAATCAGACTCATTGTGACCAGTAGCTTGAGGACTCAAGCTGAATGA
WI-8118e	40	A G	---	---	TCTAGGTTTAAATCAAAGCAATTTGCANITTTGGATTTTGGAAATGACCACCTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGGAACTGGCAATACAGAATGTAGCTTGTGTTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCCT AAAAATCAGACTCATTGTGACCAGTAGCTTGAGGACTCAAGCTGAATGA
WI-8118d	118	T G	---	---	TCTAGGTTTAAATCAAAGCAATTTGCANITTTGGATTTTGGAAATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGAATGTAGCTTGTGTTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCCT AAAAATCAGACTCATTGTGACCAGTAGCTTGAGGACTCAAGCTGAATGA



WI-8118c	44 C T ---			TCTAGGTTAATCAAAAGCAATTTGCANTTTGGATTTTGGAAATGA[CT]CACTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGGAACCTGGCAATACAGAATGTAGCTTGTTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCATTGIGACCAGTAGICTTGAGGACTCAAGCTGAATGA
WI-8118b	88 T C ---			TCTAGGTTAATCAAAAGCAATTTGCANTTTGGATTTTGGAAATGACCACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAAC[CT]GCGCAATACAGAATGTAGCTTGTTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCATTGTGACCAGTAGICTTGAGGACTCAAGCTGAATGA
WI-8171d	299 C T ---			TTTCTCTCCTTCGCGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCAGGGCCTCGGGAAG AGGGTAGGAGGACCGAGCAGCATTCTGTAGAGGAAGACAGGAAGGAGACCCTCTTGGCACACA TTTATGGAGGTTGTCCTGAAGAGAGAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAAACAATCACGGCA
WI-8171c	46 A G ---			TTTCTCTCCTTCGCGGGACCAAGGTACCTTCTGGGGCATACAAC[AG]TGGCAGCAGGGCCTCGGG AAGAGGGTAGGAGGACCGAGCAGCATTCTGTAGAGGAAGACAGGAAGGAGACCCTCTTGGCAC ACATTATGGAGGTTGTCCTGAAGAGAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACCAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAAACAATCAC
WI-8171a	46 A G ---			TTTCTCTCCTTCGCGGGACCAAGGTACCTTCTGGGGCATACAAC[AG]TGGCAGCAGGGCCTCGGG AAGAGGGTAGGAGGACCGAGCAGCATTCTGTAGAGGAAGACAGGAAGGAGACCCTCTTGGCAC ACATTATGGAGGTTGTCCTGAAGAGAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACCAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAAACAATCAC
WI-8171b	298 T C ---			TTTCTCTCCTTCGCGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCAGGGCCTCGGGAAG AGGGTAGGAGGACCGAGCAGCATTCTGTAGAGGAAGACAGGAAGGAGACCCTCTTGGCACACA TTTATGGAGGTTGTCCTGAAGAGAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAAACAATCACGGCA
WI-8314b	85 G C ---			GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTTGCAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCTTAAGGG[CT]GAGTCTCAAAACCCAGCTCAAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCACGTCTCAATAGAACTTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAAACCACT
WI-8314	78 C G ---			GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTTGCAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCTTAAGGGGAGTCTCAAAACCCAGCTCAAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCACGTCTCAATAGAACTTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAAACCACT

WI-8321	178	GA	---	---	TTTTAAATATGCCCCGTTTAGAGCAGACACAGTCACAATAAAGTTAAAAAGTTACAATGTGTCCAG TGATATACCCAGGNAATCCATTCTGGTACTTTTCAAGAGCTGCTGTATATAGTCTGAGTCTGAGAAG TCCCCTTAGATAATAGCTGCCACTTTTCAGTATGTTTCAAGATG/AJAGTATCTTAGTATCTTTCTA TTTTGCTATGGTTCTAGTTTATCAACCTACTTTTATTAGCTGAACGTGTGGC
WI-8321	178	GA	---	---	TTTTAAATATGCCCCGTTTAGAGCAGACACAGTCACAATAAAGTTAAAAAGTTACAATGTGTCCAG TGATATACCCAGGNAATCCATTCTGGTACTTTTCAAGAGCTGCTGTATATAGTCTGAGTCTGAGAAG TCCCCTTAGATAATAGCTGCCACTTTTTCAGTATGTTTCAAGATG/AJAGTATCTTAGTATCTTTCTA TTTTGCTATGGTTCTAGTTTATCAACCTACTTTTATTAGCTGAACGTGTGGC
WI-8332b	123	AC	---	---	TATGTAATCACTTTCAGTTACCCCGTGCCTCCAGAAATCGCATGTTGCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGTCCAAAGCCAGTCTTCCCCTCCCTGTCAGCCCTTAGA/AJACTAAGTAG CAGTACTGTTTGGTGTGTTTGTCTTCCCAGCAATGCCTACTGCAGCTACTTAGTAACAACCTAG AGGTGGAGGGTNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	114	AC	---	---	TATGTAATCACTTTCAGTTACCCCGTGCCTCCAGAAATCGCATGTTGCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGTCCAAAGCCAGTCTTCCCCTCCCTGTCAGCCCTTAGA/AJACTAAGTAG CAGTACTGTTTGGTGTGTTTGTCTTCCCAGCAATGCCTACTGCAGCTACTTAGTAACAACCTAG AGGTGGAGGGTNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8378b	311	TC	---	---	TGCGGGCTTAACAGGAAGCATGACTGGGAGGCTCAGGAAGCTTATAATCATGGCAGAGGCGAAGG GGAAGCAAGGACCTTCTACATGGCAGCAGGAGAAAGAGAAAGGAGAGTCTACACACTTTT AAACAACCAAGATCTCATGAGANTTCCATCGGGAGACAGCACTAGGGGGATGGCACTAAACCATAGA AACTGCCCCCATGATCCAATCACTNCAACAGGCCCTCCTCCAAACACGTGGGG
WI-8378	308	TC	---	---	TGCGGGCTTAACAGGAAGCATGACTGGGAGGCTCAGGAAGCTTATAATCATGGCAGAGGCGAAGG GGAAGCAAGGACCTTCTACATGGCAGCAGGAGAAAGAGAAAGGAGAGTCTACACACTTTT AAACAACCAAGATCTCATGAGANTTCCATCGGGAGACAGCACTAGGGGGATGGCACTAAACCATAGA AACTGCCCCCATGATCCAATCACTNCAACAGGCCCTCCTCCAAACACGTGGGG
WI-8426	184	TG	---	---	TTTAGCACATATTTAGCATTAGCCCTAAACGATACAGCAATATGTTACATCTCTGTGAAAAACAG TTGTTGTAAGTCTTAAANNNNNNNAATGTAACCTCCGACTTGTCCCTAATAGGATTTGACCNNTAA GAGNTTCTTTTGTGTGGANGGGGTGGCTTGTCTGAACCTCATCTGTGTG/CCTTGTAGCTGGTG AGGCTGGGAGTATGGANGGNCCTGGGGCCCTTGGCNATNGNATCAGTGAG
WI-8450h	61	CA	---	---	TTGAGCCTCCACAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTC/AJCA TCCTCTCTATCTAGTCCAAAGTTTAGTTTCAATCCCAATATACCAATCCATTTGTTATTTAAGA AAAAACCTCCCAAGTTATGTCAGAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGCTTATATGCAATTCAT

WI-8450g	55 T C	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTC/JACACTCCAT CTTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTTAAGA AAAAACCTTCCAGTTATTGTCAGAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450f	108 T A	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATTAT/JACCAATTCATTTGTTATTTAAGA AAAAACCTTCCAGTTATTGTCAGAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450e	125 T C	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTC/JTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450d	125 T C	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATTAT/JACCAATTCATTTGTTATTTAAGA AAAAACCTTCCAGTTATTGTCAGAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450c	108 T A	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATTAT/JACCAATTCATTTGTTATTTAAGA AAAAACCTTCCAGTTATTGTCAGAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450b	61 C A	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTTC/JA/JCA TCTTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTTAAGA AAAAACCTTCCAGTTATTGTCAGAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450a	55 T C	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTC/JACACTCCAT CTTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTTAAGA AAAAACCTTCCAGTTATTGTCAGAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8458b	60 A/G	---	---	CAAGGAAGGTGTCAGTCTTCAATAACITTTCAAGAGTTACAAAAATACGTTATTTTAA/JG/JCTA CAATTCAAGATTAGCATCCAAACCTTACAAACATGATGATACATTCGTACACACACCATACAAACCTTCAC ACCTGGCTACAGCAATGTTGACTTACATCACCATTGTTTATACITGTGAAAACTTTATTTGTGCACAGT GACATCCATTCCGCCAGACTTAATGTTATAAAGCAGCTGAGCAGAGTTCCTCA

WI-8461c	105	A T ---	---	---	CTTCCTCCAAAATCTACATGAATACTTGAAGACAAATATAACTACAACCTTACAAATGCCAAATTA GACAAAGAGANTAAATGATATAATAATAAATCTTTTATJNNNNNNNNCCTTGCTTATTACACAT TCAGGGAAGTCTAGCACCAGGACAGINTTAAACAATTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461b	38	T C ---	---	---	CTTCCTCCAAAATCTACATGAATACTTGAAGACAAAT/CJATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATAATAAATCTTTTNNNNNNNNCCTTGCTTATTACACAT TCAGGGAAGTCTAGCACCAGGACAGINTTAAACAATTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	38	T C ---	---	---	CTTCCTCCAAAATCTACATGAATACTTGAAGACAAAT/CJATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATAATAAATCTTTTNNNNNNNNCCTTGCTTATTACACAT TCAGGGAAGTCTAGCACCAGGACAGINTTAAACAATTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	105	A T ---	---	---	CTTCCTCCAAAATCTACATGAATACTTGAAGACAAATATAACTACAACCTTACAAATGCCAAATTA GACAAAGAGANTAAATGATATAATAATAAATCTTTTATJNNNNNNNNCCTTGCTTATTACACAT TCAGGGAAGTCTAGCACCAGGACAGINTTAAACAATTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-9438	77	A G ---	---	---	AATAACATGTTATGAACAAAGCTGTTACAAGTAGTAGGTAGATGACITTAATTTTGTATAAAAAAAT TAAAAAGCAT/JGJACATGCATATAAAAAATTAGATTATGTACAAAATACCAACAGTATTTACTTC TGCTCAGTAAATAAAATTTCTCCCTTTGTTTTGCTTTTTTAAAAAACATTAATTTCTGAAAAA ATCAGAAAAACATGATCGTGGAGAAATTAITTA
WI-9439b	101	C T ---	---	---	ACAGAAATTGACCTTTATTTGTTGTAATAAGCCCTGTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAAAATCCCAGTCTGCAGCTCAGTACCTGTC/JTGTGCACACTGTACCATCTCAGTCCCACCTC GCCTGTAACITTAGAAAAACAGCCCTACCCCCAGAGGGTCTGCGAGTTAATACCTTGAGAAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACCTTGACCTGTAAACAAAAG
WI-9439a	76	C T ---	---	---	ACAGAAATTGACCTTTATTTGTTGTAATAAGCCCTGTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAAAAT/CJCCAGTCTGCAGCTCAGTACCTGTCGTGCACACTGTACCATCTCAGTCCCACCTC GCCTGTAACITTAGAAAAACAGCCCTACCCCCAGAGGGTCTGCGAGTTAATACCTTGAGAAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACCTTGACCTGTAAACAAAAG
WI-9446b	75	T C ---	---	---	GAAAGCTTGATTAAAGGAGGNTTTATTTGATGTAACCTTACCATAGACTATAAAGANCATTA TAAAAAAAT/CJCCCTAAAGNACACATGCCCAAATGACCANGNCATAAGCAAAACCTTTTAAAT TACTCATCTTTCATATGTGTGTTTGTGNCCTACTNTATCATGTGCTCTCTGCTTTTGTCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT

WI-9446	75 T C ---	---	GAAGGCTTGATTAAGGGAGGNTTATTGATGNAACCTACCATCCATAGACTATAAAGANCATTA TAAAAAAATG/CJCCCTCTAAAGNGACACATGCCCCAAATGACCANGNCATAAGCAAACCTTTTAAAT TACTCATCTTTCATATGCTGTTGTCNCCCCTACNTTATCACTGTGCTCTCTGCTCTTTTGCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT
WI-9497b	185 A ---	---	ATTAAAAATGCAAGGTTTCATGTTTACATTTTCTTATCAAGTACAATGGTATATATACATTTTTT GAGATAAATTCTAGATTCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTAAATTAATCAAAGTATGTTAATGTCACCT GGAATTCATACATGGAAGGCCAACAAATAACTAAACTTGACTAATGAAG
WI-9497	185 A ---	---	ATTAAAAATGCAAGGTTTCATGTTTACATTTTCTTATCAAGTACAATGGTATATATACATTTTTT GAGATAAATTCTAGATTCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTAAATTAATCAAAGTATGTTAATGTCACCT GGAATTCATACATGGAAGGCCAACAAATAACTAAACTTGACTAATGAAG
WI-9523b	193 C A ---	---	GTGAAAAGTTTTCTATTCCATCCATACATAAGATTGCTAAGGATCATTTTGGAAAGATGTG CAGCATTGAGAAAGTTGATCTCATCATGCGAGTCAGTCAGCAGCATTTTATCTAAAGTACGTGCACA GACTCAGACAAATTACAAACTATTTCCAGCCATGATCTATGGTGATTTCCACACATTGTAC/C/AGTG AAAGCTCTCAGCTTGGAACAACCTTGTCAGGCGAGCTGCATGCACATATAT
WI-9523a	47 G A ---	---	GTGAAAAGTTTTCTATTCCATCCATACATAAGATTGCTAAG/G/AJATCATTTTGGAAAGAT GTGCGCATTGAGAAAGTTGATCTCATCATGCGAGTCAGTCAGCAGCATTTTATCTAAAGTACGTGCA CAGACTCAGACAAATTACAAACTATTTCCAGCCATGATCTATGGTGATTTCCACACATTGTACAGTGA AAGCTCTCAGCTTGGAACAACCTTGTCAGGCGAGCTGCATGCACATATAT
WI-9554	202 T C ---	---	AAAAACACAAGTTTCATACATCACAAAAACCTTCCATTATAACACAGAGTGATTATTACCAGAC AAGCATCAGTGATGATAGTACTGCTTNTAGTTGTTATGTACAATGCTGTAGATAATGCAGCCCATG CAATACACCCCAAGAACACTAGAGTCTACACCCAAAGTACAATATGATAAAGCAGCCCTCTGCAAGTG G/T/C/GCTGGATACCACTAAGAAGTCTACTGCAGCCATGTTGGTTATGATTTT
WI-9555	97 G A ---	---	CCAAAAGCCAAACCATTTCATATGATGGATTTTCATAAACATTTATGATCCTTTTGGAGTAAGTAT AAATACCTTTACATGGCTAACCTTCTAAC/G/CJTTGAAAAATCAATTTCAAGGGACTCTTTAATCA GTTAAATAATCTGCTTTAGAAAGGCACAAATGATCATACITCAGATTAAAAACAGGTAAGTATTCAG GGNTAAATGGTACAAAAAGGCTGTAACCTTTTNCITTCACATTGATCACA
WI-9625b	172 A T ---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAAATAGCTACCATATATTTGTATCTNCTCCTTGGGAAAAACCTTTGGAAAAAACAACACGCACA TAAGTATCATAACTGAGGGTTGGGACAAGTACTCTTA/TGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCATTTAAAAAACAACACACTGACAAATCTTTTC

WI-9625	172 A T ---			TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCCTGGGAAAAACCTTTGGAAAAAACAACACGCACA TAAGTATCATAACTAGGGTTGTGGACAAGTTACTCTTATGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTCATTTAAAAAACAACACTGACAAATCTTTTC
WI-9647	144 C T ---			TTTTCTGAGATTCAAGAGCTACATTTTGGTTAGTGTATGTACTATACCTTTTTTCATCCTTTCA ACATCTTTTGTACATTTTAGGTGATGCTCTGTAAACAGTGTATTGCTAGACCTAAAAATCCAAAGCT TACAACTTC/TGTCTTTACCTGATACATTTATCCATTTACTTTCAATTTGGATTTTAAAAATGTTA ACTTAATACGTCTCTTCAGATGCTCCTGCTTTTAGTTAATGTTGTTT
WI-9676n	114 A G ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCA/GjGATGTGGCTTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676m	184 G T ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGC/GjCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676l	84 A C ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676k	202 C T ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAAATAACTTGAGGj C/TjCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676j	92 C T ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676i	173 T C ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTjCjCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT

WI-9676h	134	C A	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCGCCCC C/AJATTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAATAAATTG AGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676g	202	C T	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCGCCCC ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAATAAATTGAGG C/TJGAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676f	184	G T	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCGCCCC ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAATAAATTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676e	173	T C	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCGCCCC ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAATAAATTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676d	134	C A	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCGCCCC C/AJATTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAATAAATTG AGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676c	114	A G	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCGCCCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAATAAATTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676b	92	C T	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCGCCCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAATAAATTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676a	84	A C	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCGCCCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAATAAATTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT

WI-9738b	40	C A	---			TGGACCAACACAGACAGATGTTATCCTGGTGCCTGTGTA/C/A/JATTACAACTCATTGATCACAATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAATGACTCCACATTTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTCACTTGCCTGGAGCGGGTGTGTTTTCATATGTGAGTATCTA TCITTTATTCTGTCCTTATGTTGGTGGCACAIGTGTATGCTGCC
WI-9738	40	C A	---			TGGACCAACACAGACAGATGTTATCCTGGTGCCTGTGTA/C/A/JATTACAACTCATTGATCACAATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAATGACTCCACATTTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTCACTTGCCTGGAGCGGGTGTGTTTTCATATGTGAGTATCTA TCITTTATTCTGTCCTTATGTTGGTGGCACAIGTGTATGCTGCC
WI-9756	47	A	---			ACTGAAATGTAATGGCAAGGCCACCCAGGACCTTAAATCATAAGAGTTAATCTGTGGGAAA GAGTAACACTACAAAAGCATCTAAACAGAGCAGGATGTGTAATGTGTCCCTTATCATTAGTC AGTAAAGATAAGAAAGCCCTGGTGGATCCACTTCCACAAACACACAGAAATATACACTTTTGGAAAG ATTCCACTTAACCACTTGATCTTCACTTTTATGATTTAAACCTCCGTTG
WI-9758	135	A G	---			GATGTCCTTAAGGATTGCTTGGTTAATGGGCAGACTGTGCAAAAGAGGCTGAATTGAATAAT TAGGAACTGGGAGAAATCAATCAAAGAAATCTTGTTCGCAAGGTCAATTTTATACTATTTA A/JGJTAAATAACTCTGTAGGTTCTATAGCAAAATGCTAAGTAAAGTAACCGCTGGTTTCTAAAT ATTACG
WI-9778	127	G A	---			ATTTAAATCCAGGCAGCGGGGAAAATGGATACTTTCATATGCTCTGTACCAACTATAAACTTTTG GTTCTCATGCACCAATTTTCAATTTTGCCTTCTCACTCCAAAGTACCAGTATTTTACCAATT[G/A]CTCTC ATAATTGACTTTGCTACTGGAAGAACTCTTAGAATGTTGAAATTTCTATTTACACACTTTGCCTCA AAGAATGTCAGTCAGTCAGGACTAAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116	C A	---			TCCTCCCTTTGCTCTCATGCCACTCCCTCAGGCTGCACAGAGCGTTTCTCCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACCTGCAGGACTTGTGACAATGCAGTTT[C/A]TGGATCCCAAGGAGG CTCAAAAACACTAGGAATTTGGGAGAAGAGGACCTGGAATCGGTGCTAGCAAGCCCCCAGGTGG TTTGTAGTGGACTAAAGTTTGGAGCCAGACATGGAAGGTGGCTTTGGC
WI-9841	101	A G	---			TGGAAAAATAGCTTTTATCAATCTCTGATATGCTACATATGTCATGGAGAAATGCAGATGGCATGA TATGAAATTCATTTTGAATGAATAAAATATAC/JGJTGTATGATATATATACATTAAACACTT AGGATTATACACACAATAAAACGCTGTGAAGGATAAACTAAGGTCTATCAGTGGGAAATGAGA TTGAAAAGAGGGGATGTTACTTGATATGCTGTTG
WI-9880c	222	G A	---			GAACTAACACCTTCTTCATGATGTTTCTTGTATTGGCAGTTAAATAAAATGTTATTAGATC ACTGGTCTCTGTGGGGTGTGATTTTATGATATCTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTGGACTATAAGATCCTCTTTTAAATATATTTTATATAAGCACATGAA AATGGAATGAAATAATGA/JGJTGACATAGGAATTACCTACATATTTG



WI-9880b	157	C A	---			GAACAAACACCTTCTTGCATGGATTTCTTGATTAATGGCAGTTAAACAATAAAATGTTATTAGATC ACTGGTCTCTGTGGGGTTGAGTTTTTATGATATCTCTGTTAGACCCATAAGGAGGCTGTGA GTTGTTTCTACATCCTTGGAC/AJATATAAGATCCTCTTTAAATTTATATTTTATAAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-9880a	108	C T	---			GAACAAACACCTTCTTGCATGGATTTCTTGATTAATGGCAGTTAAACAATAAAATGTTATTAGATC ACTGGTCTCTGTGGGGTTGAGTTTTTATGATATCTCTGTTAGACCCATAAGGAGGCTG TGAGTTGTTTCTACATCCTTGGACTATATAAGATCCTCTTTAAATTTATATTTTATAAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-10183	127	C T	---			ACACTGCAGGCACCTCCAAATCCTNACAGACATATGCACCTCGGAATCAACTCAGGCATGCACAGCAT CCCTGTGCTGGAGTTATTTTAAAAACAACGCCCCAGTTATCACAGTTCTNTTTTTGTTC/TTCCAC ATTTCCATAACAAAAAGAGCTACACAAAAATNNGGGGGAGANACTCTCTTTGGAGACTGACACATT TGCAGAGGGGTCATGAATAATGATTCCTCAA
FB25G10b	109	A G	---			TCCCTCAATGACAGATGAACATAATTTCTCTGGGTAAGAAATACTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAAATGGAATGTTGATTTTAGATCCTCCCCCAG TGACAAGTAAACTGAACCTGACCATAATTTATACATAAAATGGAATGTAAGAACCTATTTGGATATCC GGAC
FB25G10	109	A G	---			TCCCTCAATGACAGATGAACATAATTTCTCTGGGTAAGAAATACTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAAATGGAATGTTGATTTTAGATCCTCCCCCAG TGACAAGTAAACTGAACCTGACCATAATTTATACATAAAATGGAATGTAAGAACCTATTTGGATATCC GGAC
IB3071	102	C A	---			ACAACGCTGAACCTCCATAACAGTCAATGGTACAGTCAAAACATCACATGTACAGAACACACAATTTA GATGAACCTGAAATTTAAGNTAAATAAAATAAAATTC/AJCAATTTAGNAACAAAAATCAAAAC ATTAAGGNTCCCTGNNATATCTTAAACCCTAATGAGATTTTCACTGGNCTCAAGTCATTTTGTAGTGA GGCATTCACAATATGACCTATTAACCCAGTCTAGGGATTCTG
NIB551	161	C T	---			CGTCCCTTCCCTTTTGGATTGCAATTAAGTAGATAATATGAGAGAGAACTGACAATTTGGTTGTCC TACTGAGCTTGGGGCCAGGTGTGACTTAGGAACCCCAATCCCAAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGTCT/TTGACACACATACATGCGGCCCATTTGGTTGATTTCAGCTTT GCAAGCAGCGTAGTGAGAAAAACCAAAAGCTTGTC
S72904	51	G T	---			AGCATAGAAAGTGATTATATTTTAAATGGTTTCAAGTGAAGTCTCTTTG/TJAATTTGTGAGTTC ATTCTGGAATCTTTTGTAGTTAAATAAGGATCTTAGGACAGCACCTCGAACTACAGGCCCTAAA GAGAAATTCCTCAAAACCAAGTGTGTAACCTTCTCCCTTTCTGTCAATTTGGTTGTCTTTAAATA TTGCAAAAGTCTGTGCTAAACAGATTTTGGAGTGTTCAGTGTCTGTA

UTR-00481	115	CT	---	---	TATCTTTTATCCTGGGGCCACAGTCTTGATTATTCCTCTTGTTGTTAAAGACTGAATTTGTAAACC CATTGAGATAAATGGCAGTACTTTAGGACACACACAAACACACAGAC/C/JACACCTTTTGATATGTA AGCTTGACCTAAAGTCAAAGGGACCTGTGTAGCATTTTCAGATTGAGC
ESTC1	33	---	---	---	COCTGTAGCAGTCTTCAGCCTCCTACCCCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37	---	---	---	GCTACTACCACGGCTGCTTCGTTTGGACAAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21	---	---	---	GCCATCAAAAATTTCTTCACANTCAATACTGTTGAACAACAAGATAACACATCTTCTTGCTCATCCC ACTTGAA
ESTC107	20	---	---	---	TGCTGGCTCACCTTCCTCACANGCTGTATTACCTTTCAGAGCTGAGTGAGGCTGTGCT
ESTC109	35	---	---	---	AAAACAGGAAGGCCCTGCCCGCAGAGGCACATGNACAGGGCAGTGCACAGTGACC
ESTC110	23	---	---	---	AAACCTCACACAGAAAAAGAGGANAACACTCAGAAAATGTGATTACAGATTAGGCA
ESTC113	37	---	---	---	AAGGGACACAGTGTGCTGACAAGGTGACACTGAACANAACAGTTTTCTTTAATTGTAAAGCGGG CATCG
ESTC117	24	---	---	---	AATTGGCTCTTCTCCACATGATACNTAAGTTCAAGGTCCAAGTTCCTATCACAAITTTACAAAAAGC CTCCA
ESTC119	24	---	---	---	TGTCAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCTCTTT
ESTC122	34	---	---	---	GACAAATAACACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21	---	---	---	GAAGCCAGTATGTTGTGGCAANATTCGAGAAAAACACACTGAAAAA
ESTC128	42	---	---	---	GCAGAGGCATCAGATAAGGCCTCAGAAAGCCCCAGGCCATCATNTCCATGGGACCAGGCTGGCTCAA TGTTGGAACCTGG
ESTC129	20	---	---	---	AGTCACCATGCCAGCCTAGNATGAGTTTAGTAAGATTGGTTATGCTGGGGAG
ESTC13	46	---	---	---	GTGTATCTGGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA TCAGAAAA
ESTC130	49	---	---	---	GCCTGCTCACAAGGTAGACAAAAACATAAATCTTCAGGAAAATGAAACANGAGAAGCTGAAACAAT CTACACCTGAATG

ESTC132	30	---	---	---	---	GGTAAAGTCATAAATTACTGCCCTTAGCAAACNCIATGTTGTCAGGTTTTCTGCTGCA
ESTC137	21	---	---	---	---	CCAGTTTGGCTCTGTCCTCANAGTCTCTCTCCATGTTGGCAAACA
ESTC139	45	---	---	---	---	AGGAGCACAGCCTAAGGACATGAAGGTGAGAGTTTCTCAGAGGNGGGCTGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	---	---	---	---	CCCATTGTGTCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTCCCTTGCATGGTTAGAAAGC TTGCCCTGGTG
ESTC142	72	---	---	---	---	CCTAGGCTCATAACAATACAGTCTCAATACAAAAGACGTAATAATCTATTTTATTCAATTTAAATC AAAGANACCATTCCTATTCCTAACAAACA
ESTC143	29	---	---	---	---	GTTTACGAAAGTACTGAAAATGCTATTANTAGCTGAATTTGTGATTTCTTTTG
ESTC144	26	---	---	---	---	AAATCCATATTTCTTGACATGAGGTGCTTTTGTAGCAGCATTTTCGG
ESTC146	20	---	---	---	---	CATGTCAGGATAAGGAGCANACACCAGGATTTATACACGGTGGCAGCG
ESTC148	42	---	---	---	---	TCCTTGGTTGCTACACAGACACTTAAGTACTGTATCGCTGNATGAGGGCCTGTGGAGGCCCTCG GGGGTGGCTGGGCTGTGCTCTGAG
ESTC149	28	---	---	---	---	TCAGTTCAATTTATTTGCTTTAAGAGTTANATACCATGAGACACACAGTTCTGG
ESTC15	28	---	---	---	---	GGATTGTAATATTGCCAGCTTTGTAAGNCATTAAGCAGAGTTTCTCAGTGAICTT
ESTC150	20	---	---	---	---	CCAGGAAACAAGCAGACACANACTTATAGAACTATTTGGTTTAAAAATTATTCATAATATCAATATT AAACCTGATGTTTAAAGAACCTAATGAGA
ESTC151	49	---	---	---	---	GAAGCTAAGGCCCATTTTTTTCTTTTAATACAAATCTACTGGTGTNAAAACTCAGAGCTTAGGA AACACAGCC
ESTC155	37	---	---	---	---	TTTTTAATTGACAACCTCAATCTCTACATACATACAGTNTTGCACGAATTTAAGTGGATCAACAATT ATATTATTGATAACAACCTCATGAGCATTTTACA
ESTC156	32	---	---	---	---	GCAGCATTTGTGACAGGAGAGCGCAAAACAANCTGGCTCGCTCGGGATGGAGCGGGCGGCCTCA CCACCCTGCAT
ESTC158	35	---	---	---	---	ACCAAGCCCTGGGAATTTACTGCTTGTATGACTACANGGCTTTGACAGTCTGAGATGCTTCAGTGTGC AA
ESTC159	31	---	---	---	---	AGCTGGCAAGAGACTTCTGAGGACATCAGNTACGTTGGTCAATTTAGGGCACGGTCTGGTTCTGCA GCTTTGAAGG

ESTC16	23	---	---	---	---	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCACAGTGAATCATCACCAAGGACAGGTT
ESTC160	38	---	---	---	---	TTCTAGCATTGCTGTGCAGTGGGGCCCTGAGCTGGGNGCAGTCGGCAGTGTCACTGGGCCCGGTTTG GGACTGGGTGA
ESTC162	36	---	---	---	---	CTCTCGTCGGTTGCAAGTTGCTGTTTGTCCAGNTACACCAGTCAGAGCTCCACAG
ESTC164	31	---	---	---	---	TCATTCTCCATAGAATAITGGTTTGTAAACANCGAATACAATCCAATATATAACATTAACAACAATCC GATACATACCA
ESTC169	22	---	---	---	---	GTCTCTGGTGTGCAGGGAATCANTTTGCTGGATTAGAGGAAGGTGCCCGCTCTGTTCATGACTT
ESTC176	23	---	---	---	---	CACCTCTCCCTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA
ESTC177	42	---	---	---	---	TGGTGGCTCTTAAATACCTTCCATTATATTTTCAAAATTTTNCCTTATTCTATTAATAACCTTTTAT TCTCTTTATTCCTATAAAAAGGCAACCAA
ESTC18	29	---	---	---	---	TCAGACACTGCCGACATCAGCATTGTCTCNTGTACAGCTCCCTTCCCTGCAGGGGCCCTGGGAGAC AACTGGACAAGA
ESTC181	21	---	---	---	---	TAGGGATTCCAAGTTGCCTGGNTTAAATAATAATACATATTACAAAAATTTACACAGCTCATGCATAC CA
ESTC186	43	---	---	---	---	GCTTGACTAGCAGGGCTACATCACAAATTTATAAAGTGCCAGATNAGTGCTAATTGTCTCAGCTTG ATTTTTCACCTCA
ESTC187	24	---	---	---	---	ACCATGATTGCCCTCACACAAGCATNATCAATCGCCACGAGAGCTGGATGCCAAAAGAGTATGGCTGG
ESTC188	25	---	---	---	---	TCTATTAAACAGGGTTATGTACACACCNCTGTCAACCTCAAAACAGATGATACTCATCACTTGTCTTCCAT CTTGC
ESTC189	27	---	---	---	---	AAAGTACAATCCAGTATATGCAGAAAAGTACTCAGCATCACACTCGTGATCA
ESTC196	42	---	---	---	---	TCCTCAAATACCACCTTCCCTAACTTATCAGTCTAGTAAGCNNTTCAAAAGGAGGAAAATGGGTAC CTTTCAGGGG
ESTC197	26	---	---	---	---	ATCTCCAGTGTCTGCTGCCCTCCTCCCNCGCAAAGTCTCCACAAAGCACA
ESTC20	33	---	---	---	---	AAGATTAGGACAGACCGCGTATAGTAAGCTCTGNGGAACTCCAAGAATCTAGAGGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC200	44	---	---	---	---	TTTGGTGAAAAATCCCAATATATGAGTTTAAAAAATAATCATTANCATCATTAACAGTACTTTAAAT CAATTACTCTTTTGGCTGCAACAG



ESTC28	23	---	---	---	GAAGAGCTGGGCACGCACTGACNTTTCTTCCTCTATCCCTATAAAATAAGGAAGCAGAAATCTG
ESTC3	20	---	---	---	CAGACATGACCTACCGTCCNGGCCCTCAATTCATATTTATCTTGAGCCGCTTGTCAGGTTTGATTCGCACACTCC
ESTC31	32	---	---	---	ACAGCCCCACAGAACTATTGTAAACAATAATNTCAGTCGGTGATCATTTGTAATATACAAATACAAAGCAATTTCCTCAGA
ESTC33	25	---	---	---	AGCACTTCACGCTCCTTGACGTTGNGGACCCAGGGAACCTCCGGAA
ESTC39	26	---	---	---	AAGAAAGGAACCCACCTGGGCTTNGGTCACAGAACTCAGAGCCTGGGCAITTA
ESTC4	23	---	---	---	CCACTGAATCACACAACATGGACNAATCTCAAAATCATTATGCTGATGGAAAGAAACCAATT
ESTC40	22	---	---	---	GGCATGCTAGACAGAGGCATTANTTTGAAGATCTTTTAAATAATTTTGACTTGTTCCTCCCTTCAC
ESTC45	37	---	---	---	TTTGAGGTTTGTGCTGGAGTTTGTCTTTGTACNCCTCATCATCGAGGCTATATATTA
ESTC50	56	---	---	---	CTGCCGTGGTGAGCCCTGCCGCTGCCATGGGCCAGGAGCCACTGGTGCGGANGCGGGCAGATGTTTACCCCTGT
ESTC56	45	---	---	---	GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGGTTGGCAGGAAGNAGTGGAGGGAAGGACACCAAGT
ESTC57	20	---	---	---	AAGTGGGCCCTCCAGTCCCNCTCTGGGCACAGATCCCACCACTGCTC
ESTC59	38	---	---	---	GAAACACAAAAGTGTGAGAAAAAACTCTCAAAATTTGTCAGACTTCAGGAAAAATGATTTCCACATGGTAAGGCC
ESTC6	27	---	---	---	TCTGCAGCACTTCACTACCAATGAGCNTTAGCTACTTTTCAGAAATTGAAGGAGAAAAATGCATTATGTGGACTGAACCG
ESTC61	57	---	---	---	AGTGATTTGGCTAGGCGTGGTTCTCATCTGTGAAATTCACAGCGCAATGACAGCANCCTCTCTCCCACTCAAG
ESTC63	20	---	---	---	ACAGACAGCATCACACCANAGGGGCCACGGGAGGGTGGGGAGACGACACTTTTCCCTGGGAAAGGCAGCTCTAATC
ESTC69	20	---	---	---	GAGAGGCTAGTCAGGAGGANACCCTCAAGTTAAATCCACACACTTACTTACTGCTCATCCGTCACITTCGCTAA
ESTC7	45	---	---	---	AGTTCCCTAGAGCTGTGGGCCAGATAGTGTCTCTGAGTTGCANGCAGATGGAGATTTGGACACTG

ESTC72	37	---	---	---	GGGCTCCAAAATGGGTATTGGGCCAGGAGGCTGGCNITTTGGCGTGACGCCCTAAAAAGTGTGACC AACAAATTCACAGCTACAGGAAATCTAGAACAAAATCAAAATTCATCNCNTTGGGTGAAAAAGTTG GAAGA
ESTC74	49	---	---	---	ATGACTTCTGTCCCATCGGAACACAGAGTTTCCCCAGGNGAGCCCTTCTATCTCGGGTTA
ESTC77	40	---	---	---	GGCTCAGCAGAGGGATAGANCCCCACTCCGCATGTCCCCAGAGGGCAGCACTCCAG TTTCAGATGATGGGTCTGAGATGNTCTCTCAGGCTGCATCAGCTGCTTCAGTCTCCAGAACAGAAA GAGCCTGACCCA
ESTC81	20	---	---	---	CAAAATCAATACACAGATCCAGATATGTGAACCATATATACATATCTATACANCCATTATTTAGAC TTTCACAAACCT
ESTC82	25	---	---	---	TTTAGCTGCTATACCAAGTTTCCATAAANCTGTGTGCTGTTGGGAGGCTACAGCCTGACCACATTCT TTTGC
ESTC83	53	---	---	---	ATTGCAAAGGAAGTGAACGCTGNTCAAACACAGAAAATGGTGACAAATGA
ESTC85	28	---	---	---	CTGGTCTCTTCTGCTTGGCAATCTGCTCTCTCCTCNGGCCAGTGTCCACCCCAAGTGTCTTCCCGATGAT
ESTC89	22	---	---	---	CTCCCTCTCTCAGTTCACAGTGGAGACTANGGAGATTACAGGCAGGATCC
ESTC90	33	---	---	---	GCACGTTCTTTGTTCTCTCTCCAGAAAGTTGNAGACGCTATTTAGTTTGATTATCTGTCG
ESTC93	29	---	---	---	AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTCCTAAATTC GTGGATCTTCCCTGGCCACCGTTTGTATTGAGCTGCAATGCTTCTTGAATCTTCTCCA[CT]GCCAG ATTCCTTAAATGATCTTTCACCTAAGAAACAGCAAGAAATCTTGGCAAGCAGCATCTAGAGATAC ATCTTATTGCGATTTTCACAAAATCAAAATCAAAAGAAAGAAAGGCTTAGCTG
DWU-100	127	C	T	---	TTCCATCCTAGATATCTACTCAAATAATTGAGACAAGTGTTCAAACAGAAAGACGCTTGTGCTGAA TGTTTCATGGC[AG]GCCCTATTCACAGTAGCCAAACGATGAACAAACACCCCAAGCTATATATACCA GATGAAGGATAAACAAAATGTGGTCCATCCATCAATGGAGTATTACACAGCCATAAAAAGGAAT GAAGCAGTGTCCCTACTACACTGTGGAT
DWU-177	77	A	G	---	CAAAATCCTGGACTATCAACCTTGTGCTTAATCCCTGCAGCATTCAGGTTAATCCATCTAAGTGAC ATTTTGTAAATTCACAGGGTCCACCCCAATCATGCCAGCTTCTGTGATATGAATGAGATATACATTT ATGCTGACCTTCCCTCAAGACTGATTTTTCATGCTGGGACTTACAATATCTCAAGGAACAGCAATG TCAACAGGG[AG]TGGGAAACCCAGCCCTATCTGAGTCTTGGCTCCCTCC
DWU-286	213	A	C	---	

DWU-252	94	A G	---	---	AGTATACAAACATTTAAGCTGTGGTCAAGGCTACAGATGTGCTGACAAGGCACCTTCATGTAAAGTGT CAGAAGGAGCTACAAAACCTACCCCTCA[G]TGAGCATGGTACTTGGCCCTTTGGAGGAACAATCGGC TGCATTGAAGATCCAGCTGCCTATTGATTTAAGCTTCCTGTTGAATGACAAAGTATGTGGTTTTGTA AT
DWU-330	85	C T	---	---	GAACATTCCTCTGCAGCACCTTCACTACCAAAATGAGCATTAGCTACTTTTCAGAATTGAAGGAGAAAA TGCAATTATGTGGACTGA[C]TCGACTTTCTAAAGCTCTGAACAAAAGCTTTCTTTCTTTTGCAA CAAGACAAAGCAAGCCACATTTGCATTAGACAGATGACGGCTGCTCGAAGAACAAATGTCAGAAA CTCGATGAATGTGTTGATTTGAGAAATTTTACTGACAGAAATGCAATCTCCCT
DWU-370	231	A G	---	---	GAAAAATTAAATTGGGCAGGTGAAAAGGGTACAGATGTGCTGAGCAGACCTTTGGTTTTAAAGAG AAGCATCATTTCCCAACAGGGCAACTGTAGAGGCCAGCTGAAGAGTAAAGGAAAAGGCTGAGG ACTGAGCCTGTGGCTGGCTGGAAAAGGTGAATGTTGAGGGCCCTTCACTTCCATCACAAGAAAGTC ATTAGCGGTACCAATTCAGTGTCTGTTCTCT[A]G[GCATCTATTTCTCTGTGC
DWU-1537b	89	A G	---	---	CTCTTAACCTCAGTTCCCTCATCTATAAGAAATAGGGATTTCAGTTGTGATCACATAGCTCAGGTAATC CAGGACCAGAAACCCAGGAGC[A]GTTGGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGAACACACAAGAAATCCAGTAAGCAGCACACACTGGCTGA
DWU-1537a	52	C T	---	---	CTCTTAACCTCAGTTCCCTCATCTATAAGAAATAGGGATTTCAGTTGTGATCA[CT]ATAGCTCAGGTA ATCCAGGACCAGAAACCCAGGAGCATGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGAACACACAAGAAATCCAGTAAGCAGCACACACTGGCTGA
ESTD-ADAb	196	C G	---	---	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAAGGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCAGCTCCACCCAGAGGCCCTGGGGAATCCAGGGTCACTGTCTCTCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGGCCCTCGGCACTGAGCTG[C]GAGA CCCGCAGACCACCTCCTGAGCTTTCTGGGCCCTCTGAGTCTTGCTCTC
ESTD-ADAA	184	G A	---	---	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAAGGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCAGCTCCACCCAGAGGCCCTGGGGAATCCAGGGTCACTGTCTCTCTCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGGCCCTC[G/A]GCACTGAGCTGCAGA CCCGCAGACCACCTCCTGAGCTTTCTGGGCCCTCTGAGTCTTGCTCTC
ESTD-ANT1	160	T C	---	---	TCCTCTGTCACTTCTACTCCATTAGTTCAGGTCAGTGAAGAACTGGGGCAATTAACCAAGTAATCA TGSACTGCCAACTGCGAAACAAGAGGGCGAGTGGAGCAGGATATTATGCTACGCGGTTACCTT TTTTATGGAGGACCAGAACTGAGGCTT[C]GAGCTCAGATGATCCTGT
EST10398 2b	168	A G	---	---	TGCCTGGGGTGGCAAGGCTGCAAAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTATCTACTTGTATGATGTTTACATTTGGGGCTTGACTTTCCAAACGAGAGAAG CATTTGTTTTCTTCGGGCCAAGAAGGTATCTACCTACCA[G]ATAGTGTCTATTAGGCATTTG



EST10398 2a	147 C T	---			TGCCTGGGTGGCAAGGCTGCAAAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTATCTACTTGTATGATGTTTACATTTGGGGCTTGACCTTCCAAACACGGAGAAG CATGTTTCTTTC/TGGGCCAAGAAGGTATCTACCAATAGTGTCTATTAGGCATTTG
ESTD-C7	14 G C	---			ATATCGTGGCCTTA/GCTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD- D4S95	90 T C	---			CTTTTCATGCACGATAGGCTTTCTCTACTAATCACAGAAATTTGAGAAGAGCAAAACAACCTTTCAAGG ATAATGGGCAATCATTCTTTT/CCTCTTTAGAGCTACCGG
ESTD- GPPK2L	38 G A	---			AGTCTTCATCTGCGGTGTCCAGGTAGATCCCTTTACCG/GA/CAGAGAACTGCTCGATATC
ESTD- HRASb	82 A G	---			CTGGGCTGCCCGCAGCAGCTGCTGGCACCTGGACGGCGGCCAGGCTCACCTCTATAGTGGGTCG TATTCTGCCACAAA/A/GTGCATCTGGATCAGCT
ESTD- HRASa	37 C T	---			CTGGGCTGCCCGCAGCAGCTGCTGGCACCTGGACGG/GCTGGGGCCAGGCTCACCTCTATAGTGGGG TCGTATTCTGTCACAAAATGCATCTGGATCAGCT
ESTD- NRAMP	81 A G	---			GGAGCAGGAGGTGGGAGGGGGTCTGCTCTCCAGGTCCACAGACCAGAGAGCGGCTCAGTG TATCCCCACCCCA/A/GTGGGGCTGGGAGATGAAGAGGAGTTGATGCAGGT
ESTD-OTC	18 A G	---			GTGACCTTCTCACTTTAA/A/G/AAACTTTACCGGAGAGAAATTAATAATATGCTATGGCTATCAGC AGATCTGAATTTAGGATAAACACAGAAAGGAGGATGTAACA
EST36751 7	36 C T	---			CCAAGTCGTTCAATTTAGCTTTGCAGGTTTAACT/C/TGATTACTTTTCTATTCAAATCTCTGTA AAATTGAATATGAACCTTAGTTTCTGATCTATGGTTTCAAGTTAAACAG
EST40562	109 A G	---			CACGTGGAAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAAATCTGCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAAGTTTCACTGGATGCA TTAATAACAAAT/A/G/TTTACCTTTTGAATAATAA ATGAAGGATTTGACCTGCTTGGCTCTGGAAAGAGTATCCGTACCGTCCCTGACGTTTGAACAATACA GATGCCCTCCCTGTAGCAGTTTTCAGCCTCCTCTACCCCTA
EST18288 3	121 C T	---			GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTTCATGCAGGCTGTGACAGGATGAAGACTGGCTGCTCCCTGA/C/TGGGAGCCAGT GTGGACAGCACCCCTGGCTTTCAACACCTACGTCCACTTCCAAGGTAAAGCAAACTCTCTGCTGGCTC TGGCCCTAGGACTTAGTATCC
ESTD-AK- 168	31 C T	---			GGGAGTGACAGCTAGAGCACCAAGGGGGGCT/C/TTCAGCTGTGTTCTCATGGAGGACAGGCTTCT GCTCATCTGG
ESTD-ALB	180 A/G	---			AATCCAGCAGCTTAGGAGGCTGAGGAGGCATATACCAGAGGTACAGAGTTTGAGACCAGTCTGA CCAAACATGGTGAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGCGATGGTGGTGCATGCCGTG AATCCAGGAGGCTGAGGAGGAGATCGCTTGAACCTGGGAGGCG/GAGAGTTGTGGTGAGCCGA GATGGCACCATTTGCACCTCCAGCCTGGGCAACAGAGTAAACTCTGCTCTC

EST70523 3	182 G T ---	---	---	TTCCGGCAGCCCCCCTTGGCACCTGGTCCCTCAGGGCCACCCGCGGCACTCACCGCTCT CGCTCTCGGTAACTCCGGCGCGCGCTCTTGGACATAGCTGGACCGTTCCGTATAGGAGG ACCGGTAGGCGCTTCTGTCCCGGCGCTTGCAGGGCCAGCCCTGTCAGAGAGGGGCTCCCTGT GGTTGAGCTGAACACAGCTGTGGAGTGTCTCCACGTC
ESTD- APOA2	101 C T ---	---	---	CCAGGTGTTGGCACGTCCTGTATCCAGCTACTCGGGAGCTGAGGCATGAGAACTCTTTTGAAC CGGGAGGGGAGGTTGCAGTAGCTGACATCGTCGTGCCACTGCACCTCAGCCTAGGTGACAGAGC AAGACTCC
EST58707 7	112 C T ---	---	---	CAGTGTATCTGAAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTGGTTACAGGAGCTTT AAGTTACGATCTTTGGCTCACATGAAGGCCAAATTCGAGAGACCTCTAGAAAGATACACGAGAC CGAATGTATCAATGGACATTCAGCAGGAACCTTCAACGATACCTGTCTGTGTAGGCCAGGTTTATA GCACACTTGTACCTACATTTCTGATTGGTGACTCTTGTCTGCTAAGAACCTT
EST74167 6	137 C ---	---	---	AGACATGAAGGAGTTGAAGCCTACAAATCGGAACCTGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGGGCGACGGCTGTCCAGGAGCTGCAGGGCGGCGGCGGCGGCGGACATGGAGGA CGTGCGGCGCGCTGTGTCAGTACCGCGGCGAGGTGCAGGCCATGCTCGGCCAGAGCACCGGAGGC TGCGGTGGCGCTCGCTCCACCTGCGCAAGCTGCGTAAGCGGCTCCTC
EST43211 8	132 C ---	---	---	CGCTGGTGCACTACCGCGGCGAGGTGCAGGCCATGCTCGGCCAGCACCCAGGAGCTGCGGGTGG CCTCGCTCCCACTGCGCAAGCTGCGTAAGCGCTCTCCGGATGCGGATGACCTGCGAGAACGCGC TGCGAGTGTACAGCGCGCGGCGCGCGGCGCGGCGCGGCGGCGGCTCAGCGCCATCGCGAGCGCGCTG GGCGCCCTGGTGAACAGGCGCGCTGCGGCGCGGCGGCGGCGGCTC
ESTD- ARSB	126 A ---	---	---	GGAAGAAATGGAGCTGTGGGAAGGAGGCTCCGAGGGGTGGGCTTTGTGGCAAGCCCTTGCTGA AGCAGAAAGGCGGTGAAGAACCGGAGCTCATCCACATCTCTGACTGGCGGCGGCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTCGACGTGTGGAAACCATCAGTGAA GGAAGCCCATCCCCAGAAATGAGCTGCTGCATAATTTGACCCCAAC
EST36770 4	144 C ---	---	---	TGTAGCCAAAGTCACCTGCATCATATTGGCTGCTGGCAGGCTTGGCCAGTTTGCAGCTATAATCC ATCGAAATGATTTTTCATTGAGAACCAATATTACAGTTTGTGTTTCCATTATGAGTCCCAAAAT TCAACCTCCCGATAGGCTGGGCTGACCAAAATATACTGGTTTCTGTTTCTCTTCTGATCAT TCTTACAAGTTATAGTCTTATTGGAAGGCCCTAAAGAAGGCTTATG
EST26021 1	137 A ---	---	---	TAATGTAAGCTCATCCCAAGAGCGCTGCACCATGTTTGGAGTTGAGTGACATGTTCCGAAACCTGT CCATAAAGTAATTTGTGAAAGAGGAGCAAGAGAACATCTCTGACGACTTCACTACCAAAATGA GCATTAGCTACTTTTCAGAAATGAAGGAGAAATGCATTATGTGAGCTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTCTTCTTTTGAACAAGACAAAGCAAGCC
ESTD- BA511	29 A G ---	---	---	GGGCAACATAGTGAAACCCCATCTCTACA/GIAAAATACAAAAATTAGCCAGGTGTGGTAGCAAG TGCCTGTAGTCCAGCTACTTGGAGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTG CAGTGAGCCAAGATGGTGCCACTGCA

ESTD- BCL2	116 A G ---	---	---	AGCTGGATTAACTCCTCTCTCTCTGGGGGCGGTGGGGTGGAGCTGGGGCGAGAGGTGCGCGTT GGCCCCCGTTGCTTTCTCTGGGAAGGATGGCGACGCTGGGAGAAC[A/G]GGTACGACAAACGGG AGATAGTGATGAAGTACATCCATTATAAGCTGTGCGACAGGGGCTACGAGTGGGATGCGGGAGATGT GGCGCGCGCCCGCGGGCGCGCCGACCGGATCTCTCTCTCCCA
ESTD-BCR	69 C T ---	---	---	CAGTGGCTGAGTGGACGATGACATTAGAAACCCATAGAGCCCGGAGACTCATCATCTGCGCAAGA GA[C/T]CAAGAGGTCAGCTTCTGTGTCGGGAAAGGAGGAGGTGACAAAGCTAACTCTGCTTC AAATCAACCATCCGGTGGACACTGTGTGGCTGCCATCTGCTGGCACA
ESTD- BRCA1aa	119 C T ---	---	---	AAGAAGAGAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTAA GTGGAGAAAGGGTTTGCAAACTGAAAGATCTGTAGAGAGTAGCAGTATTTC[A/C/T]TGGTACCTGG TACTGATTATGGCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCAGCTCTAGGGGAAGGCAAAACA GAACCAATAAAT
ESTD- BRCA1bb	139 A G ---	---	---	ACTAAATGTAGAAATACTGCTAGAGGAAACCTTTGAGGAACATTCATGTACCTGAAAGAGAA ATGGGAAATGAGAACATTCCAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAATGTT TTTAAAG[A/G]AGCCAGCTCAAGCAATATTAAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCA GTATTAAATGAAA
ESTD- BRCA1cc	126 A G ---	---	---	ATGCATCTCAGGTTTGTCTGAGACACCTGATACCTGTTAGATGATGGTAAATAAGGAAGATAC TAGTTTTGCTGAAATGACATTAGGAAAGTTCTGCTGTTTTCAGAAAAGCTCCAG[A/G]AGGA GAGCTTAGCAGGAGTCTAGCCCTTTCACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGCCA AGAAATTAGAGTCTCTAGAAAGAGAACTTATCTAGTGAGGATGAAGGCTTCCC
EST51212 0	122 A C ---	---	---	ATCCTGAGCTCGCCAAATAAGCTTCTTGGTTCTACTTCTCTCTCCAGAGCCCCAATTTCACTTCTCA GAGGAAATCCCAAGCTTAGAGCCCTGGAGCCCTTTGTGCTCCCACTCAATACA[A/C]AAGGGCCCCCT CTCTACATCT
ESTD-C1R	40 A G ---	---	---	ACACAGGTGCTGGCACTGGGGTGGGATCCTCTCCCT[A/G]ATTGCTCCGGGAAGCACATTTCAT CAA
ESTD-C1R	40 A G ---	---	---	ACACAGGTGCTGGCACTGGGGTGGGATCCTCTCCCT[A/G]ATTGCTCCGGGAAGCACATTTCAT CAA
ESTD-C6	31 A C ---	---	---	CCAGTCACTTTGGGGACAGCCATGCACCTG[A/C]GCCTCTGTGTAGCCCTTTCAACCATGCATTCATC TAAGCTCTGCAAAAT
EST20118 2	119 C ---	---	---	GTCCGAATCCTCCTCTGAAAGTGGCGGGTTTAACTGCTCATGACGCTGGGCTGTGGTCCAGCT GAGGTGAGGGGCTTGAAGCTGGGAGTGGGTTTAGGACGCGGGTCTCTGCTGCATCCTAAGCTCT GAGAGCAACCTCCCTTGAAGCTGGGAGTGGGTTTAGGACGCGGGTCTCTGCTGCATCCTAAGCT CTGAGA
EST53018: 6	67 A G ---	---	---	ACAATCCAGGTACACATTCAGAAAGAGAGGGGTGGTGCAGTGAGCCTGGGTAGGTCCAGTAATCCA [A/G]GGATTGAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC

ESTD- CB22	119 C T	---	---	GGCAAGTTTATTGATAGAGAGGAAATCAAATAATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGGAGTGGCAACCCATAGGGCTTGGATACAAAAG ACAGGCAAGGAAGGGGTAGAACCATCAAAGAGGAATAGGCTGGTGAACCCCAAGCAAGGAGGACCT AGTAACATAATTGCTTCATTATGGTCTTCCCGGCTTCTCTCACACAC
ESTD- CB23	136 C	---	---	TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCATTATGGTCTTCCCGGCTTCTCTCACACATACAGAGCCCTACAGGACCAGACAGCT CTCAGAGCAACCCTAGCCCAATTACCTTCCCTTCCAGAGGACCTGAAAAACGTGTCCCAACCCGA GGTGGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAA
ESTD- CB24	145 A	---	---	ACAGGACCAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTTCCCTTCCAGAGGACCTGAA AAACGTGTTCCACCCGAGGTGCTGTGTTGAGCCATCAGAGGAGATCTCCACACCCAAAAAG GCCACACTGGTATGCTGGCCACAGGCTTCTACCCCGACACAGCTGAGCTGGTGGTGAATGG GAAGGAGGTGCACAGTGGGTGACACAGACCCCGACCCCTCAAGGAG
ESTD- CB25	146 A G	---	---	GTTTCTTTCAGACTGTGGCTTACCTCCGGTAAGTGAGTCTCTCTTCTCTCTATCTTCGCCGTC TCTGCTCTCGAACCCAGGGATGGGAATCCACGACACAGGGCGTGAGGAGGCCAGAGCCACCTG TGCACAGGTGAGCTACATGCTCTGTTCTTGTCACACAGAGCTTACCAGCAAGGGTCTCTCTGCC ACCATCTCTATGAGATCTGCTAGGGAAGGCCACCTTGATGCCGTG
ESTD- CB27	125 C T	---	---	TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAATAGGCTAAACCAATAAAAAAT TGTTGTTGGGCTGGTGCATTCAGGAGTGTCTGTGGAGTGTCTCATCTACCTAGCCTTATCTCTC TGATTAGGGAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCCAATGCT GCTTCTCTGTTTCATCTGATGGAAGTCTCTCAACACCATTTCCATACC
ESTD- D4S338	59 A T	---	---	TTTTCTGTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGA/ATATGTA TTTCTTAAACAATAAATCTGAAAGTCCAAAATTACTCTTGATCCATGGACTGCAGAATAAATGTTA TTTAGCTGTGAGAAAACAATACTAATCTTGATATGTTTCATCAGAGCCCTTGGTGACCAGGTGA TTGCCAATAAGCAGTAATATTTGAGAGGAATCTTGTTTTCAATGCAGTAG
ESTD- CYP2D6	61 A G	---	---	CAGGCCAGCGTGGTGGAGGTGGTCAACCATCCCGCAGAGAACAGGTCAAGCCACCTATGCAGJCA GGTCTCATCATTGAAGCTGCTCTCAGGTTCCCTTGGCCTGAGCAGGGCGGAGGACATCTCGG AAAAAACAATTTAACACCTTTCAATCATATACACATA/ACJATTTCCATTTTCACATAAGTCA GTTTGAGCTGAGTTTCCAAATTAATGCAATCTAAATGTCAATACTGATTAAATGCAAGTTTCAACAG ACAACTTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGATTAAATTATGCCCA TATCTGCATGTC
ESTD- D11S1873	40 A C	---	---	CATCCCCAAGCCCATGCTTTAGCCACTGGCATTTTTCGCCGCTCTGACAGATACACTCAGGCGCGT CATGCTGCACATCCAGGGGGGCCCTACCTTTGTAGTCCATGGAAAGGCTCCTCTGGGCGCGTG GGGTGTGTTGCTATGTTGGTCTGTGTAGAC/CTGGGGGCTTGGTTTCAGTTGCACCTATTGCGTT ATTGCAGATTGCTTGTCTTCCACCTGAGCGAGCCTC
ESTD- D17S33b	169 C T	---	---	

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ESTD- D17S33a	75 C T ---	---	CATCCCCAAGCCATCCTCTAGCCACTGGCATTCTTTGCCGCTCTGACAGATACACTCAGGGCCGT CATGCTGCTACACATCCAGGGGGCCCTACCCCTTTGTAGTCATGGAAAGGCTCCTCTGGGGCG GTGGGTTGTGGCTATGTGGTGGCTTTGTAGACGGGGCTTGGTTTCAGTTGCACATATGCGTT ATTGCAGATTGCTTTGCTTTCCACCTGAGCGAGCCTC
ESTD- D18S8	133 A G ---	---	TTTGAGACCACCTGGCCCAACATGGCGAAATCACATCTACCAAAATTACAAAATTAGCTGGGTGT GGTGTACATGCTATCGTAATCCAGCTACATCGGAGGCTGAGCAGGAGAAATTCCTTGAACCCQA /GJGAGGCAGAGCTTGCAGTGAGCCAAAGATCACACCCTGACACTTACAGCCTGGGTGACACAGTGGA GACTCTGCTCAA
ESTD- D3S11	44 G ---	---	AACCTGATTAGAACCTGAAATACATAATTTATCTGAAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAATAAATCCAATAAAGTACACTGTAATAAAGAAATTTAACAGAAATATCATTTGT TTATTCAAACTATTTATCACCTTATTTATTGGTAAGCCATACTAAATTTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	37 A G ---	---	AGGTTCCACATTATTGCTGATGTTTGTGATGTTTCCAGJGAGGCTTGATGTCAATCTGTATCTCCT CAGGTATCCCACCTTGAGACGTACTTTTCAAAAACCTCTACAGCCGTTGTTGTTAATTCAAGGT TGAACATAAAGTA
ESTD- D3S2b	247 C T ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTGCG TGAGTCTTATTCAAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATCCC AGAAGTGAACATACCTGCTCCTAGAACCCAGAGTCATACCTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGCTCTTTATTGGAAGGATGCCGTTGTT
ESTD- D3S2a	248 G ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTGCG TGAGTCTTATTCAAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATCCC AGAAGTGAACATACCTGCTCCTAGAACCCAGAGTCATACCTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGCTCTTTATTGGAAGGATGCCGTTGTT
ESTD- D7S399	83 A G ---	---	TGAATCTTAATTGCTATCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGJGICTCTCCTACATCATCCTTTACAAAACATTTTCATCCATGGACTCCATAC TAGAATATTGAGAAACAAACATGACAAACATTTTC
ESTD-DMb	146 A C ---	---	GTGGGACACCCAGGGCTCCAGGCTGGGCGCTTGCACGTGTGGCTCAAGCAGCTGCTCGGCCCTCCACT TCCATGGGTGTGGGCTGGGACCTCACTGTCCCTGGGGAGAGAGGAGGAGTGGGGAGGAGACA GAATGCTGATTJACJCTGTGGTGGAGAACCAAGAACTCTGGCTGTGGTAGGGGCGAGCTGCTTCCAAG ACCTCCTGATTGTAGGAAGGGGAGCAGCAGAGCGAAGAGAACAGAT
ESTD-DMa	66 C G ---	---	GTGGGACACCCAGGGCTCCAGGCTGGGCGCTTGCACGTGTGGCTCAAGCAGCTGCTCGGCCCTCCACT GTTCCATGGGTGTGGGCTGGGACCTCACTGTCCCTGGGGAGAGAGGAGGAGTGGGGAGGAGAGA CAGAATGCTGATTATCTGGTGGAGAACCAAGAACTTCTGGCCTGTGGGTAGGGGCGAGCTGCTTCCAAGA CCTCCTGATTGTAGGAAGGGGAGCAGCAGAGCGAAGAGAACAGAT

ESTD- DRD1	154 C T ---			TCCCAGCCCTATCGGTCAATATGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAAACCCATCAC ACAAACGGTCAGCACCCCAACCTGAACCTCGCAGATGAATCTGCCACACATGCTCATCCCCAAAGCT AGAGGAGATTGCTCTGGGG[C/T]TCGTATTAGAACTAAGGTAC
ESTD- DRD2	144 C ---			TCTGCCTTGGTCAGGAGGCTGCCCGCGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGACCCGGTACAGCCCATCCACCCAGCACCAAGCTGACTCTCCCGACCCG TCCCACACGGTCTCCACAGCACTCCGACAGCCCGCCCAACACAGAGAAGATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	109 C T ---			AAGCAGTGGCCAGGATGAGCGCGCAGTAGGAGAGGGCATAGTAGGCATGTGGCGGGCCCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGATTTCAAGTGG[C/T]ACTCAGCTGGCTCAGAGATGCC ATAGCCACAGAGGAGGTGCGTGATGCCAAGGGCTTCTGTGAGGAGA
ESTD- ERBB2	93 C T ---			TCCTTCAGGATCCGCATCTGCGCCTGTTGGGCATCGCTCCGTAGGTGTCAGCGGCTCCACCAGCTGG GGTGAGGGGGTGGTGGTCACTG[C/T]GGGGGCGGGTGCAGACCCCGGGCTGGGAGGACTTCA CCCCGCTCACCTCCGTTTCTGCAGCAGCTCCGCATCGTGTACT
ESTD- ETS2	43 A G ---			ACTCACAGTGTCTTTAAGTAAATGGTCGAGAAAGAGGCACC[G/G]GGAAGCCGCTCTGGCGCCTG GCAGTCCGTGGGACGGGATGTTCTGGCTGTTTGAGATTCTCAAAGGAGCGAGCATGCTCGTGGACACA CACAGACTATTTTAGATTTCTTTTGCCTTTTGCACCCAGGAACAGCAATGCAAAAACCTCTTTGAG AGGGTAGGAGGGTGGGAAGGAACAACCATGTCTTTTCAAGATTAGTTG
ESTD-F9	111 A G ---			AGATCCTGATGATTTTTCCTATTTTCTAAATGTTTACAGTTTGAAGTTTATAGATTTATGCCCA TGCTCCATTTGAGTTAATATTTGTAAAGTATGATGTTA[G/G]GTCAAACCTTCATTTTTTTTCC ATAGGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACAAAAAC
EST68787 5	144 A ---			CTTCTATGGGATTGACTTTATTTCTCCATTGCTTACCTTTTACAGGTGTTAATATAGTGAAGAAG GAAGCTTGCAGCTCATGACAAATTTGAAGCTGACAAATTACACAAGAAGGAATAAATTCACAGTCAA AGAAATCAAGCACTTTTCGAACATTTGAAGTTGTTTTGAACTTGGTGTCACTTTAATTACAACCTAG CAGACGGAACCTGAACCTCAGGGTAAGAAT
ESTD- GCDH	200 C G ---			CGCAGACCGGTCACTGTGGGGTCGGGAGTGTGGAGGAAGGAGGGAACCTGGGGGTTTAGGGACT TTCCGGGGTGACTTTCCCGTTCTGTCTTCAGAGAAAGGCGGAGAACACAGAGCCAACTGGCTAA GTGTAAAGGACCTCTGGTCGCACCCGTGTCTGCTGCCCTGTTCACTGTCTGTCTGCCGAGT[C/] G/GACTCTGTCCCGAAATTCGGAGAGCT
ESTD-GCK	88 A G ---			GTTTTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCTGCTGATCACCATGAC AACCACAGGCCCTCTCAGGA[G/G]ACAGTAAGCCCTGGCAGGAGAAATCCCCCACCACACCTGGC TGGAGCAGGAATGCCGAGGGCGCCTGAGCCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTC ACCTGCAGCCCTAATTACTCAAAAGCTGTCCCAGGTCACAG

EST34088 2	62 A T ---				GTGGGGCAACAGTGGGAGAGAAAGGGCCAGGGGTATAAAAGGGGGCCCAAGAGACCGGGCTC[A/T] AGGATCCCAAGGGCCCAACTCCCGAACCACCTCAGGGTCTGTGGACAGCTCACCTAGCTGCAATGGCT ACAGGTAAG
ESTD- GNAT2	56 A G ---				GACCCGTAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACCAAC[A/G]GGCATCA TTGAAACCAAGTTTCCGTCAAAGACTTGAAATTCAGGTAAGTGATGGTTCCCTAGG
ESTD-HT2	154 G ---				GGGCTAAATTTCCGAGCAACTTGCATAGACTGTTTTATTTGACTTGACAGGATTGCTAGAGATAGG CAGGGAGAGGAAGATGTGTACAGTTTGTACAGAGATAAAAGGATAACCTGGGGTTTTCTGTGC TTTGCTTTCACATCCCTGGGAGTTAATAGCTGCAATTTTCAAGAACGGTATACAGGGACAGCA AAGCGCAGTGGTGAAGTTTCAACAAGACACACCTT
ESTD-HT5	149 C ---				AACACAAAGCCCGAGCGAGAATTGAACCTCGGACCCCTGGTTACAAGACCAAGTCTTAACCCCT GAGCTATGGAGCCCTGCTGCTGTTGGTTTTCTCTTCATCTATAGATTGATTGCTCCTA GCATTCGGCTACCGAATAGGATGTTAGCTTGAGTAAATTCAGGATATTCCTACAAAATGAAA ACATTTTCGTGCTGTGTAATCCCTCGAAAAGGTTCT
EST37382 5	124 A G ---				CTGAGAAACAATTGGCAAAATAAGGAATTTGGCACTCCCAACCCCTCTTCTCTCTCCCTTGA CTTTGAGTCAAAATTTGGCTGGACTTGAGTCCCTGAACCAAGCAAGAGAAAAGG[A/G]CCCCAGA AATCACAGGTGGGACGTCGCTACCGCTACCGCCATCTCCCTCTCACGGGAATTTTCAGGGTAAACT ACCCAGTGGAGCCCGCTCATGCACGGTCTTGGCAGGAGTG[C/T]CTGGGAGAAGAAGGAAGATG TTCCAGGCAACACATAGCTTAGTGGAGACTC
ESTD- IGHV4-6	120 C ---				TTTACTATTTCAATGGATACAGAAATTTGGGAGTCACTATATTCCTATGAACAAAAATTCAGATTT CAGTGTAAAGTAATGTTGCCCTACATTGTGTAGTGACGGGGCAGTGGTGATCCGAGAGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGAAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAATAGTTCACAAAATACATAATAAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	110 A G ---				CAAGTAAGCACCACAATAATGTTAGCTATTACTATCATTAATTATTTATTTATTTTATTTTG AGATGGAGTCTGGCTGTGCACCCAGGCTGGAGTGCAGTGGC[A/G]CAATCTCGGCTCACTGCAAGCT CTGCCCTCGGGTTTCATGCCATTCTCTGCCCTCAGCTCCCGAGTAGCTGGGAATACAGGCACCCGCC ACTGTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTCAACCGT
ESTD-IL1B	99 A G ---				CCACTTACAGATGGATAAATGGGTACAATGAAGGGCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTACCTTGGGTGCTGTTCTCTGCCTC[A/G]GGAGCTCTCTGTCAATTGCAGG
EST74082	134 A T ---				TCCAGGTGGCTGGACCCAGGCCAGCTCTGCAGCAGGAGGACGTGGCTGGGTGAAGCATG TGGGGTGAGCCAGGGGCCCAAGGAGGGCACTGGCCCTCAGCTGCCTCAGCCCTGCCTGCT[A/ T]CCAGATCACTGTCTCTGCCATGGCCCTGTGGATGGCCCTCTGCCCTGCTGGCGCTGCTGGCC CTCTGGGGACCTGACCCAGCCGAGCCCTTTGTGAACCAACACCTGTGGC

EST45311 0	151 C T ---			GGCCCTCCTCTCTCCAAATCTGTCCCTATAGTTTCCCTCTATTAAAGTGAACATACATGCAATCTTTTAGT GGATAGATGGACACAAAGACACAGCCATTATGGGGAAGGATCCACGTGTGGCCATATTGTAAACA CATTTTCTGCAATC/TJACCTCTTTCAITTAACAGCCCTATTCAATGGCCCTTTTCTTTTTCAGTA GTACATACACAATCTGTGTCAITTTGTTGAAT
EST65258 8	80 A G ---			TGCCCCATCAGCGCGCGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAACCAGAAAT CCAGTTATTTCCJAGJCCCTCAAATGACAGCCATGGCCGGCGGGTCTCTGGGGGCTCGTCGGG GGACAGCTCCACTCTGACTGGCAGCTCTTGCAATGGAGACTTGAGGAGGGGCTTGAGGTTGGT GAGGTTAGGTGCGTGTCTCTGTGCAAGTCAGGACATCAGTCTGATTAAA
EST38216 3	26 A T ---			ATGCAGGATGAAGGTGGACAGGGAGG/TJGAGGGCCCAACCTGTCAATCCAGGGCCTGCAGATGTG CTGGACTATGGGTTTGTGACCCACTGACCTCCATGAGCATCAGGG
EST62782 149 G T ---				ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATATTAGCATTTGTTTAGCATTTACCTAA TTTTTTCCTGCTCCATGCAGACTGTAGCTTTTACCTTAAATGCTTATTTTAAATGACAGTGGAA TTTTTTTCTCTC/TJAAAGTCCAGATTTCCAGAGTTTGGTTTGAACAGCAATGCCCTGTGAA AAAGAACTGAATACCTAAGATTCTGTCTGGGGTTTGGTGCATGCA
ESTD- KRT10b	183 C T ---			CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAACTGCTAAGTTTTTCCATTAAACCACTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGC/TJTGCTTTTAAATAGT CTCTGCCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT10a	133 A G ---			CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAACTGCTAAGTTTTTCCATTAAACCACTATTACTTCTA/TJ GJGAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTC TCTGCCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT8b	231 C T ---			ACCCCTACCCCTCCCTTAGCCCGTGGGAAGCAGGAATCTCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAAAGCAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCCATAG GCTGCCTATCTCTCCCGTCTCAGGTTTACC/TJGTCACATTTGACACA
ESTD- KRT8a	21 C T ---			ACCCCTACCCCTCCCTTAGCC/TJGTGGGAAGCAGGAATCTCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAAAGCAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGAG TTTGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCCATA GGCTGCCTATCTCTCCCGTCTCAGGTTTACCAGTCAACATTGACACA
EST75099 6	82 C T ---			CACCTTGCTGTGTAGATCTCCTCAGTGGCGGCTCTACTGGGTTGACTCCAAACTTCACTCCATCTCA AGCATCGATGTCAA/TJGGGGGCAACCGGAAGACCATCTTGGAGGATGAAAAGAGGCTGGCCCCACC CCTTCTCCTGGCGTCTTTGAGGTGTGG



ESTD-LF79	142 A G	---	---	GGGTGATTTGAGGCTCAGTTAATAATTTCAAAATTGTAACGCTAGCAAAACGCAATTGGTATTAGAAAAATAAAATTTCCAATATGTAGTGTGTTATACCTGCCTCGCCATGCAGCATAGCCTGTGGAAACCAGGGAGGGCTTCCCTTACCACCCAGA
EST35879 9	142 A C	---	---	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCTCCCAATCTTGTGCTTCCACCGATGGAATGCCGGAATCCTGACACGTTGCAACCCAGGCTGTACCAATTAGGTGAACATGGCTTCGAGAGAGTTGACACAGATTCTGGAAGACAGACGCGGGATGGGGCAGGAGAGAGCTGCCTGGATGA
ESTD-LMP2	35 C G	---	---	TACACACTTTCCTTACCCATTCACTGAAACGACTGCGGCAAACTGGAGCCTTGTAGGAATGGAGTTGACCTTCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	113 C T	---	---	TGTCAGTGTCCCTAGGGGCACCTCACCACTCCAGCTTCTCAGCTCTGCCTGTCTGCTGCCTGCAAGGTTTGGTTAAATCTCAATCAATGCTCTCATCTTTAGCTGTGGGTTTGTGTTGTTCTGCTGTTTGTCTAGTATCTGACTAGCTTTTAAATATAAAAGAGATGTATCTAAACAAATAGAGATTGTTATCAGAAGTTCACACATTTATTAATAATTTTTCACCTG
ESTD-MCC	45 C T	---	---	TTGTCAGGAGTGTGCTGATGCTGCCTGCCCTGCCAGCTCTGCCCTAGCCTGAACTTCAGGACAGCTGCAG
ESTD-METH	118 C T	---	---	ATCTTCACTGCTAGAGCATCTGGTCTCTTTTAGCAITGG
ESTD-NF1	25 A G	---	---	ATTATCCAGATGAATTTACAAAACCTAGTACCAGATCCACAGACTGATATGGCTGGT
ESTD-NFKB1	107 A G	---	---	AACATGGACTTGATATTGTACAAAAAAGTTTATTTTCTAAAAAAGAAAAAGAGAAA AAATTTAAAGGGGTACTTATATCCACTGCACACTGCTGCTAGGCTTAACTGCTGATTACCTGCTGAGC AGGATCAGCCCTCATTTTGTGCTTTTGTGAACCTTTTGTAGGGACGAGAAAGATCATTTGAAATCT GAGAAAACTTCTTTAAACCTCACCTTTGTTGGGGTTTTGGAGAAAGGTTATCA
ESTD-NPPA	45 A G	---	---	TGTCCTTAGGCCAGCCCTGCTTGTCTCCCTGGCTGTTATCTTCAGTACTGCAAGAGAACACA GACAT
ESTD-NRAS	202 C T	---	---	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATATTTCTTTCTGCAGGCATATAGAAATTTGGTGGGTTTCTTTATGTAGGGTGATTTGGATACCTTTTGTGTTGATTATATAGCAATTTGAGGGACAAACAGATAGGCAGAAATGGCTTGAATAGTAGATGCTTATTTAACTTGGCAATAGCATTCCTATCTCCCTGTGGTTTAAATAAAAT
ESTD-PAI1	100 A G	---	---	GCCACCAACCCACCCAGCAGCACCTCCAACTCAGCCAGACAGGTTGTTGACACAAGAGAGCCC TCAGGGGCACAGAGAGTCTGGACAGTGGGGAGGTCAGCCGCTGTATCATCGGAGGCGCGGG CACATGGCAGGGATGAGGGAAGAGCCAAAGAGTCTCTGTTGGGCCCAAGTCTAGACAGACAAAACC TAGACAATCACGTGGCTGGCT

ESTD-PAR	120	A	---	---	CTCTTCAGGAACCAACAGTCTTCTTACCAAAACACGACTTATTTGCTGTCGAGAGGTACAACCCGTAGA
ESTD-Per/RDS	74	A	G	---	ACTTCTTCTTAAGTAAATTTAGTTAAAGGAATCGAAACTGGCTCTGAAGACATGGAGATACTGCCT
EST68308	5	29	C	T	AATCGACTGGCTTTCATTAGCTCTGTGAGTGTCTTCTTCACTTTCTGTGTTCTAGAACGTTTTCTAG
EST54045	6	39	A	G	GACTGGCAGTTTAAGCTTTCACCTTAGGCTTCTGTATACCCATGCC
					ACCTACAGACGTCGCTGGATGGTGTGTCACACCCCGAGGAATCTGAGAGCGAGAGAGGGCTGGCTG
					CTGGAGAA/GJGAGCGTGCCGGAGACCTGGAAAGGCT
					GGAAGAGATTTAAGAAAGCTTGATTGGA/CJTAATCTGGTCTTTGAGTGTGGAAGAGTTTCATGTC
					TCTGCCTGAGTTACAACAGAAATCCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAAT
					GGAGAAGTAGACTTTAAAGGTAAGAAAGTAGTTATTTTTA
					GGAATATTAAAAATATTTAAAAATACCTCCATTTTGCCTT/GJTCCTTTTAGTGAAGATGATACCTGC
					AAAAGACATGGCTAAAGTTATGATTGTCTATGTTGGCAATTTGTCTTACAAAAATCGGATGGGAAA
					TCTGTTAAGTAAGTACTGTTTTGCCCTTGGAAATGGATTTTAAATGTTGACTTTATCAT
ESTD-PXMP1	88	A	G	---	ATGAAACATGGTCTTTAAATTTATGATATGTTGTTATAGCTATCTTAAAAGGGCTTCTTTTTTTA
					ATGCAGAAAAGAGGGGAAA/A/GJGAGCGAGCTGTGGTGACAAAGGTGTTTTCTCAAGGCTCATAC
					AGATTGAAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAAAGTCTTATGAAATTTAATCTT
					CCCGAGGAATCTGAGAGCGAGCGAGGGCTGGCTGTGGAGAAGAGCGTGCCTGGAGACCTGGAAAG
					CTTTCTGGAGAGTGTGAAGAAAGCTGGCAAGGGCAACAGGTGAAGCCGAGGGCGCAGACGCAGG
					CCAGGCCACAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCACT
ESTD-RDS	127	A	---	---	CCAAGAAACGTGGATCTCCCTCATCCAACTCCGAAAGTCTGAA
ESTD-s14544	94	G	T	---	TTGGGAAGTTAGAGCCTATATTAATACGGAATTAAGGCAGGACACAGAGGCTTAATTGAAAA
EST52908	0	45	A	C	TATCCCAAAGTTGAAATGTCTCAGTTCG/JCTGTGTGGTTAGATGCAGGATTTATATGATCCGTTA
					ACCTCT
					ATCACAGGTCTCTGGTCTCTGGCCATCATTTCTCTGGGAGAGATGG/JCTGGTGGTCTGCAAGCCCTT
					TGGCAATGTGAGATTTGATG
					AGGAGAAGCTGAGAGGGGAAGAGAGACAAAGAATGACATTGATGAGTGAAGATGTC/JJGGCTCAG
EST19590	55	C	T	---	GATGCCGGAATAATGAC
EST76136	39	C	T	---	TGAAGCTTCTGCCAGCTTGCAATGTTTCTAGGAGAACCC/JJCGTCAATACCTTTATCTATAGCCTT
					CCCCTAGGCTCT
					TGAAACACCTGTGGTCCGGAGCCAGGTGTGTTCTCTCTGGAGCCTGAGGAGTTTGTGTCTGTG
					CAGTCCCGCGGCCACCTGCTGGTTGAGCCTGGACATACACCTTACCTCTTGGCCCGGAGAAGAC
ESTD-SPTB	176	C	T	---	ATTTACCCACCTGGCCATGTCCCTGGCCTGTTGTGCA/CJCTCTGTGTGAAGACCCCAACCCCTGC
					CTCCCCCAACCAAGCCAGTTTCTCTAGCAAGGGCAGGAC



EST58607 0	105 A G ---	---	CTCTGGATGGGTTACAGGTGGCAGGCACAAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCCTCACTGGAGAAACAGACAGCCACAGTGGCGGGGATGGCCGGGGAGTTC TGGTTGGCGGCACGGCTGTGGCTCGTTGTGAACGGTAGCCTTTGCGGTGGGATGCCTAAACCTTTGT TTCTGGCCAAAGGAGGGCGGGTGCCATGCTGAGATGATGGGCC
ESTD-VWF	36 G ---	---	AGGTAGGAAAGCAAAAGAGTTGATTAGTGAAGGAGAGAAATGGACCTACCTTCCACACTGTCTCTTTGG TCCCTAGAGTCTG
EST71770 6	189 C G ---	---	AGCACCACTCTCACGTCAGCCTCAGCACAGATGCTGTTCTAAGGATGACGTGCTGTTTACAA CATCTCCTCCATGAAGAGACAGAGAGTTATTTATCCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTAAGTGTGTTGAACAACAAGAGAAAACCACTGCAGATACCAGTCGTTGTTGGTGGGA AGGAGTCCCCAGTCCCAGGTGACACTGGACAAGAAAGAGCCATCCAAAGG
ESTD- TNFAb	152 A G ---	---	TTCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACTGGTCCCAAAAGAAATGGAGG CAATAGGTTTGAAGGGCATGAGGACGGGTTTTCAGCTCCAGGGTCTACACACAATCAGTCAGTG GCCAGAGAACCCCTCAGTGAATCGGAGCAGGAGGATGGGAGTGTGAGGGGTATCCTTTGATG CTGTGTGCCCAACTTCCAAATCCCGCCCGCGGATGG
ESTD- TNFAa	88 A ---	---	TTCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACTGGTCCCAAAAGAAATGGAGG CAATAGGTTTGAAGGGCATGAGGACGGGTTTTCAGCTCCAGGGTCTACACACAATCAGTCAGTG GCCAGAGAACCCCTCAGTGAATCGGAGCAGGAGGATGGGAGTGTGAGGGGTATCCTTTGATGCTT GTGTGCCCAACTTCCAAATCCCGCCCGCGGATGG
EST52418 6	113 A G ---	---	CAAAATACAGGGTCAACTGCTATGATGTTTGGAGCCCACTGACCCCTTGGTGGCTACAAGATGTCG GGGAGTGGCCGGGAGTTGGGCGAGTACGGGCTGCAGGCATACACTAGTGAAGTGAAGAACTGTGAGTG TGG
EST13586 3	89 A G ---	---	CCCACTCTATTGCCAGCCCCAGGGACAGAGCTGATCCTTGAACCTTAAAGTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCCAGTGGGCTGGCTTATCAGCCTCCAGCCAGAGCCCTGGCTGCAGA CATAAATAGGCCCTGCAAGAGCTGCTGCTTAGAGACTGCGAGAAGGAGGTGCGTCTGCTGCTGCC CCGGTCACTC
EST51976 7	123 A T ---	---	AGGCAGAACTGGGGCCCCATGGGGGGACGTGGAAGGCCACTTGAGCTCCTGGAGAAGGACCTGA GGGACAAGGTCAACTCCTTCTTTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAGATCTCTCTC CCTCCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGAGCAGCAGGAGGAGGAGGAGGATGCTG GCCCTTTGGAGAGCTGAGCTGCCCTGGTGC
EST11458 6	140 A G ---	---	CCACTTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCTCCAGTGTCTATCTGTTCTCGAGTTT CTCTGCCATGTTGCTATTGACGAGGAGGACCTGTCCCAAGCAGATGATTTACCATTTCCACAGTGGT CCCAGTAAACATTTCTATGAGCCAGGAGAAAGATACGTTATCTCTGCAAGCCGGGCTATG TCCCGAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC

ESTD- AT3aa	60	C T	---		AGACCTCAGTTTCCTCTCTGTAAGGAGGAGTTTGTTCTTGATCTCCATGGGCCAGC[C]TAGCA CTGGTGCCTGTGAGTCTGATCATCAGGTAGAGAGATGGACAGGTGGAGAGAAATTTGAAAGGGCA TTGGAATTCAGAGCAAGAGACAGATATTAGAGCTGGGAAATGTGG
EST39852 8	106	C G	---		CGGTCTCCCTCCAGGTATTGTTGCAGAGGCCGAGATGACCTCTATGTTCTCAGATGCATTCCATAAG GCATTCTTGAGGTGAGTACACCTTCCCCACTCTT[C]G[GGTACAGAAAGAGATGCATGAACA GCAGGAACACGTGGAAAGGCCTGTTTCCAGTGTAAAGGCATGCAAAAGGCCTCCACAGGCTGCTAT AATACAGCCCT
EST62448 0	112	A G	---		ACCTGGTGTGCTGGTGTGAGTGAACCTGTCTCTTGCCATTGCCGCCCTCCTGGGGCCCGTGG TCCTCTGGTGTGCTGGGTAGTCTGGAGTCAACGGTGTCTCT[AG]GTGAAGCTGGTGTGATGGCA ACCCTGGGAACGATGGTCCCCAGGTGCGATGGTCAACCCGGACACAAGGGAGAGCGGGTTACCC TGGCAATAT
EST36027 2	120	A C	---		AGTGACTTCCAAGGAAATGGTACCCAACTTGCCCTTCATGCGCCTGCTGGCCAACTATGCCTCTCAGA ACATCACTACCACCTGCAAGAACAGCATTGCATACATGGATGAGGAGACTGG[C]A/CJAACTGAAAA AGGCTGTCAATTCACAGGGCTCTAATGATGTTGAACCTGTTGCTGAGGGCAACAGCAGGTTCACTTAC ACTGTTCTTGATGGCTGCTCTAAAAGACAAATGAATGGGGAAGACAA
ESTD- COL2A1cc	112	A G	---		AGAATGTATATAGTCTCAAACTGGGCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTCTCTGCTCACTT[C]A/GIGGGTGTTCAGAGTGAAAA GGTGAACAGGGTCCGCTGCTCCAGGCTCCAGGTTCAGGTAACTCAAGCATATACAATACTGCGCT TTGGTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD- COL2A1dd	97	C T	---		TGAGAGAACACCTAGTCTCCATCCTCTCTCTCAATGGCAAGAAAGTTAAGTGAOCTATCTAGGGC AATAGACTGAGTTTGTGGGACCTGGAAAC[C]TJGGACTTCTTCTACTGCAGCAGACAAGACTTA CCCAAGAGAGATTAAATGGCAAGATATACAATACAAATTTTATTTGACCAAACTATCATGGAACA GCATT
ESTD- CPT2	150	A G	---		GCCGCAATGCCCGGAGTTTCTCCAATGTGTGGAGAGGCCCTTGAAGACATGTTTGACCTTAGAA GGCAATCCATCAAAAGTTAAGTTTCTGGGCAGATGAAAGCTACCATCCTCCTCATCATGAAAC TGGGAGGCCGGCAT[AG]GTGCTCATGCCGTGTAATCCAGCATTTTGAGAGGCTGAGCGGGTGGAT CACTTGAGGTCAGGAGTTTGAGACCAACCTGGCCACAT
EST12274 0	135	A G	---		CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTGCTTCCAAATAGAGCCCTTACCAAAGTGAT TACATAAAGAAAGTCAAGTGGTTTACCTCTCATGACCAAAATATCTTCCCTCCTTAGGATGAGGTG A/GTGTAAATGACCGATGGGGTCAGAACTGTTCCTGTCCACCATGGAGGATACTATAAAGTGTGAAGA TAAATTCAAGCCACAGAGCTTGCCAGATC
EST76807	91	G	---		ATGCTAAGGGGATCGGACATGAAAGGACCCCTGTGAGCCGATTTGCTCTATCTCCAGCGGCCCTGTGATC CAGCTCACTCATCAATGGGGCAGTCAAGCCAGGCAAGGCACTGGGCTCCGGAGGACTCACCACTGCCCCCT GCTGCCATGTGGGACTGGTGAAGTTGAGGACTTCTTG

ESTD-SSA1	111	C T	---	---	TTCACATTTGTGGATTGTTCTTTGCTGTGCAGCACCTTTTCAACATGATGTGATGCCATTTGTCCAAGTTTGCTTTGGCTGCCTGTGCTTGTGGGATATTTGAAGAGATTC/TJTTGCCAGTCCAATGTCTCTAGAGATTTCCCAATGTTTCTTGTAAATAGTTTCATAGTTTGAGGCCTTAGATTTAAGTCTTTAATCCATTTGATTTGATTTCTGTA
ESTD-RVR1	109	A G	---	---	CTTCGTACGGGAGGTCACGTCTCCGCCCTCTTTCATGGACATATGGATGAGTGTGACCATTTCCCTCTGCTGACAGTGTACGACGACGACAGCTTGTCTACTATAGAG/GJGGGAGCTGTGTGCACTCATGCCCGCTCCCTGTGAGGCTGGAGCCACTGAGAATCAGCTGAGTGGAGCCACCTGCCTGGGGCCAGCCACTCCGAGTCCGGCATGTCACTACCGGGCAGTAGCTAGCGCTCAOCCGAGG
ESTD-WT1	70	A G	---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCTCTTACTCTCTGCTGCTGCAGGATGTGCGA/GJCGTGTGCTGGAGTAGCCCGGACTTTGTACGGTCCGCACTGTGAGACCAGTGAGAAACGCCCTTCATGTGTGCTTACCCAGGCTGCAA
ESTD-F2	100	C	---	---	GATAAGTACACTGAGGCCCGCAGGAGGTTATTGCCTAGTAGGCCAACTGTGTCATGCACGCTTAAACCTCTGCACCAATGGCTCCAAAGCCCGTAGGGGAACCTGGGGGATCTAGGGGATGGGTGAGGAATGGCCCCAGCCAGTCCCGCGGTGCTGGTCCCAACAGAGGAGGCCGTGGAGGAGGAGACAGGAGATGGGC
ESTD-PBDA	103	A G	---	---	TGGATGAG GCAGCCAGGAGCGCTGCACCATGCCCCGCATAGATCGGACCTCAAGCTCGACTTCAAGGA/C/TJGTCCTGCTCGACCTAAGCGGAGAGCGCTCAAGAGCCGAGCGAGGTGGG
ESTD-12839	122	A G	---	---	CCTTCTATGCCCCAGATGGAATTCAGTCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGTCTGAGCCGTGGCTGGGAAGGCGAGGACTAATCCAA/GJTTCTCTACCCGAGCTTGCTCGCATACAGACGGACAGTGTGGTGGCAACATTGAAGCCTCGTACC
ESTD-CTLA-4	48	A G	---	---	TGCAAAACACAAAAATCTTCTCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCCCTTTTGCTCCTAACATCTATGTACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAG/GJTTCAAGTCCAAGGCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGGAACCTTGAAATGTTATTCAAC
ESTD-EST54419	96	C T	---	---	TGGATTTCCAGTAGGTTTCAGTACITATGAATATTAIGATACCTTAGCTTAG ATGGCTTGCTTGGAATTCAGCGGCAAGGCTCAGCTGAACCTGGCT/GJCCAGGACCTGGCCCTGCACTCTCCTGTTTTCTTCTCTCATCCCTGTCTCTGCAAGCAATGCACGTGGCCAGCCTGCTGTGGTACTGGCCAGAGCCGAGGATCGCCAGCTTTGTGTGAGTATGCATCTCCAGGCAAGCCAC
ESTD-8	88	A G	---	---	GATCAAGCAGTGCACACGGGTACGATGGACAGCTCTCCACAGTGCACCATGAGATGGGCCATATACAGTACTACCTGCAGTACAAGGATCTGCC/C/TJGTCTCCCTGGCTCGGGGGCCAAACCCCGCTTCCAAGGCCATTGGGGACGTGTGGCGCTCTCGGTCTCCACTCTGAACATCTGCACAAATCGGCCTGCCTTCGCTAATTTGAATGATATTGTTGCTGTGGGACCTGAGCACCTTTTATGGCACAAATGATCACTATTTCTTGACCCCTACTTAC/GJATCCTGGGAGATGTTATTTGGGTTTAGCGTGGTGTGTTGTCTATCTATAGTCCCAAGTGAA

ESTD-PS-1	99 A G ---	---	GGGGAGTAAACCTTGGATTGGAGATTTCATTTTCTACAGTGTCTGGTTGGTAAAGCCCTCAGCAACA GCCAGTGGAGACTGGAACACAACTAGCCTAGJTTCGTAGCCATATTAATTTGGTTTGGCCTTAC ATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAGCTCTCCAACTCCATCACCTTTGGGCTTGT TTTCTACTTTGCCACAGATTACTTGTA
ESTD- B3AR	104 C T ---	---	GGCTGCCAGGGTTCCGTGGGAGCGGCCCTAGCCGGGCGCTGCTGGCGTGGGGTGGCCACCC GTGGAGGCAACCTGCTGGTCACTGGTGCCCATCGCCTGAGACTCCGAGACTCCAGAACCATGACCAA CGTGTCTGACTTCGCTGGCCGCGAGCCGACCTGGTGATGGGACTCCTGGTGGTGGCCGCCGCCGCCA CCTGGGCGC
WI-567b	48 A G ---	---	TCTCACACTGACCCCTTACCTTCATCTCACCTCTGCTGCCCTTGGTTCAG/JAGCCCTCATCTCTTTTA CAGGATCCGCCACAGCATCCCACTGATCTGGCTTAGGCTCTCTCTCCAATCCATTCTTCAAAAG GCTGCCACTGTGATCTTCCCAAGGATCTGATCTGATCTACCATCTTGGTTCAGCC
WI-801c	58 G T ---	---	ATGGAACTTTCTTCCATAATGAATGAGGTTCTCAATCCATTACACATCCCTTTCTTG/JAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTTGCAGGGGGTGGGGCTGTGC ATCTGTGTATGTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACCACAGAGATTAA CATCTGCCACCTC
WI-801b	58 G T ---	---	ATGGAACTTTCTTCCATAATGAATGAGGTTCTCAATCCATTACACATCCCTTTCTTG/JAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTTGCAGGGGGTGGGGCTGTGC ATCTGTGTATGTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACCACAGAGATTAA CATCTGCCACCTC
WI-1099b	76 A G ---	---	GAAATTCACCTATACAAGAACTATTTCTCTAATATTACATTAGTCTCATTTCTGAAATATTAT TTTTTACA/JGTACCCCTTTGATTTTGTATTGATTCATTTGTAACGAGAGATTACAATATCAGTAACGC TGTTCAATGATAGTGTATCACAAATGCTAAATACITTTGGGTCAACATCAAAATTAGAAAGAAA CTTACAAAGTTTATTGCTTTAIGGTTTA
WI-2529	71 C T ---	---	AGGAAATGGCTGATACTCTGCTGGTGGCTTCATTATAGTAAAGGAGATGTAATTGCTGATGAGCCTCT CAA/CJTJTTAACTGCTGCTTCAGTCAGTGAACATTTAATGAAGTCTACACAAATTAATTAGTGT AAGTTGTAATGCTGAATAAGCTTGAATAAAGTGAAGAGAGTTAAAGAGGAGACAACTGTGCTTT TTAAGAAATAGAAGAGTCACTTTCATTAGAAATGGCTTTGGGATGACAAGTA
WI-10088	205 C G ---	---	TAAGGGCTGTCTTCCCCAGAGGCCCCACGGGACAGAGAAAGCATCTTGATACCCAGGCCACAAA TGAGCAATCCATAGATACTACATATAAGAGAGACCTGTACCTATGAGGTAACTGAGGATGAAGGA GTGAGTCATATTGGGTGGCAATTAATGACCCAGCCTCCTCTCTCAAGAGACTTTTACATTTTAGAC AGG/C/GJAGCAGAAAGCAGCAAGGAGAAAGGAAGT

WI-2625	98 G A ...	---	---	GGGAGTCTGGCTGTAGTGGTAGACAGCACTGAAGGATGGAGGAGAGAGAGAAACAGGCAGAA GCACTGGTAGTTAACAGGCTTATTAGGA/GA/CAAAATTGATGATACCTCCCTGAGGACTCGCAG AAATTACGAGCAGTGGACAGGGTTATCTGTGGTGAATTCAGTTATCCACTTGCAGGAGGAAAGCCA GCCAGCAAG
WI-2924	54 G A TAGG	---	---	TCGTGTGCATATTTCCCTCTTTGACTCTGACCTCCTAGTCTCTCTTATAGG/GA/JACCCTGTGATT ACACTAGGCGCTACCTGGATTATTTAGACAATC
WI-2939	72 G T GTGCCTT	---	---	CCATTGTGAGGTTGGGTGGGTCACCTTGTCATTCCTCGCACTCAACAAAGTGGCTTGTCTCAGTGC CTTTG/JCAAGACCTTCCCTCAACAAGAATGTCTTCCATGCTCCCGTGTCTTTGAAAATTCGACT TTATCCTGAAAACTCAGCTGCAGTGTATCTCCGGTATAAAGCCACTCCTG
WI-3203	99 G A AGACGAG	---	---	CTTGCTACCATGTCATTTACAGCATACACCCCTCAGTGAATGCCGTAAACCCCATTTATAAACAT CTTGCCATCGAAGGGTTATGCCGAGACGAG/GA/JCCACACAAGGCAATACCTTGAAGTGACTTGGA GAATAAAGATTGTGGATGGATGAAGCAGAGAGAGATGCTAAAAGTGA
WI-3473	101 A G GCGCTAGGGA	---	---	GGAAAAGAAACCTGAAGGATGAGTAGAAGTTAATTGGGAGATAGTTGGTATAGGCCCTGTTTGGGA GATTGCAGAGAGGAAAGCATTTTAGCCCTAGGGA/GA/JTAGAAAATGTTGGTGACATCAGGGCT ACACACTTTTCTGTATGCTCTTCATCAAA/GJTGAGGCGTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTTGCTTGGCTCCCC
WI-1796b	29 A G ...	---	---	ACACACTTTTCTGTATGCTCTTCATCAAA/GJTGAGGCGTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTTGCTTGGCTCCCC
WI-1796	29 A G ...	---	---	AGTCGTCCATCTTCAGGGTCTAACTCTGGATCTGGCTGCAGAGTAGGAAAGAGATGGGGTGAGT AGTCACATTAGGTATTTCCAAATAA/C/JTAAAAATGCCCTCGAAAAATATCTCTCCCATGTGCCCTGTC TAAATATAACATTTTCCC
WI-4360	93 C T AAATAA	---	---	GCTGAGCTTTGTGGCAGAGCCAGGGACAATTCAGCTGCCGGATTTTAATAGATTCTGCAGCACTGCAA CAGGAACCAAAAATCAGTCTC/JGGGTAACTGAGAGTGGTTTTTCACACCCAAA
WI-1959b	87 C T ...	---	---	GTTGTGCCCTGTAGCAGACACAGAGGCA/GJAGAGGAAAAAGCCTTTTTGGTCCAGGGGCTTACAC TGAATCCCTCAACAATGCAAGATGAGCTAATGGTCTTAGAGGTATAATCTAAGTGTGAGAAAAACA AAGGTATAGGGTTTG
WI-1973b	28 A G ...	---	---	CTTGAGTATCGTGGATTTTGGTATACACAGAAATGGGAGAGCTGGAACATAATCCCCCATATACCA AGGACAAATTGATCTGTTCTACAAATTATACAGTAGGAGACATTATGTTCCATGACAAATGGTAAT TTTTAA/C/JGACAGTTTTTAATTGAGTGAAATTACCATAAAAAATAATAATAGTAGCAGCTAATATT TACTGAGCTGTTACTAGGTGGCTATAAATAGC
WI-1980b	140 C T ...	---	---	



WI-2015b	190	A G	---			TGTCAGATAGTCGGTCTCTACCTAGGTGCAGTAGCATGCTAGGAGCTATTAAAGTACACAAATTATGCT ATATATTTATACAAATACAAATTACTTGCAGATAGCATGACCATGCTAGTGAACCCACACAGACTAT GTGTGAATCGTCTATTAGGGTTTGTCTATAAACTCTACATGGTGTCTTTTCCAACTT/WGJCATATACCTT CTAATACCATAGAG
WI-754b	49	C T	---			GAAGGCACAGGAGAGATGGCTGTCTATCCAGCCAGGGAGAGAGC/CJACATTTATTGGTAA TCCTATAAAGTGCATCTTTAAATTTGTATTTACTTTAGA
WI-754	22	T C	---			GAAGGCACAGGAGAGATGGCT/CJGTCTATCTACCAGCCAGGGAGAGAGCCACATTTATTGGTAA TCCTATAAAGTGCATCTTTAAATTTGTATTTACTTTAGA
WIR-1b	56	A G	---			AGGCAATCAGACCTACAGAGAGAAACCCCAATAAAACTCTGATGATCGTACATCC/WGJGCGCTG GAGGTGATGCCTCTCTGAGGACATGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-1	56	A G	---			AGGCAATCAGACCTACAGAGAGAAACCCCAATAAAACTCTGATGATCGTACATCC/WGJGCGCTG GAGGTGATGCCTCTCTGAGGACATGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-3b	72	A G	---			TAATTTAAATGGGCCAATAACACAGTACTTATCTCAGAGCATTTCTCTAAAGGCTAAATAAGAA GAAGT/A/GJCTAAAGTTATTAGCTCAGAGCCTCACACATCTCAGTGACTGATAAACAAATAAGCA AAGCTGGTGTGAGATAAGA
WIR-3a	69	A T	---			TAATTTAAATGGGCCAATAACACAGTACTTATCTCAGAGCATTTCTCTAAAGGCTAAATAAGAA GAJ/TGTATCTAAAGTTATTAGCTCAGAGCCTCACACATCTCAGTGACTGATAAACAAATAAGCA AAGCTGGTGTGAGATAAGA
WIR-4	47	T	---			GAGCCTTTCTAAATTAAGGATTGTGACTAGCAACCTCCTGTACAGATTCCTGCTCACACATGTGCA AGGCAGCAGCAATTTGCCAGCTGCC
WIR-5g	209	C	---			CGGGACAGAGACAGAGAGAGAGAGTTCTGCAGCATTCACAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCACAGAGCCCTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5f	196	C	---			CGGGACAGAGACAGAGAGAGAGAGTTCTGCAGCATTCACAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCACAGAGCCCTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5e	194	C	---			CGGGACAGAGACAGAGAGAGAGAGTTCTGCAGCATTCACAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCACAGAGCCCTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG

WIR-5d	191 A	---	---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGTGCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAAACACAGG TTTACGTCCAG
WIR-5c	177 C	---	---	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGTGCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAAACACAGG TTTACGTCCAG
WIR-5b	159 A	---	---	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGTGCCACTGTT AGGTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAAACAC AGGTTTACGTCCAG
WIR-5a	37 A	G	---	---	TAACCCCTGAAACTTTGTCTCTCTCATCTCAGGGAGAACACAGACTTCATGTTAAGACCCAGAA[A/C] CGCAGTCTGGGGTGGGGCAG
WIR-6	63 A	C	---	---	TTGCGTACTATT[C/T]AAGCATCTGTAGAATATTGAATACATAGTCTTGAGATTGATC
WIR-7	12 C	T	---	---	GGCGTCTATGACTATCTCTGGTCAATTGATTGACTAATGATTCCTG[C/T]GCCCTTG
WIR-8	46 C	T	---	---	AAACAGAAAAATAGAGGTTATAAGGATGAACTAAAGTTGTGAGAAGAGGATGA[C/G]CTGAAG AAAGAACTACTCTCTTTTGACCAATAATACAAATGGGAAACACTGGAAACCATGGCTTGATTACT GACAAC
WIR-2	56 C	G	---	---	TGTCCTTGCTTATGCCTGCCCTTTTCGCTTGGCAGGATGATGCTGCTATTAGTATTTCACAAGAAGTA GCTTCAGAGGGTAACCTAACAGAGT[G/A]TCAGATCTATCTGTCAATCCCACGTTTACATAAAA TAAGAGATCCTTTAGTGCACCCAGTGAATGACTGACATTAGCAGCATCTTTAACACAGCCGTGTGTTCAAAAT GTACAGTGGTCTTTTCAGAGTTGGACTTCTAGACTCACCTGTTCTCACTC
WI-7069	93 G	A	---	---	GGTCATTTCCCTTTTATCTGTCAGGCAGCCAGCTCTGACTT[A/T]CTCTGTTTCTGTCATCTCTCCC CCACATACCAACTCTTCCACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18694	41 A	T	---	---	CCTATATTCA AGTTTGGAAA
WI-18612	37 A	G	TGC	TTGTATTGCTG CTTGCAAT	CACACTGTTACACACCTATATTCAAGTTTGGAAATGG[A/G]TATTTCGAAGCAGCAATACAAAAGTA TTCATGAAGAAATGCATAATCTCTGAAAAATTAIGAAAACATCCCT

WI-18517	87	C T	CAGGAATCAG CAGCCTGA	TGTTTGACAA GTGCAACA	TTAAAAATCACTAGGGCTCACCCCTCAACACCCCCCTCCATTGTGTAACCTCTACAGCCTGCATGCG ACAGGAATCAGCAGCCTGACGTCGTTGTTGACCTTTGTCCAAACACAACTGACTGC
WI-18668	76	C T	GGCGAAAAAC TAGGCAAAAA	GCTAAATTA CTGCACCTTT GC	CGATTGACAACCTTTATTTTCAACCTAGGTAAACAGTCCAAAAATCAGTGTAGATTGGCGAAAAACT AGGCAAAAAACG/JAGCAAAAAAGTGAGTTTAAATTTAGCAAGGCTCAAGACAGTATGTGGAAGGAA GGTGAGATTTCCTCTACT
WI-18680	75	T C A	AGCATCTGGA	CCTCTGAATA TACAACGGAGC	TAAACATACGAGTACTGTACACGCAAGCATGCATCCCTGAGTCTGAGTGAGGCTGTCACTCTAGC ATCTGGAAJTCJGCTCCGTTGTATATTACAGGAGGGA
WI-18704	99	A C	GGGTTCTCCGA GGGGTAC	TGAAGGCCCTG CTGG	CACCCAGGCTGTACCCAGGCTTCTGTGCGAGCACACACCAAGGGCAGGTGGGCTTGAAGGAGCC CTTGAGGAAACACAGGGTCTCCGAGGGGTACJACJCCAGCAGGGCTTCAGCTTAAAGTCG
WI-18673	29	A G	---	---	TGTGGCAACCTTGTTTTAAATGCAAAACJAGJACTTAAATTTACAGCACATTCATAATGAACCAAC AGGAGAGTTGCTGACTTGTAAACATATGAATATATAAAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAAGCGCATACAAGGAAG
WI-18640	121	T C	GTCGTGGGGTG GGG	GCAATACCAC TGAAGAGGAC A	ACCAGTCATGTTTATTTGGAGGTTAATCCCTATTAGGATATGAAGGATTGAGCAACGATTGAGATT GTGTTCTCACGGAGGGGCTCGGGCCAAAGTCTGCGGGTGGGGGTGCGAGATTCJGTGCTCTCTC AGTGGTATTGGGAGC
WI-18533b	91	T C	---	---	GGGAGAGGAGGTAGATTGCCAAATGAGGCATTTTTTAACTCCCGGAGATTTCTCTCTTTATTT TATATTTTCATTTTCATCCTAAJTCJTTACTGAAGCCATTTCTTTGGTTAACTTTAGA
WI-18533a	59	T G	---	---	GGGAGAGGAGGTAGATTGCCAAATGAGGCATTTTTTAACTCCCGGAGATTTCTTCJCTTTA TTTTATATTTTCATTTTCATCCTAAATTTACTGAAGCCATTTCTTTGGTTAACTTTAGA
D11734	83	A C	TCATCTGATAC CTTGTTTCAGAT TTC	AACCAGGATA AGGCTACAAC ATTT	GAGCATATGCTGTCATGAGGACCTTTCTATCTTACATTATGGCTGGGAATCTTACITCTTTTCATCTGATA CCTGTTCAGATTTCJACJAAATAGTTGTAGCCTTATCCTGGTTTACAGATGTGAAACTTT
D49493	159	A T	CCTGAAGGAA TCTGGGAATT	ACTTTCAGGCC AGGC	CAGGACTTGTGGTGCAGCTGCAGACACAGAGCACAGCTCATGGGAACATCATCTGGGCCCCAGAGAG AGCTGCCGCCAGTGCATCATTAGGGGTCTTTTCATTGCTAGTACTAGCCCCCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAATJATJGGCCCTGGCCTGAAAGTGGCCCATCATACCCACTGTT CT
EST10030	98	T C	CATTTTGTTC TCTCAAGTCCC	GCAGTGGTGT ATGGATGA	TATTTTCATAGAGGAGACCTAGGAGGAGGTTGACACAGCACACTGCTCAGCAGATGACTTAAATTTT CCCTTAGCCATTTTGTCTCTCAAGTCCCTTCJTCATCCATACCACCCTGCTGATTG
EST10052	24	G A	GCTCACTTCTG GAGGCTG	TGTGGAACCTC AATCTTAGACT TC	TATTTGGCTCACTCTGTGGAGGCTGGAJGAAGTCTAAGATTGAGGTCCACATCTGTGAGGGCTTC CTGTTGAGTCATAACCTGGTGGGAAGTCAATCATGTGGCAAGAGAGAGGGGCTACAGAGCAAGAGGAA A

EST10605 2	118 C G ---			CTTGGCGTAATCACAGTTCTGTATTATACAAAAACTTTGTTTTCTCTGACAAAACGTGACACATAGA AACAAATTTCCAAATGGACAGGAACCTAAATTTGTGGAGATGCCCATGTG/GTTGTGAGACTTAA AAAAAGAAAAAGATCCC
EST11048 0	61 T G TAATCT	CTCTCAAGTAG ATAAGAGGCA	GCTAAATTTTC AGAAAGAATT TTGTTT	CATGTGTCATCCCATGATTGAAAAGACATGTTGCTCTCAAGTAGATAAGAGGCATAATCTT/GJAA ACAAAATCTTTCTGAAAATTTAGCTTATGACTCATTACACTGCAACCCAGAGAAGGAGCAC TATGGAGGCCAGAGGAAGTGACACTATATGTGGAAGTCTGAAAGAAATGAAGTGTCAACACAAAA TTCTATATCCAGCTAAATATCATTTAAGAAATGAAG/GT/GGAAATGAAGGCAATATCAGATAAA TTTGATGGAGAAATCCGAGGCCCTGCCAGCATCCCAAGTAGATTCTTTGGACGAAGAAAAATCCT TCTGTGGATTCAGCTTTACGGCTTTCTCTCATCTGCTGGTG/C/TTCTCTCAGAGCTTTAATGTCCGT CCTGCTCTCCGAGTCAG
EST11349 9	109 C T ---			GAATCTGGGTATTAAATAGCGGGTGCACAGGAGCACATAGGAAGAGCATCCAACTACTTTGGAG CCCT/GJAGGAGTTTTAGAGAAAGCTGGAGCCGAGAGCAGTAGTAGGAGGTAGCCAGACCAA AAGGAGGAAGGAGTGGAA
WI- 16632a	71 A G TGGAGCCCT	CCAACCTACTT CTAAAAACTCC	TCCAGCTTTCT CTAAAAACTCC T	CCAGGAATAAAAGAAAAAGAGTCAGAGGAAACAGTCTTTGATGTTATGAGGCTGAGACACTACTC TTCTTCAG/GJAGTATTTCTGACTATAAGTGAATAAATACATTGAAGACTTCAGGAGCTCA CTTGCCATTATTTGTGCATGTTGTTCTTAAAGGCTTGTAAGAGATAACTTGGAAATGTGGGAAC ACATAGATCCCAGAG/GJATTTAAAGGGGCTGGAAAAAGTAGCCTTAAGAC
EST11772 6	74 A G ---			AGAGCAATGGTGGCATCAATAAGCAGCTCATTTTGATTAC/GJAGGTATACATGAAGTAAAAATTC ATGAAGTAAAAATTCATTATACCAAAAAAGCCTCCACAGAACTTTTCATGCACCCTGAGCTATGTGAAC TGAAAAGTAACAGTGGGAT
EST11795 3	82 G A ---	CAATAAGCAG CTCATTTTGAT CTAC	ACTTCATGAAT TTTACTTCATG TATACC	GCCTAGTAATTCAAAAAGGAACATGTTGTATAATAACACTCAGTACAAAAGTCTGT/GJATCCAGG AAGTGACCAGCCCGACGTGTGCTATGACCCCTCTGAACCTCCCATTTCCATAGTTTTTGAATC GTGAAAAATTTTTTATCTGTACGCTTTCC/GJATTATATTTATCTTGCTTGTATTCAGCACCC CACCGATTTCAGGCAGTGTCTTAAACTGCGCTGTGAGCTGTAAAAAGTCTTCT
WI-16644 42	42 G A TAC	TTGTATAATA ACACTCAGTA GCAAAGTCTGT	GGCTGGTCACT TCCTGGAT	CCCTAGCAAAATGACTTGGAGTTGTGTCCTCAATACCAAGTTACATACTGTTGCCAAAATTAAGCTCTC TTCCCCAGAGGCATTAACTGAGATTAT/GJGGAAACGCACAGCAAAATTGACGATGCAGCTTTTAA CCTTTTTA
EST12005 9	56 A G CAAAGTCTGT			ATCTTGAGGTTTCTGGCCCTGTCAG/GJAGGAGTACATCTTTTACTTACCACAGGTGAGAACCTTAT AAGAAACTGTGTAGAAAAGATATCAGGTCAGACTTTTAAAGGGCTCTTATCAGCTCAATAAA
EST12055 9	32 T C ---			
EST12492 1b	95 A G ---			
EST12492 4	25 A G ---			

EST12502 2	52 C G			ATACTAGGGAGAAAAACCAACTGGAGGCAAGTCCACAGGTCCACACTTGTCA/C/G/CAGGCAAGTAT AAACAAAGTGGGGTTTCGATGAAGAGAAAAATGCTCAGCGGGGAAATGACCATTTTAAAGGGCCATGTG GTGCTCGAGGAGTTAGAGG
EST12619 8	105 T C			CCAGAGAAAAAATTAGAATGTATCGGTAAAGAAATAGGAATGCATATTTCAACTCACTGTCACAAA CAGGTGTTTATTATCCCAAATGACAGTGTGCTGAGAT/C/GATGCATGTGGCAGACGAG
EST12620 0	67 A G			TTTTCTCTCTCTTCATTATTCATTGTTTCAAAACACTGTCTAGTACCAACATTGTCCACCGGGC/A /G/TTGAGAAATACAATATTGAAGAAGAGTCACTGCCTGCCCTCTGGAATAATCAGAGTATTGA
EST12817 9a	22 C A			TTGGGGTTCTCCAGGATCCAG/C/A/CTCGTAGCTGATGTGCATGAGGTCTCATCCATGCTCCACGG GTCTTTGGAGTGACCGGATGGGAATCCCATGTTGCTTTGGGTACTCCATCAGGTCAATTGG
EST12941 8	23 T A			TCTCAGCTTCCACCTGACCTGCA/T/A/CAACAGCCAGTTATTTACCAGAAATTTGTTTGGGTTTCA ATGTAGTGTATTAGCTTTAATACACTGCACCTGTTTG
EST12949 2a	52 A G ATACTGTT	GGCTTTAATCA TAACCTAATA	TGTGTCCTGT GGGTCTC	AGGAATTCATGAGGCTTTAATCATACCTAATAACTGTAAAAACAACAC/A/G/CTGTCACTTG CAGAGACCCACAGGACACACATCTCTCTCTCACATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104 C T			ATTTTTGTTTTCTTAAATGAAGCATAATAAACAGTTAAATTCAGAAAAATCATCTATAGTTGA GTGTAAACTCCCTTAAATCAGTCTTCTAGGGCCACA/C/TTGGAGCAGAAGCAGCTTCCCACCCAAG CACCTCTGAAT
EST13117 6	66 A G			TGCTGTCTGCATCAGTCCTTTTAAAAATTTAATCGCTTTATACAAATGACACCAATAAAATGAC/A /G/TAATTTAAAGTTTACAATTTGAGAAGCTGACACGTGTGTCATACAGACACACCTCATTTTACTGTGC TTTACTG
EST13121 6	44 C T			TCTGCTTTAAAGATTCTTCATAGCTGCTTAGGTTTGTCTTCC/C/TTAGCATATTCAGCTATAATCA CCTACATTCCTTCACAAATATTTCTGTGTGTGCCAGGCGAGTCTCTCACTGTCCCATGAATAGCC AGTCTTATTCCACTCT
EST13226 6	74 T G			AACTGTTTACTAAACAAAGGTGCTTTAATTTGAAAAGCATTTGAGGAAATAAATGAAATAGTCT GGCCATTT/G/GACTAACCAAGTTCTACAAATTTACATATCCGTCACTCAGATGAGCATATACCAAG TCAGAGGAAACAAAACATG
EST13230 6	72 G A AGAGACGC	GCTCAGATGTG	CCGGCTCCTGT ACAGAGA	GCATCATCAGCGGCTTTACTGAACITACAACCAACTGCCGCTCAATATGCAGCTCAGATGTGAGAG ACGC/GA/TCCTGTACAGGAGCCGGTACTGTCTTCAATCCTTTGCATGCGAGGTGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70 T C TCTCAGGCT	AACCAGATTT	ACAAGAGGGTT TGACAAAAGA	AAAGATATAAAAAACAACTCCCATCAGTAGCAATACAAGTTATACATTTTAAACCAGATTTTCTCAGG CC/T/C/TTTTGGATACCTTTAGTAGTTAACTGCTCTTTTGTCAAAACCCTCTTGATATAACCA

EST13278 2a...	51	A G G	CITTCACCGAA CAATATTTTAG	CATATCTTGG GTGGTGAGAA	TTGCGAGAACGTTTTACAAGCTCCAAACCTTTTACCGAACAAATATTTTAGGAG/GJATTTGAAATTTAT TTCTGTAGTTCTCACCACCCCAAGAATATGACAGCTTG
EST13282 0	99	A T	CCACACATTTT AGTCCAAGA	GATGGAATAAT TGAGGAAGGTT	GCTCACTAGATGAGCATTGACCAAATATTTAGATAATACCTGTTGGGAAAGTGCTGAATTTACTAGCC TGCCTGAGAAATCCACACATTTTCAGTCCAAAGAT/JAACCTTCTCAAAATTTTCCATCTCCCATCAGA G3
EST13290 9	39	A G CTT	CAATTTT TAGA AGTTGGGTTT	AAATCACTTCA TGGAATAITTC A G	AGCTCATCTGCAAGCAAATTTTAGAAGTTTGGGTTTCTT/JGCTGAAATTTCCATGAAGTGATTTTT TTTTCTGTGCTTAACCTTCAGTTACTTAAAGACCTAAAGACAAAGTGGTATCACATCACATATTTTGT ATGTTGGGCTTTTITG
EST13518 2	45	C G ---	---	---	GAAACATCCTCCAGTAGATTGAGGTTAAATGATTCAGCATTTC/JGACITTTAAAAATTTACCTCA ATGTTCTCGGAGTCGTCATAGTTTAAATGACTTCTGCACCTTCTTATAACCTTGATIG
EST13522 8a	66	A G ---	---	---	CAGGTTGGTGAATCTCAACTAGGAGCTATTTGCCCCATCCCCACCCGCGAGTGTCTGGAGAC/J G/GTTTTGATTGTCACAACCTGCGAGAGGTGGTGCTACTGGAATCAGTGGGTAGAGGCCA
EST13568 6	69	T C ---	---	---	CTTTAAGGAAGTGAGCCAGATGAATCCAATGACCAACCTGGTTGAGAGCCATTGGTCTAGGAGTAGA AA/JC/GCACACAAGGAATAAGGAGAGAGGTTTCGGTTAGTTGAGGGGAGAGAAAGTTTGAAGCA TTTCAAGCTAAGTAATGGT
EST13785 0	101	C G ---	---	---	AAGATTACGGACCATAAGAACTGCCCCCGACCCATACACACAAATTTATAGCAGGTAAACCCAA CTGAAGGGAACAAAGTAATGACTTCTTGAACAAA/C/GJTGATTACGAAAGTGAAAGGCTACAGGG TGATTACTA
EST14038 1	25	A G ---	---	---	CCTCAACCATCTGTAAACCCGAGCC/JG/CAGTGACCCGGGACTTGTGCTTCCCCATCCAGCCCTCT CCTATCAGCATCCGCTAAGCGTCAGTCAGCAGGTG
EST14083 7	23	A G ---	---	---	CAATGGTGTCATGTGAACATAT/JG/JACCTATTTCATAAAGTTAAAAATAATCCCTTCTTGCAATCA CAGTGCAAAAGGCATGAGGGTGAAGTCACTCTGCTAAATGACCGAAACAGGAGGTAGGAGG
EST14221 5	42	T C	GCATGCTAGA CAGAGGCATT	GGAACAAGTC AAAATATTTT AAAAGA	AAATATCAATGCATCTTGTGGCATGCTAGACAGAGGCATTAT/C/JTTTTGAAGATCTTTTAAAAAT ATTTTGACTTGTCCCCCTTCACACTATTTTAAATGT
EST14812 2	50	A G ATA	CAAGTCAGCTT CTACATTCTGA	TAAAGATTTTAC TTAAATCCCAT TATGTACT	TTTCACTTAGTACCAAGGATGCTTTCAGTGCAGCTTCTACATCTGAATA/JG/JAGTACATAATGGG ATTTAAGTAAATCTTTAGAAAGTCCCGAGTTTGCCTTTTCTAACATTTTCATATCAGGTGAAAAACAAT TTTTTCATATGGGTGATT
EST14815 3	128	A T A T A C T G G T T	CATACCCACCC CGGGAATAACA	CGGGAATAACA GTACCCGAA	TTTGTTCGGCAATACATAGTGGCAATGCAGGTGAGTTGCGCGCTCTCCCTGCTGACCCAGTAAT TCACCGACAAATGGCGCACCTTAAATAAATTTGCCCGTATCACCACCATCTGTT/JA/JTTCC GGTACTGTTTTCCGTA



EST16151	53	C	T	---				AGCCAAATTCAAACGAACTCTATCAAAACACACAAAGGCCCTAGAGGAGAGATTATC/TAAATGAACGCT AAATAATCAAGGCAATTTTGATCTAAAGCATTTTGCTTAGCTCTACAAAGGCATGAATGAGGTGT GGTCACGTTTTGTATAGGA
EST16182	54	G	A	---				CATTGGTTGGGTAGGGAAGATAGTAGTGTGCAAAATAAAATGGTAAACACAGCAG/GA/AAATGGAA TTATAGCTTTCTTTTCATATAGGGAATTGAAATTTATTTACTGAGGGTGATAGGCAGAAAGTAGTA
EST16183	59	A	G	---				GCAGGTAACCTGTGGTTACAAACGATATTGTTCTTCATAAAGAAAGAAATATCTAGTTG/GA/GTAG AGGAAGGCACGTCTTCCTGGCCCTCTCTCGTTTCATATTTTATGTCACGTCTCCTAACGTGGGCCGTGT GCAAGAGATCTTTGAGA
EST16198	28	G	A	---				AATCTAGGCTCTTGGCTTTCAAAATCA/GA/ATACAGACAGATAAGAGCTTTAAGTATTTTCGCATTT CCCCAGAGGAAAGGTCAGCATATAAACCCACATGGGTACATGCTCACGCACATGGTGTC
EST16229	52	T	C	---				TGTGAACCTCGAATTCGCTTGTCGAAGTCTTGACAGTTTCATTGGGAG/GC/JCCCTGTGCAGCC CTTGCCAGTTTCCACGAGGCAGGATACTCCACTAGCTGATTCAGACAGGCAGAGGCTGCA
EST16229	45	T	C	---				TGTGAACCTCGAATTCGCTTGTCGAAGTCTTGACAGTTTCATT/JTGGGAGTCCCTGTGCAGCC CTTGCCAGTTTCCACGAGGCAGGATACTCCACTAGCTGATTCAGACAGGCAGAGGCTGCA
WI-16816	124	A	G	TGGGGTTA	GGAGCCATTGT	GCCTAGATTTT	GTTCAGGACAG	CAGACTTTCTCACACCTCATTGGCTGGAACCTGGGTACATGCACATCCTTGAACATATCTGGCAA AGGGAATGGTCATCAAAATTGCTTAAGGCCAAGCAGGAGCCATTGTTGGGGTTA/GA/JACTGTCC TGAACAAAATCTAGGCTC
EST16269	49	G	A	---				GCCACTCTCCTGTGGCTTGCTCCTGTGCCAGCTGCTGCCAGTGCCACA/GA/JTGGTCTAGCCTCATGG CAGAAGCAATTTAGCCAACTCCTGGTGTGCTGCCACTCTCTTCTTCTCCGCGCTGGGCTCACCACG TCTCTCTCTCAATC
WI-16824b	83	G	A	---				GTACCCOCAGCCCAATGCTTCAGGAATAAATGATGGTGCTGCAGCTGTGTCTTATGAAGAAGTCAG AAGCTGATAAAGCTGG/GA/JCTTACACCTTTAGCACGGATAGTTTCTGTGTCCTCCCAAGTGGGTGTGGA GCCTTCCATTATGGGAATA
WI-16824a	47	T	C	CAGCTGT	TGATGGTGCTG	TTCTTCATAAG	AA	GTACCCOCAGCCCAATGCTTCAGGAATAAATGATGGTGCTGCAGCTGT/JC/JTCTTATGAAGAAGTC AGAAGCTGATAAACGTGGCTTACACCTTTAGCACGGATAGTTTCTGTGTCCTCCCAAGTGGGTGTGAGC CTTCCATTATGGGAATA
EST16445	96	T	C	---				TGCTTTTATTAAATCCAGAACGGCATGCTACAGATACTGTACAGCATGAACATTTATTTCATTACAAA AATGGCTTCCAAACCATTAAAAATGAAC/TTC/JGGAAATAAGAGCATAAACGGAAACAGTAACATCA
WI-16857	47	G	A	A	GCTAATGGCA	TGTGAATTGGG	AAGACCACT	TATAATCCATCTCCCAACACACACAAAAAAGCAGCTAATGGCAAT/GA/JACTAGTGGCTCTTCCCAA TTCACAAGACCTGTGCTCAAAATGTTTTCCTGATAATGTGGAGAAATCTGCTCTTTATGTA



WI-16879	79	C T	GATACAGGCC ATATTCCCA	CAAGGCTTCT AGAACTAGAGT CC	AGACAGGTCAAAACAACTCCTAGGGATAAAGATATAAATCCAGCAGCAGCATTATTTCCAGATACAG GCCATATTTCCCACTATAGGACTCTAGTTCTAGAAAGCCTTTGGGAGAACAGCCACCCAG
WI-16882	99	A G	GAAAATGCCA CGTCTCTGAC	GACACATGTCA GGTAAATCGC	ACATGAATGGCAACCTCTAGGTGGGAGAGACAATTTCTCCCCCTTACCCCAAGGTTACTCTGAC AAGGCTATGAATGAAATGCCACGCTCTGACAG/GGGGATTACCTGACATGTCATCTCCCT
WI-16888	70	G A	GCTAACTTTGG GCAGGTTC	TTGACCAAAAT TAA	GTAGTAATGTTTCATCACTACCCGGGGAGAGCAAAAGAACCATGGAACGGTAGCTAACTTTGGGCAGG TTCTG/AJTAAATTTGGTCAATTCAGAACATTTCCAAAT
WI-16895	75	C T	ACTGGCCTGT GTTGTTC	GCTATACTCT TCTAGGCAGTG GG	TTTGTGTTTGTATTATTTGGCTCCCAACATCAGAACATAAGTTCCATGAAACAGGAACCTTTGGCCTGTG TTGTTCACTCTCCACCTGCTAGAGATAGACA
WI-16890	74	G A	AAGAGTAAAG ATGGCGCTAG	CAAAATGAAG TATCGTTCTA TAACAGA	AGTTTTCAGTATGTGTTAAGGAGTTATATTCGCTATGACTTTTCATCTCAGAAGAGTAAAGATGGCG CTAGAA/GAGTATCTGTTATAGAAACGATACCTTCTATTTGGGCTGAACCAAGTGAAGGT
WI-16918	93	C T	CAGCCATTAA CACCAGCAC	TCCGTATACAG AAGTGGCATC	GGAAAGAAAAATAAATACTACCACCTTCTCTGCTGCTACACAGAGCACTAAAATCTAGGAAATTTGAC TTTACTGCAGCCATTAAACACCAGCACCTGATGCCACTTCTGTATCAGGAACCTTAACGTGACAACC ATGAAAGGTCCTCTGAAAAG
WI-16947b	127	A C	GGAAAGCAGA CCTGGGG	ATGTGATTGCC CGTGG	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAATAGGCCTGGAGCACAGGATT TGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAGCAGACCTGGGGGACJCCA CGGGCAATCACAAGAGATG
WI-16947a	58	C G	CATGGAATA GGCCTGGAG	GCCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAATAGGCCTGGAGC/GJACAGG ATTTGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAGCAGACCTGGGGACCA CGGGCAATCACAAGATG
WI-16966	43	T C	AAATGCACAC TACATAACAA	TGCAAGTTATC AGTATAAAAA CTCATATT	CATTTGTTTACTTTAAATGCACACTACATAACAACCTAATAT/CJCTTAACTTTGGTCCAACTATTT AGTATAACTAATATGAGTTTATCTACTGATAACTTGCAATGCCATTAA
WI-16995	55	T C	GAGCAGTAGA GACTGAGGTA	CATGTTGATT CCAGCGT	TTGAGTGCCAGACATCAAGCATAAGAGAGCAGTAGAGACTGAGGTAAATAGTATTT/CJACGGCTGG AAATCAACATGCCCTCTCTCTGTGAAAGTTGTCAGCATGGAGCTGAGAGGCTGAGTCAATCT
WI-16992b	60	T G	---	---	AAATACATGGTGTCAACCTCAGCTAAGCACCCAGAAAGTACACTGTGCGCCCTCATCTGAGAT/GJGTG TAGGACTGAAGGGAATGTGTTTGGGGTTTAGGAA
WI-16992a	46	G A TC	AAGCACCCAG AAGTACACTG	CACATTCCCTT ACAGTCTTACA C	AAATACATGGTGTCAACCTCAGCTAAGCACCCAGAAAGTACACTGTG/GA/JCCCTCATCTGAGATGTG TAGGACTGAAGGGAATGTGTTTGGGGTTTAGGAA

WI-17010	23 T C	TTCAACAGGA	AATAATACGGT	ATGTTTCAACAGGAAAGCCATGTCATGACATTCATAAACACCCGTATTATTAGAAGCTCATTTAAT
EST17127	74 C T	CACTCGGCAC	GGGAGGGCAGG	TGTTTAAATGCAGACAAAATAAAGGCTAACTAAAGGCAGATCCAAATGACCCAGTGATCAACCTAGA
9b		AGACAGAGT	GGTG	GGTCCACAG
WI-17040	94 T C A	AATTCCTTAT	GGACTATGGCT	ATCCGCTCTCCAAACAGCATCCAGGCCGGGCATCTCCCCACGATTTTATAATACACTCGGCACAGA
		CATCTCAAGCC	TATTCAGTGAT	CAGAGTCCTTGGGAGCCATGGSGCACCCCTGCCCTCCCCAGGCTCCCTAAGTAACAACCT
			G	CACGCGTTCATTAAATTTGGTACAAAGCATGAACACTCAGGACAGATTGGCACAATACATGCAGTTC
				GAGAATTCCTTATCATCTCAAGCCAGTCATCACTAGTAAGCCATAGTCCCAAGTCTCGTTTTCC
				AAATCTTCTCATATGT
				TTGTTTGTGTTTCTCTCTCTCCCAAGGGATTACGTATAGGTCCTTAACAACAGGGGATC
WI-17044	47 G T G	GCCAAGGGAT	GGGATCCCT	CCCCACTTATAGCTGACAGCAGCAGCTGCAACCACTGACTCTCTGCAGATGGCAGGGAATCGAAT
		TAACGTATAG	TGTTTAAGA	CAAAAGAAAAGCAAGTG
				GCATGTGTTGGAGCAGATCTCCATGGTAAGCCAAAAGTGGACTTGTACGCTATAACTACTCTT/AJG
WI-17021	62 T A	TGGACTTGTCA	TGTAGAGTTAG	CAGCTGCCACTAAGTCTACAGGCACAGTAACACTTATACAGGAGCAGCATGCCAAAAGTGCCTGG
		GCCTATAACT	TGGCAGCTGC	GAGGTGCCAATAAATCAA
WI-17065	90 T C	CCAGAAAGGA	CCCAAGAGAC	TGTAAAAAATGTAGACATGGGGGAAAAAACATTCGTAAATCAACATGTGCTGTTTCTACTTCCGGTA
		AAAGCATAAA	AATGAAATCCT	CCAGAAAGGAAAAGCATAACTTT/CJAGGATTCATTGTCTCTGGGT
				TTCATAAGGTTGTACAGCCAAACATCACTGTTT/CJATTCCAGAACATTTCAACATCTCAAAAAGA
WI-17066	32 A C T	TGTACAGCCA	GAGATGTTGAA	AACTCGCACCCATTAGCAGTCATCCCTGTAGCTTCCCTCATAGGCAATGGCAACTGCTGATC
		ACATCACTGTT	AATGTTCTGGA	
			A	
WI-17074	86 T G	---	---	TGCTGACTGTGATGACTTAGTAAGGCCATCACAGGTTGCCAGAACATCTACTCACTGTTCCAAGCAT
WI-17104b	108 T C	---	---	AACTCTCTACACAGGCCIT/GCTACATAGGAGTATATTTGGCCAAAGACTCACCACTAGAAAGTGATT
				CAGATGAGAACTCATGCTGGCTCATGTGCAAGCTTCCCTGATGCTTTGGAGCTTTCCCATTCATCCA
				AATCAGAAAGCAGTCAGTGGCCCGTGGTTCCAGACGGCTT/CJCTCTTTGTTAAGAAATTA
WI-17114a	37 T C	TTTCCATCAAG	TTGTATTATAA	AGCGTCCAACAGATGTTCCATCAAGGACTTTGTTT/CJGTCCTTCACTCTGCTATTATAATAC
			ATAGCAGAGTG	AAGCTACCTCCCAAGGCCAGATGCTCTAAGTGCTAAAGAAGACTGCAGCCACAATCAGAGTTACAT
			AAGAGAC	GGGA
			TTCTCAGAATC	
			CTGGAAGATAT	CGTGGCTGGACTAAGTGCTCTTCCATGTGGACACATCTCCACTGAACAGGATGAAATTCAGATAGTC
WI-17150	76 T G	CTCTT	G	TTCTCTCTT/GJCATAATCTCCAGGATTCAGAGGGCTCTCTTTGTCTGCTCTAATTT
				GAAATCGAATACGTCCATTCTTTGTAAATAACAATAACGTT/GJAGGGCAAAAGCAAGATTCGTG
				TAAACCAACATTGGAAAGGGGACACAGGGAGGGGCAGAGGGGAAAGGCCAGATTTCACCGGTTT
WI-17163	43 A G	TAACGTT	TTTGGCCT	CCCTCCACATCTGCAGACAAA



EST20824 8	115 T	AGTCGGGAGT GCTGATTG	AAGATTTTATC TTGGACCCGA	GTGTGGAAGCCGGAGTTTTATTATTCAAATCAGTCTCTGAAACTCAGGGATTGAGGTTTTTA AGGATAACTTGGTGAGTAGAGGGCCAGTAAGTCGGGAGTCTGATTGTTGTCGGGTCCAAGATAAA ATCTTAGG
WI-17347	50 A	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGCGTA	TTGGTTAAATGATGCCAGATGGGTACATCCTCAGAACTTCTCAGCCTTAVGIGTAGCACAAGTGG ATGCTTGAAGAAACTCAGTCTTGGAACTCAGACAGCAATGGACGGGATGAGTGGGACCA
EST21904 b	128 G A GTG	TTCATATGGCC ATTTTAATAA GTG	GGCAGGTGTC AGAAAGCAT	TGATTGTGGTCTGGAGCAGGTGGCGAGTTCAGTAGGAGCAGAGGAAAGTAGACGCAGTAGAAAT GAGACTGGAATCAATAGAACAGAAAAATGTACTAGGCTTTTATATGGCCATTTTAAATAAGTG[G/A]TA TGCTTCTGAACACCTGCC
EST22111 3	82 T C T	GAAGATCTGT CTGGCATTTCTT	TGGAAAAACA GCCCCAC	CAAAACAATGTAGACATAAGGGAACAAATTCAGAGAGCTCAAGTCACCATGTTTTGTCTAAGAGAAAT CTGCTGGCATTTCTTTCGTCGGGGCTGTTTTCCAAAGGCACA
EST22197 2	78 T C	AATTATTCTGC TATTCCTGCCA	ACCATGAAGG ATGCGGT	GTTTAATGATCACTCAACCAAAATCCACAGGAGAACTCTTAATGTTTACAAGCACCATAATTTCTGCT ATTCCTGCCATTTCACCGCATCCTTCATGGTAGAGTATCACAAAGTAAAGTTTCTGGTTGTTTCATC TACTTAAACCA
EST22311 9c	92 T C ---		---	TTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATATACATAAAAAATCCACCACCTGTAAACAG TAGCATTCAATGGTTTTTACTCTATTCGTCAAAGCTGGGCAACTATCAGTACTATCTAATTCAGAA CACITTCATCATCCAG
EST22311 9b	54 A G ---		---	TTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATATACATAAAAAATCCAGTAAATCCAGTAA CAGTAGCATTCATGGTTTTTACTCTATTGTCAAAGCTGGGCAACTATCAGTACTATCTAATTCAGAA CACITTCATCATCCAG
EST22311 9a	41 T C GAGTTATAA	GGATTAGATC ATCTTTTTATT	TTGAATGCTAC TGTTTACAGTG G	TTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATTCACATAAAAAATCCACCACCTGTAA CAGTAGCATTCATGGTTTTTACTCTATTGTCAAAGCTGGGCAACTATCAGTACTATCTAATTCAGAA CACITTCATCATCCAG
EST22319	19 A C ---		---	TCGAGGAGCTCTGAGGAGCAGCACCAGGGAGCTGTGTCCAGGGCCACCCGTGCAGGGCAAGTGTG GTCCAACTCCTTCCCTCCCTTACAAAACCTCCAGCCTCACCCACACAAACACTGGCTGACAGGCCCTTCT TAAGCCTTTTTAACGT
EST22433 c	103 A G AA	AAGACATGTT CACCAAGTGA	CAGCTTCAGCT TAACTGACAGA AGTTTCAGTTT	GATGTTAATGACTTTCTTTGAGATATGATGGAAAAATATCCAGGTACACATGGAAAAAGACATGTT CACCAAGTGAACCAATCTAACCGAAAAAGCTTTACCAGTGTCTGTCAGTTAAGCTGAAGCTGAAAAAT CTGGGAGCTTGACATGCTG
EST22657 9	71 A G TTATCTGCACAT	AAATGGATCC TTATCTGCACAT	GCATGAATTTT AGTTTCAGTTT	TATCCATTTCAAGAAAAAAATGACTTAAAAATACAAATTTCTATCCAGAAATGGATCCTTATCTG CACAAAGTCAATTGAGAAAAAAATTCATGCAAACTGAAACATGCTTT

EST22993 5b	71 T	ATCCTTTTGT CTACCCCC	TTGCCGTGTAA TTTGACTGTAA TG	GCCTTTTATGTCCTCTTTAAACATCAAAATGTTTATAACACACTTGATCCTTTTGTCTACCCCCA ATTC/CATTAACAGTCAAAATTACAGGCAATATAATAGGCTAACAGAAATGCTTGCAATTT TTATTTCTCAGCTTACCAATTTGTGTAATATCTCTGTACAAAGGTGTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTAAATTTTATTAATCTTTGCCCTT/AJAGGTTTTGACAGTTTTGTGCTTTCT T
EST23021 0	108 T A	---	---	ACAGAAATTTAAACATGCAAGTTTTCATTTACATTACCTTTGCAGATTGAAGAAAAA/C/GJAATATTAG TAGTTACTATTAACTTAGGCAAAAGCCATTTCTTG TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACCTTGTCTACTCTCCCA AGTGACACTAGGCAATGTAAGCTCCAGAGGCAG/A/C/GCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGGCTCACTG AAAGGCTGTAGTTTGTGTTTTGTTTTTCTT/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAAGTCCAAGGCTAGAGAAAGATATAGGCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA CTGACACGTCCTGTGTGGGGGGTCCATGTGGCGTGTGTGAGTGAGACATTTTACTGCGTCCC GTCCCGCCAGCCCT/A/GJTCGCGCTGTCTACTGGCCCTTGTCACATTTGTATTTCTGCTTGGTGAAA TACCATCAGCCTTCC
WI-17387	55 C G	CCTTTGCAGAT TGAAGAAAAA	GCTTTGCCTA AGATTAAATAGT AACTACT	ACAGAAATTTAAACATGCAAGTTTTCATTTACATTACCTTTGCAGATTGAAGAAAAA/C/GJAATATTAG TAGTTACTATTAACTTAGGCAAAAGCCATTTCTTG TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACCTTGTCTACTCTCCCA AGTGACACTAGGCAATGTAAGCTCCAGAGGCAG/A/C/GCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGGCTCACTG AAAGGCTGTAGTTTGTGTTTTGTTTTTCTT/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAAGTCCAAGGCTAGAGAAAGATATAGGCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA CTGACACGTCCTGTGTGGGGGGTCCATGTGGCGTGTGTGAGTGAGACATTTTACTGCGTCCC GTCCCGCCAGCCCT/A/GJTCGCGCTGTCTACTGGCCCTTGTCACATTTGTATTTCTGCTTGGTGAAA TACCATCAGCCTTCC
EST23669 1	101 A C	AATGTAAGCT CCAGAGGCAG	CCTTCCCTCC TGTAAGC	ACAGAAATTTAAACATGCAAGTTTTCATTTACATTACCTTTGCAGATTGAAGAAAAA/C/GJAATATTAG TAGTTACTATTAACTTAGGCAAAAGCCATTTCTTG TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACCTTGTCTACTCTCCCA AGTGACACTAGGCAATGTAAGCTCCAGAGGCAG/A/C/GCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGGCTCACTG AAAGGCTGTAGTTTGTGTTTTGTTTTTCTT/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAAGTCCAAGGCTAGAGAAAGATATAGGCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA CTGACACGTCCTGTGTGGGGGGTCCATGTGGCGTGTGTGAGTGAGACATTTTACTGCGTCCC GTCCCGCCAGCCCT/A/GJTCGCGCTGTCTACTGGCCCTTGTCACATTTGTATTTCTGCTTGGTGAAA TACCATCAGCCTTCC
EST23733 9	31 T G TT	GGCTGTTAGTT TTGTTTGTGTT TT	TGCACATTTAAA TCCCATCAAT	ACAGAAATTTAAACATGCAAGTTTTCATTTACATTACCTTTGCAGATTGAAGAAAAA/C/GJAATATTAG TAGTTACTATTAACTTAGGCAAAAGCCATTTCTTG TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACCTTGTCTACTCTCCCA AGTGACACTAGGCAATGTAAGCTCCAGAGGCAG/A/C/GCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGGCTCACTG AAAGGCTGTAGTTTGTGTTTTGTTTTTCTT/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAAGTCCAAGGCTAGAGAAAGATATAGGCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA CTGACACGTCCTGTGTGGGGGGTCCATGTGGCGTGTGTGAGTGAGACATTTTACTGCGTCCC GTCCCGCCAGCCCT/A/GJTCGCGCTGTCTACTGGCCCTTGTCACATTTGTATTTCTGCTTGGTGAAA TACCATCAGCCTTCC
WI-17470	83 A G	GTCCCGTCCG CCAG	CCAGTGACGAG GCGA	ACAGAAATTTAAACATGCAAGTTTTCATTTACATTACCTTTGCAGATTGAAGAAAAA/C/GJAATATTAG TAGTTACTATTAACTTAGGCAAAAGCCATTTCTTG TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACCTTGTCTACTCTCCCA AGTGACACTAGGCAATGTAAGCTCCAGAGGCAG/A/C/GCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGGCTCACTG AAAGGCTGTAGTTTGTGTTTTGTTTTTCTT/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAAGTCCAAGGCTAGAGAAAGATATAGGCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA CTGACACGTCCTGTGTGGGGGGTCCATGTGGCGTGTGTGAGTGAGACATTTTACTGCGTCCC GTCCCGCCAGCCCT/A/GJTCGCGCTGTCTACTGGCCCTTGTCACATTTGTATTTCTGCTTGGTGAAA TACCATCAGCCTTCC
WI-17519	55 T C A	GTGTCTAGC TAATGAATGC	AATTATTATT TGCAGGCAATA CTC	ACAGAAATTTAAACATGCAAGTTTTCATTTACATTACCTTTGCAGATTGAAGAAAAA/C/GJAATATTAG TAGTTACTATTAACTTAGGCAAAAGCCATTTCTTG TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACCTTGTCTACTCTCCCA AGTGACACTAGGCAATGTAAGCTCCAGAGGCAG/A/C/GCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGGCTCACTG AAAGGCTGTAGTTTGTGTTTTGTTTTTCTT/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAAGTCCAAGGCTAGAGAAAGATATAGGCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA CTGACACGTCCTGTGTGGGGGGTCCATGTGGCGTGTGTGAGTGAGACATTTTACTGCGTCCC GTCCCGCCAGCCCT/A/GJTCGCGCTGTCTACTGGCCCTTGTCACATTTGTATTTCTGCTTGGTGAAA TACCATCAGCCTTCC
EST25356 3b	95 C G	---	---	ACAGAAATTTAAACATGCAAGTTTTCATTTACATTACCTTTGCAGATTGAAGAAAAA/C/GJAATATTAG TAGTTACTATTAACTTAGGCAAAAGCCATTTCTTG TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACCTTGTCTACTCTCCCA AGTGACACTAGGCAATGTAAGCTCCAGAGGCAG/A/C/GCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGGCTCACTG AAAGGCTGTAGTTTGTGTTTTGTTTTTCTT/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAAGTCCAAGGCTAGAGAAAGATATAGGCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA CTGACACGTCCTGTGTGGGGGGTCCATGTGGCGTGTGTGAGTGAGACATTTTACTGCGTCCC GTCCCGCCAGCCCT/A/GJTCGCGCTGTCTACTGGCCCTTGTCACATTTGTATTTCTGCTTGGTGAAA TACCATCAGCCTTCC
EST25356 3a	26 A C	---	---	ACAGAAATTTAAACATGCAAGTTTTCATTTACATTACCTTTGCAGATTGAAGAAAAA/C/GJAATATTAG TAGTTACTATTAACTTAGGCAAAAGCCATTTCTTG TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACCTTGTCTACTCTCCCA AGTGACACTAGGCAATGTAAGCTCCAGAGGCAG/A/C/GCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGGCTCACTG AAAGGCTGTAGTTTGTGTTTTGTTTTTCTT/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAAGTCCAAGGCTAGAGAAAGATATAGGCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA CTGACACGTCCTGTGTGGGGGGTCCATGTGGCGTGTGTGAGTGAGACATTTTACTGCGTCCC GTCCCGCCAGCCCT/A/GJTCGCGCTGTCTACTGGCCCTTGTCACATTTGTATTTCTGCTTGGTGAAA TACCATCAGCCTTCC
WI-17581c	99 C T	---	---	ACAGAAATTTAAACATGCAAGTTTTCATTTACATTACCTTTGCAGATTGAAGAAAAA/C/GJAATATTAG TAGTTACTATTAACTTAGGCAAAAGCCATTTCTTG TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACCTTGTCTACTCTCCCA AGTGACACTAGGCAATGTAAGCTCCAGAGGCAG/A/C/GCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGGCTCACTG AAAGGCTGTAGTTTGTGTTTTGTTTTTCTT/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAAGTCCAAGGCTAGAGAAAGATATAGGCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA CTGACACGTCCTGTGTGGGGGGTCCATGTGGCGTGTGTGAGTGAGACATTTTACTGCGTCCC GTCCCGCCAGCCCT/A/GJTCGCGCTGTCTACTGGCCCTTGTCACATTTGTATTTCTGCTTGGTGAAA TACCATCAGCCTTCC
WI-17581b	86 T C	ATTCAACATT ACTACCAGTT CAATTGATAA	CGTCAATGTAA ATTGCGCT CATTCCTATAG	ACAGAAATTTAAACATGCAAGTTTTCATTTACATTACCTTTGCAGATTGAAGAAAAA/C/GJAATATTAG TAGTTACTATTAACTTAGGCAAAAGCCATTTCTTG TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACCTTGTCTACTCTCCCA AGTGACACTAGGCAATGTAAGCTCCAGAGGCAG/A/C/GCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGGCTCACTG AAAGGCTGTAGTTTGTGTTTTGTTTTTCTT/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAAGTCCAAGGCTAGAGAAAGATATAGGCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA CTGACACGTCCTGTGTGGGGGGTCCATGTGGCGTGTGTGAGTGAGACATTTTACTGCGTCCC GTCCCGCCAGCCCT/A/GJTCGCGCTGTCTACTGGCCCTTGTCACATTTGTATTTCTGCTTGGTGAAA TACCATCAGCCTTCC
WI-17596	86 A G C	TAACACTCC CAATAT	CTAGAAATCGA CAATAT	ACAGAAATTTAAACATGCAAGTTTTCATTTACATTACCTTTGCAGATTGAAGAAAAA/C/GJAATATTAG TAGTTACTATTAACTTAGGCAAAAGCCATTTCTTG TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACCTTGTCTACTCTCCCA AGTGACACTAGGCAATGTAAGCTCCAGAGGCAG/A/C/GCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGGCTCACTG AAAGGCTGTAGTTTGTGTTTTGTTTTTCTT/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAAGTCCAAGGCTAGAGAAAGATATAGGCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA CTGACACGTCCTGTGTGGGGGGTCCATGTGGCGTGTGTGAGTGAGACATTTTACTGCGTCCC GTCCCGCCAGCCCT/A/GJTCGCGCTGTCTACTGGCCCTTGTCACATTTGTATTTCTGCTTGGTGAAA TACCATCAGCCTTCC

WI-17623	46 T C ---	---	TGTTGGTTTAAATTTCCCATATAAATTAATGGTGGGCACATTT/C/GCATGTGCTTACTGGGTC ATTCATATATCTTTTGTGAAGCATCTGCTCCAAATCTTTTGCCTGACTTGGAGTTTTTGGT
EST26419 1b	46 T C ---	---	ATTTCATACAGAGATACAAAGGCAACTATGTGCAGCAACAATCTGA/T/C/GGGCAGTCCAAAATCTCT TGGGAGGAAGTAAATTCATGGTAAATGTCATGATGGCTGGTTCCAGGAGAAGGTTCAAAGGAGGTAG AGAGAGAGACAGAGAGATG
EST26419 1a	35 C A AG	CAAGAAGTTTG GACTGCC	ATTTCATACAGAGATACAAAGGCAACTATGTGCAG/C/A/AACAATCTGATGGGCAGTCCAAAATCTCT TGGGAGGAAGTAAATTCATGGTAAATGTCATGATGGCTGGTTCCAGGAGAAGGTTCAAAGGAGGTAG AGAGAGAGACAGAGAGATG
EST26780 5	69 G C ---	---	TCAGCTTTAATTTAAGGGACATGTAAATAAAAAAGATGCAATTTGACAGGACAGCAGACTAGTTCAAGC AG/G/C/JAGGTTAGACCAGTAACAACAACCAAGAAAGCAAAGTGTCTGTTTCCATCTTGGCTTTTACCA CACTTACAAACTGATACCC
EST26900 7	39 A G ---	---	TACTTCAGTTTAAGGCCAAATTCACACAGAGACTGTCTC/W/G/GAGACGGGCACAGAACCCAGACACC GTAGAAACACACCACCATGTCATGACGGGGAAGCAGAG
EST27152 1	101 C T ---	---	CAAAGGATTTTATTTTGTCCCTAAAAAGTAAATCTAGAAAAATAGCAACCCACTGCAAGAAGAGATT CTATAC'AAAACATTTCAATCATCTCTCTCTC/T/JTTCACATGGTGTACTCTTTTCATGTACACAT CATCGAAACACAGACTGA
EST27504 0a	33 G A ATT	GCTGGTGTGAT GCTACTGTAAAT G	TTTTTGACATTTGCAACAATTTAATAATTTATC/G/A/CATTACAGTAGCATCACACCAGCAGTCAAT AATGCCACTTTAGGCAAAAAGTCTTTCAGTATTTCTGTGTACACATCTGTGTTAACAAGAACCCATACATT GGTAAATTCATTCT
EST27662 4	51 C T CTCCAGTCTG	TTATGGAAATG GCTTATGTAAAC C	ATCTTAAAGGACCATTAGAAAAAGGCCAGTCACATTTCTTCTCCAGTCTTG/C/TJAGGTTACATAAG CCATTTCCATAAATCTATAGCCTTCTCTTAGAGTAACACACACTCTTGTITTAGGAATGTTC
EST27788 3	100 A G ---	---	ATTTTATTAGCGGTACAATTCCTCAAGGTGTAAGGGTGAAGGAAAGGCCGAAAGGCAGGCAAAATACAT TATTGAGCTGAAAACAACCTTACATTCAAGGAC/W/G/GCTTCCAGACAAGCCATGTAGAACCAGCAT GCCITGGGACTGTGTGGAT
EST27828 4	58 G A AGAACCCAC	GTGCAGAGAGG TACTCCAAAGTA C	TCCTTAAAACTTTCTCTTCTGTGGATCCAGTGACGTGGAAGTCATCAGAACCCAC/G/A/GTACTT GGAGTACCTCTCTGCAACCAAGATAGCTGGCTGATTTCTGCTCAGTCACAAATTTTACTTGAA
WI-18369	58 G A ACAATC	AATAAATTC AATCTGTCAC TTATCCATTT	TAAAAATTTGAGATACATTTCCCAATGTAACCAATAAATTTCAATCTGTACACACAATC/G/A/AAATG GATAAGSCCTCTTGACAAATTTCTGCCACCTCCGTTTAAACGCATCAGAACTCAATCTTATCTC
EST28036 4	37 T C ---	---	TCCCGCTTCCAAAAGCTTTATTGGCAATATGCTCTA/T/C/JAAAGAAATGATCAATCTGTGCTCT AAGTCAATGGAATGAAGAGCTGTGTCAGGGGACACACCCACCGCTGTGAAGGAGACTGCTGTGTG TCCACCTCTTATTCATAG

EST28483 7	31 T A	GGAGTAAAG GTGTTCTCT T TAAA	TTTCTCGCATT TAITTTTATAC CA	CATTGGAGTAAAGGTTCTCTTTAAAT/ATATGGTATAAAATAAATGCGAGAAACATTAAAC GGAGAAATGTACAGACACAGACAGAGACATGAGTTTGTTCTGACTGTGACACATTGGTGAAA
WI-17724	50 T C	TGGGOCCTCC TGTC	TGGGTTGGCAG TGTC	AGAATTGGTCTAGTAATGTTTCAGGATTTCGGTGATGGGCCCTCCCTGTC/TG/GGACACTGCCAACCC CACAGCTGGAGGGGCACCTAAGGCAGTCATTTTGTGATTAGA
WI-17730b	68 T C	...	...	TGAGCCTGGGGAGAAAGACACAGAGTGAAGTGCTATTAGTTACATCATACCAAGGTACATACTG TT/C/CACATGATTTATGGCTGTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGCA
WI-17730a	39 A C	GACCACAGAA GTGAAGTGCT ATT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGGAGAAAGACACAGAAAGTGAAGTGCTATT/C/CJGTTACATCATACCAAGGTACATA CTGTTACATGATTTATGGCTGTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGCA
EST29041 5b	53 G A	GGAACAAACA CATTAGGCAT CA	GGTATTGTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTTCATGAGGAACAAACACATTAAAGCATATTGTCACT/G/A/GCTAACTCCT CAAAACAACATACCCCTTTATTTTAGCCCATGAAAAAC
EST29128 4	58 A G	...	...	CTTTAGAAAGGACACCAGTCTTGTGGACTTAGGGCCTACCCCTATTCCAGCAGGTGCC/AG/JTTATT TCACCTTGTTACGTCGTGAAGGACCGTTCCAAATGAGGTTACAGTCACAGGTTCTGAGCAGACATGA GTTTCTGGGGACACT
EST29912 3	103 C T	CTGOCAGCTT ACAGGCT	GCGTAAAGTGC TCATTCTCTG T	ATTTATTAGTATCTGCTGTTGGGGTGGGTGGGAGATTGTTGAGATACTGCAACAGACACAAA AGCAAGAAAGAAACATTTCTGCCAGCTTACAGGCT/C/JACAGAAGAATGAGACACTTACGCATG GCCATGATACACAGCAGTGA
EST29936 8	121 G C	...	...	TATTGGTATGCTTAGGGAAGATTCTGATTTAGAGATAATAATCTTAAAGTTAACTCACCATGAAA TTTAACTTCTGTACTGGCTTCACTGATGAGGCAGTAAACTACATAGGGATAAA/G/CJAGCTCAGTA TCJGGAATCAJGCTTCTG
EST30223 2	99 A G	...	...	AAATAATACATCATGGGAATGGGATATCCATCCCTCAAGCATTTATCTTTGAGTTACAAGCAA TCCAATTACACTCTAAGTTATTTAATAATTC/JAGGATTTAATTTCTTCTAGTTCAATCTTGGGA GG
WI-16260b	86 G A	...	...	CTTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAGAAAAGACCCAGA GTTTCAACATATAGTAGGAGC/G/A/ATAACCCAGGCTCTACCTTCCCTTCCGTGAGAACCTCGTGGGAC
WI-16260a	59 G T	TGAGGTGGATT CAAGAAGAAA A	CTACCTATATT GTGAACTCTG GGT	CTTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAGAAAAG/JTACCC AGAGTTTCAACATATAGTAGGAGTAAACAGGCTCTACCTTCCCTTCCGTGAGAACCTCGTGGGAC AAGAGAAACAGGAAATATTGTGCTTTCTTG/G/AJGCTGTTTCTTATACCCCAATATCATAGAATT GTTGTTGCTTCTATAATGTTACAGCTTCAAAATCTTTGCTTAATCAATCCAAATGAATTACCTGAATT TTCTCTCTTGTTCAAA
WI-17835	30 G A	TG	AAACAGGC	

EST31951 4	87 C T	GGGTGTCGAG CCAACA	CCACCAAAAT CACTCC	ACAGCCATTATTATGTTACTGTTAAATATCAGAGACTGAACATATTTTACTCTTTTAGCAATGACA TCGGGTGTCAGCAACA/C/TGGAGGTGATTTTGGGGGAATCTTATCACAATATTCT
EST31968 8b	95 T G	---	---	CGAATTTGCTCTCTTATTTTGTGATTCTAGTAATCCTAAAGATTTGGGGGGGGTACTATAAGT GCATTTTATAATGGGATTTTCTGCTT/GJAACCTGCCACTGATCTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCC
EST31968 8a	75 T C T	GCGGGTTACTA TAAGTGCATTT T	TGTAAGAATCA GTGGCAGTT	CGAATTTGCTCTCTTATTTTGTGATTCTAGTAATCCTAAAGATTTGGGGGGGGTACTATAAGT GCATTTT/CJATAATGGGATTTTCTGCTTAACTGCCACTGATCTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCC
EST32063 2	103 C T	---	---	TCCATGGATGAACAGACGCTACCATGCCACATCCCCACTTCCCTCCGACCAGATGCTGTGGCCAGAGC TGGCTTCCCTTCCAGACCTAGCTGGCTTTGTAGT/C/TGTTCCAGGCCCATTTGAAATAGCAAAAGGCAC AGTCATGTAGCACTCGG
WI-16303	65 A G	---	---	AAGGCTTCCAAAGCATTTCAAAGGCATTTGGGTGTGTGCTCTAAGTTTCTGGTCACTGCAGCCCCQ/AG JTCTGATTAGGGAGACCCCAAGCCAGTAACAATATGGTCTTGGCAG
WI-17800	29 C G	GGGAGCACAA GAGAACTCA TT	TTTCTACAAT TAATCCAGTC TT	TGGACATGGGAGCACAAAGAGAACTCACT/C/GJAAGACTGGGATTAATTTAGGAAATATTTACAG TTTCCACAAGTCAGAAAGAGCTAATCCCAACCTCTGTATCTGGAACATACACTGCTGCCATTTTCTGC CCATGAAGGGAAATACCC
WI-17857	34 T G C	CCTAAAGTCTG GGATGACTTTC C	TGGCTTAGGT TCTACTTGATG T	AAACTGTCATTCTCTAAAGTCTGGGATGACTTTCCTT/GJATTCTACATCAAGTAGAACCTAAGCCAAAT TCAGAATCAGAACTCCTTTTGTCCATCAAAATCCAGCTAACCCAGCTGAATTAATGTTTCAATCT GTATCTGATGTAGTTAACCATGGCCTGTGATGATTAATGCTATAGGAAGGGAACAAATCTTTA TAGTGTCCAAAGATAATTAATCTTGGTTTAAATCTTTGCCAGCAAAAGCAAAATAT/ATCCGACTGAC TGCTCCTTAGTCTGTGATC
WI-17860	121 T A	TTTGGCAGCAA AGCAAATA	ACTAAGGAGC AGTCAGTCGG	CAGCAACCTTTTTTTGTTTATAGCCTACTCTCAAAAATTGTT/AT/TTTTGTGTGATTAGTGACAACG GGGGAATCTACAATGCTCACATCACAGTAACCTACCA
WI-17866 EST33301 4c	43 A T	ACTTCTCAA ATTGTT	AATCACACAA A	GAAAAAAGTCAAAATGTTCCCTTTATGGGTGATGCCACCACCTGATTCCTTCACACAAGCATGATC AATCGCCACGAGA/G/A/ACTGGATGCCAAAGAGTAIGG
EST33301 4b	80 G A	---	---	GAAAAAAGTCAAAATGTTCCCTTTATGGGTGATGCCACCACCTGATTCCTTCACACAAGCAT/G/A/ ATCAATCGCCACGAGAGACTGGATGCCAAAGAGTAIGG
EST33460 1	63 G A	AGCGTGGTTTT CAATACTAAA CA	CTGTATTATT GTTAAATATTT GCATTGTT	CTATCCAAAGATATTTATTGCAAGGTGGTTTTCAATACTAAACA/G/A/GTAAACAATGCAAAATATT TAACAATAATACAGTGATTAATAAGCCATGGCATATCCAGTTGATGTAATACCTTTGCAA



WI-17904	50 A G	AAAGCATGAC AATAAAATGA ACAC	CGCTTATGTTA ATAGTAATTC CG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACAAATAAAATGAACACIAGITACGGGAATTAC TATTAACATAAGCGATAACATCAAAACATCTGGTAAATGCAGTTAAACAAACACACAAATGA GTTTTTCTTTGAGTGACACAAGCTTGTTCATTTTGAGAAAATGTGTGCCAAATACTCAAGTGTGAA TJAGJGATTTTATTAGTTGTTCTCGCTAGTAGTTTGGTATCTATGAAAAAAGCAGCTAGTTTCAGC TTACAAATCACACAAGT
EST34149 5	69 A G	TGCCAAATAC TCAAGTGTGA GAT	AACACTAGCG AGAACAACTA ATAAAATC	TGGGAAAACATAAGTTAACTCAAGAATAIATCCAGTCTTTATGTTACTAAACATTTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCTC/AJTACAAAGATTAAAGAAACCTTACCATCAAAACACTTC CAGTGCATCAA
EST34343 8	95 C A	GGACCATATG ATATATAACT TCTTAAAGC	--- CAGAAATTATG TGATAATACT CCTTCC	GGTACACAAATTTAATGGAAGGAACACACAGGTATGTTGAAAGAACATCAGTACAGCTGGAGACAGG GAGGGACCATATGATATATACTCTAAAGC/CJTGGAAAGGAGTTATTATCACATAAATTTCTGGGC GCTACAGAAGTTTTTCATCA
WI-17982	98 C T	GTAGAGCGGA GAGGAAACAG	--- AGGCACATGGG CAGC	CTCAGTAACTCCGGTGTATAATCTGCCATTTATTGATTTATTATGATAAAACACCTCTCATTTGTGA AAAACAGCTAAGGGTGACATCTCCAGACCCCAACCACTGTCCCTGTATGTJACJCTGCTGAGAGTCC ACATTTTGGAAATCCAAT
WI-17993	118 A C	GTAGAGCGGA GAGGAAACAG	--- AGGCACATGGG CAGC	CCCATCCAGAAACCCCACTGTGATGGTGGAGCAGCATGAAACAAACATCTCCCAGGCCCTCGCAGT AGAGGCGAAGGGAACAGJAGJGCTGCCCATGTGCCTGTCTAAAGACGCCACCCCTCAGGTTGATGT CACCTGTGGGAGACCGGGT
WI-17136	33 C G	--- CAGGAAACAG	--- AGGCACATGGG CAGC	ATTCCTTTATAAAACACCATGTGCTCCCTAAAATGTJGJATTCACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAGACAGAGAAATGTGTCCCT
WI-18041	24 A C	--- CAGGAAACAG	--- AGGCACATGGG CAGC	GCCACTGAAAAAAGGTGCTCTCCJACJGTTTTCTAACTCCCTGGACTCCCTCATTTGGAACCTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTTAGACTTTGCTGTATTTTAAAGGCAGTGTGATGCTCCAGGAT TCAAATACCTAATCA
EST35164 8a	57 A G	CACAGCCCTGC OOC	CCCTCTGGATT CTGAATCTCAA	TTGAACCAAGGCCCTAACAGATGACTCAGCAGGGCCCTCAAGCACAGCCCTGCCCCCAJAGJCTTTGA GATTCAGAATCCAGAGGGTGTCTCAGTCCCTTGGTTAGGTGCTTCTGTGACATTTCCCTTG
WI-18052b	67 A G	--- CCTGAGTTCTT TCATGTACGA C ATC	--- CTCAGGCAGCT CTGCTGT	AGCGAATGAAAATGCTACATAGGCTCCCTGAGTCTTTTCATGTACGAATCTJCTGGTTACACATCTT AJGACAGCAGAGCTGCCCTGAGGGAGGGTTGTGTTTAAATGCTGATGCTCAGCACAGTGTGCTGGC ATGGCCATCCATGCTTT
WI-18052a	50 T C	GGAGTGGGG GAGTAAAA	CGTCAOCCCTGC TTCCA	AGCGAATGAAAATGCTACATAGGCTCCCTGAGTCTTTTCATGTACGAATCTJCTGGTTACACATCTT AGAACAGCAGAGCTGCCCTGAGGGAGGGTTGTGTTTAAATGCTGATGCTCAGCACAGTGTGCTGGC ATGGCCATCCATGCTTT
WI-18054	46 G A	GGAGTGGGG GAGTAAAA	CGTCAOCCCTGC TTCCA	CTGTTGTGCTGAGAACAGAGGGGTCAAGGGAGTGGGGAGTAAAJGJATGGAAGCAGGGGTGACG CATGCAGGAGTCCAGACAAAAGACGGGTGATTTGCTCAGGTTGGTAGCAACAGAGGTAATG

WI-18084	54 G A A G A	GTAGCTGCTA AGCTGTATTTC	CCAGTGGTATG ATTGTGACATT C	CAGCTGCCAATCATCTCTCAAAACCCCTGGGTAGCTGCTAAGCTGTATTTTCAGAG/AG/AAATGTCAC AATCATACCACCTGGGAGAAAGAGTAAGCACAGTCTATTAGGTGCCAAACTGGGGTACCTGGGAG GCAGAAA
EST35347 2	97 T C A A	GCATAAAATT TTCCAGTTGGT	CCCTCGGCAOC TGCT	TTTAGCACCATCTTAGTGGAGCAGGATCTTGATATGGGGTGGAAATTTTGTGTATCTGGGCTTCAT GGGATGCATAAAATTTCCAGTTGGTAAGT/CJAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGG CAGGCA
WI-18070	28 A C	AACCCACTAC TTACTCAGAT	AAAACATA AGAACTGGA GGTTTT	AAACCCACTACTTACTCAGAGTGTGTAT/CJATATTAACACATGAAAGATATAATCTTAGAAAAA ACCTCCAGTTCTTATTAGTTTGAATTTCTGTACTCAGAAGCATTTTAGGTGCAAGGATATAA
WI-18080c	80 C T			TGGCATAAAGTTTGCAAAATATCAATATCAAACTAGTCTCTCTTTGTAAATTAATACTACTATGCCGTG TTTGACITTTAT/CJTCTTAAGTAAATGAAGCCAAATGCAATGTTAATCCTTCTCCTTTGGTGTAT
WI-18080b	65 G A			TGGCATAAAGTTTGCAAAATATCAATATCAAACTAGTCTCTCTTTGTAAATTAATACTACTATGCC[C/ AJTGTGTGACITTTATCTCTTAAGTAAATGAAGCCAAATGCAATGTTAATCCTTCTCCTTTGGTGTAT
WI-18080a	41 T C	GCAAAATCA ATATCAAACT AGTCTCTC	CAATTTACATA AGAGATAAAA GTCAAACA	TGGCATAAAGTTTGCAAAATATCAATATCAAACTAGTCTCTCT/CJTGTAAATTAATACTACTATGCC CGTGTGTGACITTTATCTCTTATGTAATGAAGCCAAATGCAATGTTAATCCTTCTCCTTTGGTGTAT GTGGCATCCTATAAAGCAGCCATGTGTGAACAAATGATATGCACAGAAAGCATACTTCT[G/A] TGGCTTTGTACACGGGTTTCTTCAAGAGGAAGATGACTCAGCCCTCCAGCTTCTGCAGTCTAGC TTAGGAGAGGIGITGAA
WI-18086	63 G A			AACTACATAGTATGGTGGCTGGCTTAGAATCAATGGGTAAAGCCTTTAGTGTACCTTTGGTATTCCTC TT[C/CJTGTGTATGAAGACAGACACCTCTGCTGGAGGACTCATTACAATGTAAGAAAGGGGTGAG TCAGT
WI-18115b	71 C T			AACTACATAGTATGGTGGCTGGCTTAGAATCAATGGGTAAAGCCTTTAGTGTACCTTTGGTATTCCTC TT[C/CJTGTGTATGAAGACAGACACCTCTGCTGGAGGACTCATTACAATGTAAGAAAGGGGTGAG TCAGT
WI-18115a	70 C T	TTAGTGTACCT TTGGTATTCCT TT	AGAGGTCTGTC TTTCATACCAA A	AACTACATAGTATGGTGGCTGGCTTAGAATCAATGGGTAAAGCCTTTAGTGTACCTTTGGTATTCCTC TT[C/CJTGTGTATGAAGACAGACACCTCTGCTGGAGGACTCATTACAATGTAAGAAAGGGGTGAG TCAGT
WI-18136	78 A G			TTTTGAGAAGCAGCTCTGTAAGGCAAGGATGCAATCAAAAAATGGCTTTGAGGATTAATCTTCTCTTTA GGTAATTTGCA/GJTAAGACAATAAAGCATTTTAAAGTCCACTGCCGCTTAGAAACT
WI-18169	115 A G	CCATCTTCCG GAAGCTC	GAGTCTGCTT GTGCTCCA	GGCAAAATATTTTACATCACACCTCGAATCTGCCAAGTCTTCCACTATGAAGGCAATCGTAGAG TGTGCAGGAGGAAAGGTGTATCCAAAGCAGCCATCTTTCCGGAAGCTC/GJGTGGAGCACAAGCAGA ACTCGGTGGGTAGAGTGA
WI-18190b	26 G A			TGAAAAGAGTCGACACAGCGGACACT[G/AJTCATAAGTGGAAACAAAGGATGAAGCTAATCATGGAG GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAAATGAGCTGGAGACATTAATCCTGGCGA

WI-18190	62	A	---	---	---	TGAAGAAGTCGACACGCGGACACTGTCATAAGTGGAAACAAAGGATGAAGCTAATCATGGA[G/A] GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAATGAGCTGGAGACATTAATCCTGGGGA
WI-18181	100	A	C	CAGATC	CGTTTACCAT TTGTTAAGCTT TTG	GACAGTGAACAACATTGAAACACAAATACAAACAAACATTAGGAACAAGAAATGTGTAATCCAA TGTGTGAAAATATATACAAACACTCCCTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAACGTA TGTGTTCTTGAAC
WI-18215	78	A	A	CTGCCCTC	AGCAGAGTTC CTCCCTCTCT OXXX	ATTATACAAGCATTCCTGAGTACAACTAGGGGACAGGTATTTACAAAAACAAATAGAGCAGA GTTCTGCCCTC[G/A]GTGTGGGGGGAGAGAGGGGATTCAGCATTTGGTGGAGTATGTTAATT CCCTCAAGTTAATCCTTC
WI-18232	60	T	A	AA	TGGTGTGATT GTGATACACTT C	CATTTCCGAAAATCTGATAGTTAAAATATCCCGTCTGGTGTGATTGTGATACACTTAAGT[A/G]AA CCCCTGAAAACCTTTATTTTGAATTTGAAGTTTGTCTAGAAAACCTGGGCAGAACTTTTACACTTCTG AC
WI-17892	76	T	C	ACA	GGAAAACCTG AGTTTGAGATC GAGACA	TTTAAAAATGCTTAGATTTCTCTCAGTATTTTATCAATAGTGTGTAAGCTGGAAAACCTTGAGTTTGAG ATCACATATTC[CTGTCTC]ACTAGTCTATTCACCTCTGTGGGCATTTCCGCAGAAAGTGCC AATATCCCCAAATGTTAATCGTAACATACT[G/A]GAAAGCTGTACAGTAGAAGTGTAGCAAAAAT TGGATGOCACAACTTATCTCACCATTCTTCAAGCAAGTGAAGTCAAGATGTTCTTGCCTATATC TGCAAAAGATCGAACAG
WI-18266c	119	C	T	---	---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATC[CT]ACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124	T	C	---	---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACATTC[CT]GAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97	C	T	TTCAAA	AAATAGGAAA TATGGACTATC TTTGTGCA	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[CT]TGCACAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73	A	G	AA	GCTGTCAGCTA TTGTTATTCA	CTGAGCCTCTGGATATGTGGTTTAGTGTCTATCATTAAATTTGGAAAGCTGTCAGCTATTGTTATTTT AAAT[A/G]TATCTCTGCTCCCTTTTCTCCTTTTCTGGGATTCATCTGCAATGTTATA
WI-18330b	66	A	G	---	GGAGAAAAGG GAGCAGAGA	AAACATCTACAGCTGTCTAGGCCATCCTGTAAGAAATCAGGATAAGAGCTGAGGAAACAAGAGG A/G]TATGAGGCAGTGAGTCAGGACTATGCAAAACCATATAAAATAAAGAACATAATTTTGTGAT TCACA

WI-18330a	49	G A A G A	TCCTGTAAAGA AATCAGGGAT	AGTCCTGACTC ACTGCCCTACA	AAACATCTACAGCTGCTTAGGCCATCCTGTAGAAATCAGGGATAAGAGAGCTGAGGAACAAGA GGGATATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAAATAAAGAACATAATTTTTTTGTTGAT TCACA
EST37564 5	85	T C A G A	AAATTC AAGC CATCTACAAA	CTATGGAGGOC TCAATGAGA	AAATTAGTTAGCCATAACAGGCTGGAATTGCTGTTAGAATACTGCATGTTATTTAAGCTAAAATTC AAGCCATCTACAAAAGATTTCCTCATTGAGGCCCTCCATAGGCTGCAACACATCAAAAGGCATTAC TGTA CTGGAGAGGACTGAG
WI-18327	104	G A T T	AACAGCTTT CGTTAGGCTAG	CGCATACAATG GCTCAGC	CAAGGGATTTTATTACCTACAACAAGTAAGGAGGACAGCTGGGGCAGTTTCCCAAGAGCAGTACCTC CCAAACAATGGTGAAACAGACTTTGCTTAGGCTAGTTTGAGCTAGCCATTGATGCGGAGGCAGA GT
EST37624 6b	102	G A ---		---	GTGGCAAGAGCAGCTAAACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCACGCTGATGG CCTGCAGTCTCTGCCGTGCTTGGCTCTCTGGACGGAGATTCATTCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
EST37624 6a	58	C T ---		---	GTGGCAAGAGCAGCTAAACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCACCTGATGA TGGCCTGCAGTCTCTGCCGTGCTTGGCTCTCTGGACGGTTCATTCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
WI-18357	89	C G GCATCAA	CCAGCCCTTA GCATCAA	AAGGACTCAA AGACTGAAGAT GA	AATGTTTTAAAGTCTCTACCGTCTGCTGAGTGGCCCATGAAGCCAAAGCCCATTTCCAGACATTTCAGA TAATCCAGCCCTTAGCATCAAAGCTCATCTTCACTCTTTCAGTCTTTGAGTCTTCCAGCCAGGTCCCAAGCTT GTGGACCCAGAGACAAGCC
WI-18012g	117	A G ---		---	TTTTATCTGGGTACAGCTCCTTCTTAATGGCCCTGAAGGTCACTCCTTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTCGTGAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012f	113	G A ---		---	TTTTATCTGGGTACAGCTCCTTCTTAATGGCCCTGAAGGTCACTCCTTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTCGTGAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012e	112	C T C C C T	GCCACTTTTGC C C C T	TCAGCGTGTAT CAGGAAACA	TTTTATCTGGGTACAGCTCCTTCTTAATGGCCCTGAAGGTCACTCCTTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTCGTGAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012b	46	T C ---		---	TTTTATCTGGGTACAGCTCCTTCTTAATGGCCCTGAAGGTCACTCCTTTCAACTTTCCAGACTTGGAA AGATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTCGTGAAGTGTTCCTGATACAC GCTGACGTTTCGAGGG
EST38390 4	75	A G C T C T G C A T T G	GCAAAAAGGA CTGATTAAATAA	GCTAAAGTCAG CTGATTAAATAA ACTTAA	CATATCATAGCCAGATCTACAACCCAGAGTAATTTCCCATGTTATGTTACATGGCAAAAAGGACTC TGCATTGTAGATTAAGTTTATTAAATCAGCTGACTTAGCATTTGGGAGATTATCTGGAT

EST38512 7	91 T	TGACGATGCC AATACTTCG	CACCTGCACTCT GGGAAGC	TAATAAAAGCTGACCAATTGGTAAACTGTGTCTGGACTGAGAGAAACAATGAAAAATCTGTAAT ACCTGATGACGATGCCAATACATTCGT/GTCTCCAGAGTGCAGTAACTGTTATAGCC
EST38519 0	24 C T T	CCTGCACTCC TAAAAGATCT	TCGTTAGGAC TTGGGGA	CCTGCACCTCCTAAAAGATCTTTTC/TTCCCCCAAGTCTTACAGAATGGTATATCTCTGGAAAA AGATGAACGTCATCAATGGATTGTGCTGCTCTCGTTTTCAGCTTTGATTTTTTTGCTTGAGAACCTTG TCCTCCTGCTGATTT
EST38575 1	66 T C A A	GAACATCCCA TGTTCTGTT	AGGGAAGGTA GTATAACACAT	AGTGGTCAATGTAAAACTAATGGGGACACCAAGCCCTCAGGAAGAACATCCCATGTTTCTGTTTAA T/C/TTCTCTTATGTGTTACTACCTTCCCTTCTCTTCTTATACACATAGATTTTCTTAAATTGCAGC CCA
EST38616 9	101 C G C T T C	CCTGCTCCGCC CTTC	GAGGAATGGAT GGTGGC	CCATCTAGGCAGGCTACCTGAGCTCTCTGTCTCCAGAGTGGTGCCTCACGCCGGGGCCCGCTGG AGTCCGGGGCCCGCCCTGCTCCGCCCTTC/C/GGCCACCATCCATTCTCCAGGGG
EST38652 8	59 T C C A T T T C A A	TCTGAACCTGGG CATTTCAA	TTGCAAAAATG AAGGAAAAA	TATAGTAGGTACTTCTTGTCTGCAGCAGGAATTTATTCAGTCTGAACCTGGGCATTTCAA/T/CJGCGTG GTATTTTTTCTTTCAATTTTGCAAGTAAAAAAATCAT
EST38654 5	42 T C G T T T T A C A	AATGTCATTT TAATATATCA	CAGTGATGGTC CTTAATCTTCT	CTCAAGCTGAGAAATGGTCATTTTAAATATATCAGTTTTACATA/T/CJAGATAGAAGATTAAAGACCAT CACTGAGGTACATAGCTCAGAGGCGAGAGTTAAGATTGGACCCAGGCGTGGTTCCAGCATATA
EST38707 9	75 A G ...		ATC	GGATCTCACTCACCTGGGACAGCCTGAGAGGGACATCCACCAAGACCTACTGATCTGGAGTCCCA CGTCCCGJAGJAGGCCAGCGGGATGTGTGCCCTCTCTCCCAACTCATCTTTCAGGAACACGAGG ATCTTGTCTTCTGAAA
EST38759 2	86 A G G T G A T A T G G	TGCTCCCTGA GGTGATAGG	TCACCATCGTG GACTTAAGG	TGACCTTGATTTCTCACTAGAGGGGAGAAATCACCTACCTTTTGGATGCCCTCCACTCTACTTGT CTCCCTGAGGTGATATGGJAGJCTTAAGTCCACGATGGTGACCTAAACTCAGTTTAAATTTCTTGCC TAGCAGCACC
EST38775 1	40 T A C	AATCAATAGG AGAGGATTGG	GGCTTTGCTCT GAATTCAAA	GACTCTCAACCAAGAGAAAATCAATAGGAGAGGATTGGCT/T/ATTTGAATTCAGAGCAAGCCCT CTTACTGAGAGGTGAGCCCGAGCCCTCCAAATGCCCTTTCATGAGTTAGGATCTCTAAGTGGTAC AAACAACCAACATGGTGG
EST38815 4	91 C A C A	TGTTATGAGA ACCCATTACA	GCTGACTGGCA CATGCTTT	CACCCCATATTTGACCAAGGGATGAAGCCCTAGCCATGCTCTTTCACTTATGTGTTCATTCAACAAG TGTTATGAGAACCCATTACACA/C/AJAAAGCATGTGCCAGTCAGCAGATTCTGTATAA
EST38858 4	98 C T T G A C	CACGAGTAAA AAGAAACTCA	GGAGCGAGTCC AAGGAGAA	TCCTTACTGTGCTTACAACTTTCTCCCAAGTTTGGGTGGTTCCATATTGTTATTGTTATTGTTA TTCAACACGAGTAAAGAAACTCATGAC/C/TTCTCCTTGGACTCGCTCCTCTCCCCAATCTCGAT ACCGACTGCACGTGG
EST38865 2	72 T C T G T G C A T G C	GCTGTAGAATT TGATGATG	GGAAGGACGG AGGACACAG	CCTTAATGGATTTACAGCTCATCTGAGTCTCTGCTGTGTTCTCTGAGGAGCTGTAGAATTTGTGCG ATGCT/CJCTGTGCTCTCCGCTTCCCAATAGACATATGCGAGGCGAGGCAAGAGCATGCTGGA TTTGCTTATGTTGTTAA

EST38878 9	47 T C	AAACATCATT ACTAGCCTAG ATCCTAA	CCTTCAATAAA TCTCATGTCT CA	CCAATGAGAACCAAGTAATTAAACATCATTACTAGCCTAGATCCTAAATTCJTGAGGACATGAGATTT ATTGAAGGGAATCCTCAATTAATATGAACATTTCTTGAGAAATGGGAAATTTGAAACATTCCTCC TTATTCATGTCTATCTCACACATTCCTTTATTTATTTTATTTTCTCAATTTCTCAATATCGGATTTGTC TCATGAGAAATAATGGCTGAGGGAGCTGGCACGGCAGTCTTCTCAJG/CJGCTCCCTGGATAGCTAAAT TTA
EST38882 6b	113 G C	TGTCATCTCAC ACATTCCTTTAT TCTTTT	CGATATTTGAG AAAGTGAAAA CAA	TTATTCATGTCTATCTCACACATTCCTTTATTTTATTTTATTTTCTCAATTTCTCAATATCGGATTTG TGCTCATGAGAAATAATGGCTGAGGGAGCTGGCACGGCAGTCTTCTCAGGCTCCCTGGATAGCTAAAT TA
EST38882 6a	35 T C	GCACAGCATG GCTAAAACG	GGTATTTGTTG ATTCCCATCTT T	GCACTAACTAACTTTTCATTTTGTGGATTGCACAGCATGGCTAAACGJGJTAAGATGGGAATCAA CAAATACCATTTGAAGATATGGAGCAAGAGAACTCTCACATACCTGCTGGAGGGAATATAAAAT
EST38909 5	47 A G	GTTGAGGGAA ACTTATAACCT	TGTTGTTTTGT GAAACAAGCG	AACTGAATGGCAGTGAACACACTACACATCAAACTTAGGGAAATGTGTTAGTGTGACGTTGAG GGAAACTTATAACCTCACJG/CJGCTTGTTCACAAAACACAGCAGACAAACAGAGATTTCCAACTC CAGCAATGACAGGGCTAGGG
EST38911 9	85 A G	TGAATTCCTTT GCTGGG	CACTGCAATCT CACCCC	TAAACATTTCCCATTTGAATTTCCCTTGGTGJG/CJGGGGGGGGTGAGATTGCAAGTCTCAAGATAAA TATCAAAATATATCAAAACTTCAAAATTTGCTATGCTTTCACACACTGACATGAGCCACAAACATTT CCTTTACAGGGGACTGTAC
EST38955 5	30 G C	GGACCTTCGG TGACC	CTGGCAGGGAG CCTG	CCTGCTATGATGCCTGGGCAGATCCCGGACCTTCGGTGACJG/CJGAGGCTCCCTGCCAGGGCTTGG CCCCTGACCGGGCTCCCGAGCTCGGCCCTGACTGTGGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST39002 0	42 G A	GGTGTAAAG CCTAAGGAAT	ATCTCGGCTGG CGGC	CACGTGGCCCCCTAAGTTCCGGGCTCTCCTCAGTCTGGATGGCTGTGGAAAAAGCTTGGTGGTAAG GCCTAAGGAATJGJAGGGCAGGGGGCGATGCCGCCAGCCGAGATGGTCTGTAAAGCTGTGGGTC AAAGACCTAACTTCTGGA
EST39004 8	79 T G	TCCCTATTATT CCATGATATTT TCA	GAATGGTTTGT GAAAAATATA TTGATAT	AAAGATAATGTATCATCACAAACGCAACATATAGAAACATAAAAGAAAAATAAGTATCCACCCTAAAT CCCTATTATTCATGATATTTTCAJTCJAGCAACTAGTATATATCAATATATTTTTCACAAACCAT TCAGTTACAC
WI-16398	90 T C	CCTTGTCTC AATTTTAAAC CCT	TAAGGGCTAAT TCCCTATATA AAAG	GGTTGTCTTCATGATTTTCTCATTTCTCATAGGTTTCTGTGCTTGTCTCAATTTTAAACATJ T/CJCTTTTATATAGGAATAGCCCTTAAACTGTGGTACATGCTGCCAAAAATTTCTCCCTCCAGTT
WI-16403	69 T C	GCTTTAATGGC TACAGAAAGA AGG	CCAGAACCCAG ATGTGTTTAAA AA	GCITTAATGGCTACAGAAAGAGGCTJGGTTTTATTTTCTTTTAAACACATCTGGTTCTGGCAGC AAGTTATATTAGCATTTAGAGCAATAGGTGCCCTGAA
WI-16406	24 C T	AGG	AA	

EST39236 0b	57 C	TCATCTGAGA ATAAACCTTCCT G GTCT	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCTTTTATTCATGATTGTTTTCATCTGAGAAATAAACCTTCTGCTCTAAATTTTCCAA[C/G]ACTATGTT TAATGATGACTCAGTACCTATAATGAGACTGGAAATATATTACCTGGCAAATGAATGAGGTGCTC TTT
EST39294 4	63 G	CCTGAAACAG T GATGCC	GCACAAATAA ACATAGTACCG AGAA	CAACAGACCTTTGGTTTGGCTCAGCTCACCTGGTGACAGGAGACTCCTACCTGAAACAGGGATGCC[G/I] TTCTCGGTACTATGTTTAAATTTGTGCTGAGCCAGCAACCTCGAGTTACCCGGCCTTTTACCCACAGCC AGCTCTGCTTGTCTGCAT
EST39366 2	72 T	C ---	---	AGAAAAACATTCTGCTGATCAGAGGAAGATGATGTAGAAAAATCAGAAATCAGAACTGAAATTCCTAAA ATCTAT[T/C]ACACTGAGAGGAAAAATGAAAAAGAAAAATGTTTGCATAAAAGCTTTTCCCTGACTCTCA GAGGGGTTCAGA
EST39371 9	86 A	CATTGGATT G GGTGAGAGG TT	TGATTTGAGAC ATTTACATTT TT	AAAAAGCTGTAGCTGGCAAGTCAAAGTTTATTTATGTGTGTAATTTCCAGTTGAGCATTTTTCAT TTGGATTAGCGTGAGAGG[A/G]AAAAATGTGAAATGTCTCAAAATCAAAATGCTTCTTCTAAAGATT GACATTGCCAACCTGC
WI-17177	23 A	G ---	---	ACAAAGTACATATCCAAACCAACC[A/G]TCCATCCCCACCTGTGOCCTATTCTTCTTGTGTTTCTTT AGAGCCTTTTCAGCTATTTCCTGTGAAGCAAACTGCAGAAAGCCTCCCCGTACTCTCTCCCTGGAA G
EST39428 8	31 C	GTCCCCACA T ATTTGATT	GGTCCCTTATG AAGCCACC	AGGTTCTGTGTTGCTCCCAATTTTGATTC[CT]GGTGGCTTCAAGGGACCCAGGATTCGCAIT TTCTGGGTGGGCGCTAGGTAATTTCTGTTGCCCTTTGGTCCACAGAGACAAATTAAGAGATCAGGCT GGCTGTGC
EST39430 2	45 A	GGCAGAGGAA TAACTGATGTT C	CAGGGGTGCGG GTATTG	AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAACTGATGTT[C/A/C]CAATAACCCCGACCCCTGA CCCAGTAOCTTTCCCTCAGGCCAGGCTCCGGTGGAGGATGCTCTGGG
EST39446 7b	117 C	CTACTGACAT AGGACTTCA	TCCTGGAAAAC TGACATAAAC	AAAGCCCTGTAAACTGAAGCTAGACAACGTCAACTTTGGAAAGAAAATAACAGAACCTATTATAT ACGTAATACACTTTCATACCTGCCTACTGACATAGGACTTCAGAGTAATA[C/T]GGTTTATGTCAGT TTTCCAGGATTGTTCTCCC
EST39465 2	80 A	AATGCAGGAG G GTGSC	CAATCTCGGCC CCTCT	ATGGTGTCAATTAGAGGGCCACAGGGGATGGGGAGTAAAAATAACATAAACGAACTGAACAGAAA TGCAGGAGGGTGGC[A/G]AGAGGGGCCGAGATTGGGTGTTTCAGGGCAGAGAGGTGGAAGACCAG
EST39501 0	81 A	AAAGATTCCT GTAGACATCT AACATTAG	CACTTGCAATT CTGAAGGCT	TGCTTACAACCCATAACCATAGGCCATGTGTTGACACATTCTTGACCAAGCCCTAAAGATTCTGTAG ACATCTAACATTAG[A/G]TAGCCCTTCAGAAATTGCAAGTGCAGGTTCAAGTCAAAACCAATTC CACAAAATGGGACTGCTGAAGAGGTGGACAGTTGGACCTTACTTTGGTGACCCCATACATTGTGGTCA CATGCTTTAGCCATAC[A/C]CATGGTAAACATTGACTATGGAGTCTTGTGAAAGTGAATGTGCGGATG GCTATGTAGACATAAAGA
WI-18387b	84 A	C ---	---	

WI-18387a	57	A	G	CCTACTTTGG	GCTAAAGCATG	CACAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATACGAGTTTGTG
EST40601	78	A	G	CGTGGAACCT	TGACCAAAA	GTCACATGCTTTAGCCATACACATGGTAACATTGACTATGGAGCTTTGTGAAGTAAATGIGCGATG
9	78	A	G	GAAACAC	TTCTTGAAGA	GCTATGTAGACATAAAGA
				AGTGATCAC	AAGCGTC	TCCCAGGATGTTTATTCAAAGCTGTGGACGGTGAACATTAAAGACAAAGAGGTGACTCGCGTGA
				ATCTTCAGGAT		ACCTGAAACACAG/GGACGCCCTTCTTCCAAAGAGGGCTGTGGCGATCAGGCCACTCAAGG
EST41935	32	A	G	AGGT	GCACCCCTTC	TCCATTCAAGTGATCACATCTTCAGGATAGGTAG/JATAACAGTGTGAAGGGTGTGCTCATTTTCTTC
				CATTCTGGTCT	ACACTGTTA	AGCTGTGAGTAGAGGAGTCTCCCGAGAGTAGCAGTTGTTGA
				TTATTTTGGGA	AAAAGTATTT	ATGTCATTCTGGTCTTTATTTTGGACA/C/JGTAGCATGTTTAAACAAATCAGTTTTCATAGGCAA
EST43091	28	C	T	CA	CTAC	CCTTTGAACATCAAAAGAAATACAAATATATTTTTCACAAATTTCTCATCAGTGTAAATTC
WI-18420c	108	T	C	AGGAAGTTTC	AAATCTCAGC	AGAGACAAACAAGAAGATAAGGAAATGGGAAGAACAGAGAGTGAATTTAAAGCAAAATCTTGA
				GAATAAGGGA	ATTGCTATAAG	TTTTCATAGGTACTTCATGGGA
WI-18420a	38	C	T	AA	CCAAGATTTC	AGAGACAAACAAGAAGATAAGGAAATGGGAAGAA/C/JTAGAGTGAATTTAAAGCAAAATCTT
					TTTAATTTAC	GGATTGAGATTCCATTAAACAGGAAGTTTCTCAAAAAAATCAAAATTCAGTGTATAGCAATGCTGAGAA
WI-18425b	101	T	C	AGACAGATTTC	TC	TTTCATAGGTACTTCATGGGA
						AGCTGATCAGCTGCTGTTACTGTGTTTATGTGTGGCCCAAGGAAAGCCAAAGATCAGACACCTGTG
					---	CTAGACAGATTCAATGCACACAACAACAGAGGGT/CJGGGGTGCACACGGCGGAGAGCCAAAGAC
WI-18425	81	A	C	A	CCTCCTGTGT	TAGGGC
					TGTGTGA	AGCTGATCAGCTGCTGTTACTGTGTTTATGTGTGGCCCAAGGAAAGCCAAAGATCAGACACCTGTG
						TAGGGC
					CTCCTGTGCT	AAATTGAGGTCGGGTGGAACTATAAAAGGAAAGGAAAGAGAAATCAAGGGAGGCCAAAGTG
WI-18449	129	C	T	AAGTGGGACT	CTCCTGTGCT	GGAAGCTGTATTGCTGATCTAAGCTGTCTCCAGTTCCTTTTGGCTCTAAGTGGGACTA/C/JTC
						TGGATACAGTCAGGGGAG
WI-18457	120	T	C	---	GTATCCAGA	ATCGCTTCATTGAAGCTGCTTAATTTCTCAGTCAACTGGTGGCCCAAGACATTATTTTATTCCT
						AAATGTCCAAATATCTGCCTGATGCTGTGTTTGTGCACATTGGGGCCACAGT/CJAAATAGGCTAAA
					---	AGGAGTCCCACTGCT
WI-18462	39	A	G	AGAGTGA	TTTAGGCTTTG	GGTGCTATAGCTGCTGTATACCCACACAATGGCAGAGGTGA/JGTAGAAACCATCTCAAGCCATAAAA
					AGATGTTTCT	TATTTACCATACATCCCTCACAGCAAAAGTTTGTAACTCTCGGTTTAGGGACTCCATTGAG
WI-18476	60	C	T	GAGG	GCACGATGGGA	TGAGGACGTGTGACAAGCTCCAGAGGGGTGGGGCCGGGTGAGGGTGGGGGCTGAGGGT
					GTGAAC	CACCTCCCATGTGGCCCTGGCCGTCCCTCCACTCACCCACACCTGGCCCGAGTCCACGTTGAGGT



WI-18491	109	G A	AACAAATGGT AGGTGGTATT AATACTATT	CGTGTGCATTT TCTTGTATCC	CTAATGAGATGAATACATGGAAGCGGTTTAGCAGAGTGCCTAAACACACAGTAAGTAACCAACAAAT GGTAGGTGGTATTAACTATTATTATTAATCCAGAAATGAC[G/A]GGATTACAAGAAATGCACA CGT
EST50757 b	79	C T	GAGCTCGAGG CTGCTTCT	ACCCCTCACCC GCCC	AGCCCOCTCCACTCCACTGCTTCCACAAAGTCGGCTCCCGAGAGCTCGAGGCTGCTCTTTTATAT GTGAGGGCC[C/T]GGGGGGTGAAGGTCAGAGA
WI-17675	103	T C	GGACATTTGG CATGGTGACTT	GGGGAACCAAC CAGG	GATCTTGAAAGCAGCTAGAACTAAACATCTTACCAGGTGCTGAAGAAAGTGTCTTCGTTTAAAT TGCCAAGCAGGGATGTGGACATTTGGATGGTACTT[C/C]CCTGGGTGTTCCCCATAGATTACCCAT TGCCCTCTAATGGTGCTA
WI-16543	67	G T	AGATAAACTA CATTTGGGTTT	GATTTCATATT ACAGGGGACTT	GATCCATTACCTAGGGTAAATTTCTCCTGAATGTCAAAACAAAGAGATAAACTACATTGGGTTTGG[ G/T]AAGTCCCTGTAAATGATGAATCAAGAATCCTCAAGTGTCTTGCCACCCATTTAAACGTATT TTTGTTAAGGCTGAAGTT
WI-17687	107	C G	GCCAAAAAGG TTGGGGA	TTACTTTTGT CCGACCAGCA	ATCTGAGATGGAAGAGTTTCATCCCAAACCATCTCCCCCTGACCCCGAGTCCATGGAAAAATTGTC TTCCACAAAACCGGTCCCTGGTGCCAAAAAGGTTGGGAA[C/G]TGCTGGTCCGTACAAAAAGTAATT G
WI-17690b	79	A G	AGGCATTTTTC TAGCTGTGTTT	CAAGAGTTATG GGTCTGAATC	ACAACATGTGAAAGAGATATGTTGCTTACTCAGAGTGAGGCAATTTTCTAGCTGTGTTGATTT GGCTTCCCTAT[G/G]ATTCCAGGCCCACTACTGTTCTCACATCATCTGCTATGCTGCTG
WI-17690a	63	G A	AGGCATTTTTC TAGCTGTGTTT	CAAGAGTTATG GGTCTGAATC	ACAACATGTGAAAGAGATATGTTGCTTACTCAGAGTGAGGCAATTTTCTAGCTGTGTT[G/A]A TTTGCTCCCTATAGATTTCAGGACCCCACTGTTGCTCACATCATCTGCTATGCTGCTG
EST51717 b	128	C T	GCGGAAGACA GTGAGCTGTT	TTGAGGCAATA ATCCAGCTC	GATCCAACTCAGTGTCTAATCTCATCATCCAGATTTATCTGAAGTGGAAACCCCTCCGACCCCA TGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCGGCGGAAGACAGTGAGCTGT[C/T]GAG CTGGATTATTGCCTCAAA
EST51717 a	39	C T	---	---	GATCCAACTCAGTGTCTAATCTCATCATCCAGATTTAT[C/T]GAAGTGGAAACCCCTCCGACCC CAATGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCGGCGGAAGACAGTGAGCTGTTCGAG CTGGATTATTGCCTCAAA
EST53012	97	C T	TGTCACCTTG GGGCC	GGCTCTGOCCA GGCC	TTTCCAGGTTGACAGGTTTATTCACCCCTTCCATCCCCATGGCCACCCCGAGGAGGAGACAG GTGTGCTGGAGTCTGGTACATTTGGGGCC[C/T]GGCGTGGGCGAGGCCCACTGGGTTTACATTTCTGT GGGCGGTTGGGACAC
EST53349	96	A G	TGTTGAAAGC AGTCACAATG TAC	CATCTGGATAT CTTGTACATT TT	AAACTGCAATAACAAAAACAGAAAGTCCAAGAGGCTAAAGTCTAAGCTATAATTACACATG AAGTATATGTTGAAAGCAGTCACAAATGTAC[A/G]AAAATGIGACAAGATATCCAGATGTTTAA TTTCGAAATGTCTCCATGACTTGACAGACTGAGAGCCAGCCAGCCAGGAGACCTTGAGAACT TAAACAC[A/G]GAGCATTTATTGTTAGAAAGGGCAAGTCTTACACTCAAAATAGGTTTTAACATGAAC ACATTAAGGGGAGATGGCC
EST53389	74	A G	CA	C	

[illegible]

[illegible]

TIGR- A003P30	117	C G	---	CCAAACCTCCT CAITCCTATAA	TTAAA	---	ACAAAGTTCAAAAGGAGAACTTCCTTTGTTTTAATGCAGCTGTGCTCAGAAGCCCTGTGATTTCTTAGGA AACCATCTGGGTTTAGCCCAATTAGAAAATGCAGTTTAAAGCAGTGTCA/C/GJACTGGCTGCCTGAA GGTACCCCTGGAGATACT
TIGR- A004S34	156	C T A	---	CCAAACCTCCT CAITCCTATAA	TTAAA	---	GCTTGCTTTTATGTTAGTTTCGGGGGAAAGGAGGGGCTGACAAACCGCAGACATCTGGACACCAGC AAGGGTCCAGGGGAGTTTGCAGAACTTCTTTCCTTGGCTAACAGTCTGTATGTGACAAATAGCCA AACCTCCTCATTCCTATAA/C/TCTTTAACAAAAACAGTTAGCTGTTTACAAAAACAGTTAGCTGTT TACATG
TIGR- A004T44b	97	A C	---	CCAAACCTCCT CAITCCTATAA	TTAAA	---	AACAACAGTGTAACTTTAACAGGGGATGTTAAAGTAAAGTACAGGAAGATAAACCAAAAATGAT TGAGTATGATAAGAAATTTGCATGGCGATT/CJAAATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAAAGAAACAATATAG
TIGR- A004T44a	69	G A TGA	---	CCAAACCTCCT CAITCCTATAA	TTAAA	---	AACAACAGTGTAACTTTAACAGGGGATGTTAAAGTAAAGTACAGGAAGATAAACCAAAAATGAT TGA/G/ATATGATAAGAAATTTGCATGGCGATTAAATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAAAGAAACAATATAG
TIGR- A004V08	60	T C GGCATTCTCT	---	CCAAACCTCCT CAITCCTATAA	TTAAA	---	CCTACAATCCTATAATTTGCAAGGGTTGGGAAGGATGCAGGAACAGGCATTCTCTTAT/CJGCC TTTTGTGGGAAGGATCAATTTGGGTGCATGCACCTTAGGGGACAAATTTGGGCAGTAGCTGTCAAAATTC AGTAGCTGTCAAAATTTCAAA
TIGR- A004V26	125	A G	---	CCAAACCTCCT CAITCCTATAA	TTAAA	---	TCTAGCTATAAGACCAGATTTTAATATTCTAGATATAGAAATTAACAGAAATAATCTATTGAATTGA CTGATTACAAAATGTTAACAGCTGGATAAACGGTAAATATGCATTATCTTCACATGA/VGJAAGGT TTCAGTTTATAAATGCTTAAATAGTGTATCTATTGCTTAAATAGTGTATCTATTGG
TIGR- A004V28 a	29	A G CGATCTC	---	CCAAACCTCCT CAITCCTATAA	TTAAA	---	CCAGGCTATAATGTTGTGGTGGATCT/CJGJCTCACTGCAACCTCCGCCCTCCAGGTTCAAGCAA TCTCCTGCCTCAGCCTCTTGAGTAGCCGGGACTACAGGCACCCGCCACCGCCTAACTAATTTTIG TATTTTTAGTAGAGACATTGTATTTTTTAGTAGACACAGG
TIGR- A004X20	25	T C GA	---	CCAAACCTCCT CAITCCTATAA	TTAAA	---	TAAGTTTCCCTCTCTCTGTAGGAT/CJGJCTCCATGTTACAGTCAACTATAAACATGGCTCATGT TCACTCTGGCTTCGCTCAGAGGAGTTGATATTTTGGAAAGTGGTACCTTTGTCTGTGCTTTTCA GACCAACCGCTCTCTTCAATTTCTTCAAGGCTTCCCTCCAAAGGAGTTAAATCATCATGTCCCAATC ATCATCATGTCTT
TIGR- A004X30	26	T C CCAC	---	CCAAACCTCCT CAITCCTATAA	TTAAA	---	TTTTGAAATCTTAGAGTAGAACCCCACT/CJACTCTAGTAACTTGTATAAAAATTAATAGTTTT AAACACTTCCATAAAGAAATTAGGGGTGCCAGCTCCTTGATTTCCCCCTAGGGATAAAGATATCCAT GTTAGGGATAAAGATATCCATGTAC
TIGR- A004Z04	102	T G ATGCAAACT	---	CCAAACCTCCT CAITCCTATAA	TTAAA	---	CACGGTATATGCCTTATATAGTATATATACAGATCGTACACAATATATTTAACAGTTTGACATG GGGTCCACAGTACCTTCAATTTGGGTATGCAAAACIT/GJTTGCTTTTCATGAAATTTCTAATATAAGG ACTGTGCTTCTTCATATTCATATGGACATTATACAAAAATACAGTCTCTTTAGTGATTTAAGACGTC TCTTTAGTGATTTAAGACTG

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TIGR- A004Z19	85 C T	GAGAACAACT GCAGCAATTTT	AAGATGTCAT CGGGAAGA	TAAGTGGAGACAAGTTTATTGGAGAGCTTGACACCCCTCTTCGCCCTAGCTTGAGAGAACAACCTGC AGCAATTTTCTTTTCTTTTCTTCCGATGACCATCTTTTGGCTGGCGGCCAGGCCCTGGGTGTC TCCCATATCGCTGCTTTAGTGAGACTGAGGATCTGGTATAGGAAACAGATC
TIGR- A004Z42c	89 C T	TTGGGGAGGT AGGAGACT	CAGGCTGCOG GTGC	GTCTTAGCAGAGGAGATAACTTTGAGGACAGCCCCCAAGGCCAGCTTCAGGCTTCAGGGGCGGGCA GGGTGGGGAGGTAGGAGACTTCCTGGACCGCAGCCCTGGCTCCAGCTTCATCATCTGTGTCTCTT CATCATCTGTGTCTTC
TIGR- A005D17 c	81 T C	---	---	TATGGACTGTGTAGAAATATGATTTGGACAAGAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGCCTCTGTAGATCTCTTGGCTCTCTGTGCAGGATTCCTTCTTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTACGACAGTCAAACTCTTACGACAGTCAAAACAC
TIGR- A005D17 b	79 G C	GGGGAACCC AGCAAG	GAGAGGCCAA GAAGAATCTAG AC	TATGGACTGTGTAGAAATATGATTTGGACAAGAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGCCTCTGTAGATCTCTTGGCTCTCTGTGCAGGATTCCTTCTTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTACGACAGTCAAACTCTTACGACAGTCAAAACAC
TIGR- A005D44	97 G T	TTAACATTATT GAACCTTAAAA CTGTACAC	TTGTCTATTAT TTAAGGCCAAC AAAA	CATCAGTAACATATACACAATTGGTCACTCAACTGAACCTTGCCTCCAATATATTTCTATACAATACTT AACATTATTGAACCTTAAACTGTTACACTGCTTGTGGCTTTAAATAATAGACAATGATTTTGG TCTATTACTTAGTGATAGACAAAGTATTACTTTGTTAGACAAAGTATTACTTTGTTAC
TIGR- A005E31b	27 G A	---	---	GGAGTTCAAAATTTATAACACAGGCCTCTG/AJCTCACAGTGTACTGGCTAGGCAAGCTTTCAGAC ACAAAGCCACCTGCCTGCCATGTGATAGTACTCTTGGCTGCTTGCCTTACAAAGCCACCTTCTAT TTCATACCAATACCTTCTATTTCATACCAATAAG
TIGR- A005E39	182 G C	AGTAAGGTTA CTGCACCTTAC	---	CTCAGTGTAAAAACTTTGTTAGGGAAAAAATAATCCAATGGATATATGGGAAGAGAGTG CCAGGCTGGATGGTGTGCTGAGACAGAAATGACCCCTGGGCTCCTTTATTTTCTTTTCAACAGGACC CCACAGATAATTTGCGGTATGTCATGAGGACTGGGATGCTTCTATTG/CJGGAGTCTCTATT
TIGR- A005E42a	42 A G	AGTAAGGTTA CTGCACCTTAC AGAG	CCTAAATCAGG GGAAATTGAG	GCTGAGTTTGTATCTTAGTAAGGTTACTGCACCTTACAGAGAGTCAATTTCCCTGATTTAGGA AGCGATGCTAATGGGTATTGCATAGGTGTAAGTATAAAATGTTGTATTTAAGAGAAATCCCAAG CTTGGTATAAGGCAGAAAAATAATGGTATAAGGCAGAAAAATAATAG
TIGR- A005E46	76 A G	CACCTGACTCG GTGCTTTAC	COCTGGCTGTG AGGTAATGT	ATGACAATGATGATAGTATTAGCCTACCGTTTGTAGCACTACTGCTGCTATCAGGCACTGACTCGG TGCTTTTAC/AJGTACATTACCTCACAGCCAGGGTTGGCAATGGTCAATTTTGACAAATGGTCAATTTG ACAC
U20979	24 C T A	GCAGGGGTGA CGTATGTAGA	GGGGAGGACAC CCTAAGC	AGAGCAGGGGTGACGTATGTAGAA/CJTGCTTAGGGTGTCTCCCAACAGAGCAGATACTTGAACCG ACTCAATTCCTGTGTAAAGAGACATTTGTCTGCTTCACGGAGCTCCCAAGGTGTCAGAGTTCTAT ATAGGATGCTGGATTAGTTCCTTTGATATTGTAAAAATTTCCCAAGAGCCGCATATGAATCTGCC

X57830	106	G C C T	AGTGGAAACCA ACGATCATAT	CATTGACAGAA TAAATGAGGC A	GTGGCAACTGTGGAAGGCACACTGAGCAAGTTTACCTATCTGAAAAAATAATATGAGATTGGA AAAAATTAGACAAGTCTAGTGGAAACCAAGCATATCTGTCATGCCTCATTTTATCTGTCAT GAAAGCGGGGTTCAATGCTACAAATGTGCTTGAAAAATGTTCTGACAGCATTTTCAGCTGTGAG CTTTC
X74070b	72	T G T G G A T C	CTTTTAAAGAA ATTTTGTTTA	GGGCTTAAAAA TATTAGAGATC TAGATTT	AACCTGAAGAAGTTACTGGAGCTGCTATTTTATATATGACTGCTTTTAAAGAAATTTTGTATTG GATCTG/GGATAAAATCTAGATCTCTAATAATTTTAAAGCCAAAGCCCTTGGACACTGCAGCTCTTT CAGTTTTTGTCTTATACACAAATTCATCTTTCAGCTAATTAAGCCGAAGCCCTGGGAATCAAGTTT GAA
Z48804	44	C T		---	ACTGCCGAAGTGTAGCGGCCCCCAACCTTGCTCTCATCACAG/C/TTJAGAGCTTCTCCCGAAGGG CCTTTAGGATAGGAGAAAGGTTTCATGCACACACAGTGTGAGAAATGGAAGAGCCCTCCAGACCACT CTACAGCTGCTCTAGCCTTAGTTGCCACTAGGAAGTTTCTGAGGCTGGCTGTAAAGTAAGTGAAGG TCCA
D28513b	133	A G		---	ATGACCAAGCCACCACATTTAGAACITTTGGCTGCCCTTGGAAAGTCCAGAGCTGGATCTCTCAGCTCC CGCCCCAGAGGGTACGACCTTTGGACATGGCTCACAAGCAGTTTTTATTGACTGCATGAATGCJAV GJTGCGGTGCAAGCATGAACCTTTGTTTAAATCAAGAGGCTTACATAATTTTAAACCAGTTCTGCTTC AGCTGTACATA
D29833b	85	A G		---	CCACTCCATCCTGATGCCCCCAAGTTATCCACAGCCTCCTCCCGACCAAGACCTATCCAGCTGGACC TCCATTTTCCCTGTAAATCTCCAACTGATCCTACCTCCCTACTCCTGCACCCCAATAATGAA CAACTGCAGCAGGTGCCACCACCACCAACCAAGACACCACTACCTTGTAACTACTGCTTCTGCTAC
D29833a	21	A G		---	CCACTCCATCCTGATGCCCCCAAGTTATCCACAGCCTCCTCCCGACCAAGACCTATCCACCTGG ACCTCCATTTTCCCTGTAAATCTCCAACTGATCCTACCTCCCTACTCCTGCACCCCAATAATGAA CAACTGCAGCAGGTGCCACCACCACCAACCAAGACACCACTACCTTGTAACTACTGCTTCTGCTAC
D31762	82	G A		---	CTCCCTGCCTCCTCCTCCTGCTGATGCTCCGTCCTCAACAGCCGAACCTGCTTGAATGGGGG GAGGGGGGTTTCG/JCTTTCCTTCTCTTGGCTCCCTCTTATCTCCACAAACCATTTCTCAATAAA GCCAAAAATCTTCTCTTCTCCCTCAGGCCACCTCCTGCTCCTCCTGCTGCTGGCTTTT CTGGA
D37931	64	T C		---	ATTATCGGAGTGGTTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCATTTGAGCTGTCJ CCCAGGCTCTGCTCCTCAGCTCATTTCTACTCTTTTCTCTATATAACTCATTTCTATTAATACAT GCACCAAGAGATATGGAGACATAAACCTGTATGAATGAGGCTGGGCTTTTCTGTAAATAGGCTTCC TTT

D63807	101	C T	---	---	CAGGCAGGACTTCAGTGTACAGTATCCCTGCCCTTCAGTCTCTCTTAGAAATCACATCTGTGTTCATCC ATTGTTTAGAGGAGTGTATTTTCTGTTCCAC/C/AGAGAGGACTTTTGTTCACAAATTGGATCAC AATGCAGAGGAGTCTGTCTCCCGCGTCTCGGTCTCGGGGGGTGACCTGTCCAGATGAC
D90145	21	T C	---	---	TGGGAACATGCGGTGACCTC/C/JACAGCTACCTCTTCATGGAAGTGTATGCCAAACAGCCACA CTGGGACTCTCTTAACITTAATTTTAAATTTATTTATCTATTTAGTTTTTATAATTTATTTTGAT TTACAGTGTGTTGTGATTGTTTGTCTGAGAGTCCCGCTGCCCTCCACCTTCCCTCACACAGTGTG TCGGTG
EST14035 1a	59	T C	---	---	ATTATCACTCTCAAAAATTTTGGTGTGTGTTTAAAGTACTTTCTATTATTATGAGCCCT/C/JGAGGA CCAGACATGTTATTATCAAGCCCCCTATATACCATCTAAT
EST16668 5	71	C T	---	---	GCATTTTAAATTCACATTTGAATCAATTATTACTATTATGATGTTTACATAACAATTCAGTATCAIT ATG/C/JTGTAGATTTTCAGATGTAGGTCGTCAATACTGAGCACITATCT
EST16904 7	57	C T	---	---	ACAGACTATCGCCAACTTATAATGCTTAAACTTTTATGATCAATAGTAATAAATTACA/C/TJGAGATA TTACACATTTATTATAAATAGGGTTTGTGAAGATGATTTTCCCAACTGTAGGTTAAACAT
EST21863 9	49	A G	---	---	TTTTAAGTACCAGAGGCACTGCTGGAACAGGATGAAAACTGATACACC[A/G]GTTACTACTTACTC TTCACCTTTCAAACTGATTCCTCCCTAAAGACTTCTACTTAGCAAA
EST21885 6	80	G A	---	---	GGCTGTAAGTAGAATCAAGGTTTAAGAACATTTTATGCATTTATCCACAAACATTTTACTGAGCATA CTAGGTGCTGGGA[G/A]JGTGACAGTGAGCAAAAAACAAA
EST22623 8a	26	A G	---	---	ATTTTAGTGCAATGACAAAGCCCAA/GJAGAACAGAGGATCAAAATAAGATTGAAATGTATTACC TTCATCAAGTATACGAAAGTTTAAACAAAGTATGGGAGT
EST22644 2	98	A G	---	---	AAAAATGATTGAATTCAGCAAGTACATTTATGATCTATCTACATTTTAAACAGCACTAAAAATAA AAATTTTAAATGATTATCCATTTATCCAG[A/G]AAATGTGGAAGATGGCTTTTAAACCC
EST23587 1	31	T A	---	---	CCTCATTTATTTAAAAAGACGGACATAAAAAA/TJATATACAAACAAAAAACCCAAAGTCACATTTACG GAGGTAAAAACTAAAAAGTCTGATATGAAAATATGGTGG
EST24246 7	106	T C	---	---	AAAGATCTGGCAATTTACACATCACTTCAAAATATTTTGTAAATTAATTTTCCATGAGTATTTTTTCA TGTCGAAGCATTTTAACTATCATTTTAGCGTAAATACC/T/CJGAATAACCCATAGTTACAGAATTGG GTCTGTGAACCTCAATT
EST24308 3	45	A G	---	---	TAGTTTAAATTTTCTGAACCTTTGGCTTATAAAATTTTCTCAACTT[A/G]CATTTAAAAATGTATCAAT GCACCTTCTTCAGTAGTACCAGATGAAAATATAAACCTCGTTC
EST24435 6	73	G A	---	---	CTTGAACCTCTGGTCTCAAGTGGTACGTCCGTCTCAACCTCCCAAAATGATGCGATTACAGGCATAAG CAGCC[G/A]TGCCCTGACCCACATTTCTTTATCCGATCTGTGATGGACATTCAGGTGTTTC
EST25089 6	25	T C	---	---	TATTGTTGCAATTATCAAAATGGTTA/TJ/CJAGTTTCAATTTAAAACTGTAATGATTCTCTATGTATAAA ACAGCTTTGAAGTTGTAAATGTAGTTTTCCAATCGTTAGTTAATGCTACATT

EST25476 9	33 GA	---	---	AATGATCTTTATTTTCAGACCTGCTCCTAAAA[G/A]CTTTCCTCCTCTAAAAACCAACACA AGAGGTCTCTTGTGCTTTCCTTTCCTGACTGTGGCGGCTGGAGCTTGACCGTCTGCTGA
EST26183 2	70 TA	---	---	AGATAATGCATTAGAGCTGCCCTCATTGTATCTTGATTAACCTTTGTAAGATTGATCTCTAAATAAG AT[T/A]ACATCTCTGGGTACTGGGAGTTAGAACAA
EST27231 1a	28 TC	---	---	AGAAAAAAGGTGCTACCAAGACTCATG[T/C]GATAGCGCTTCTTTAGGCACATATTATAGCAT CAGATGAAAGTTCTGTAATCACACACACACTGTGCTCTAACAAACACGGTGACTCTGA
EST27816 5a	26 TC	---	---	CAACTCAAGGTACAAGACAAATTGCAT[T/C]TAACATTGTTATAAATAAAAGGAACATCAGATCAAT CAITTAAGGGCTCCAGAGTGAACAGCATCTTCATAACITCCATGTT
EST28588 0	78 AT	---	---	GTTTAATTGGCGTAIGTTCCACAGGCTGTACAGAAAGCATGATGGCTTCTGGGGAGGTCTCAGGAA ACTTACAATCA/TJGGTAGAAGGCCAAAAGAGAGCAGGCATCTCTCCATGACCACAGCAGGAGG AACAGACAGAGGAGGGGGAT
EST30226 5	25 AC	---	---	TACTCACCCGACATACATATCTCA[C/G]TAGAATTAGCTATACTGCATACTAACTTCATTGTAGT AGGGAATATAAACTACTGAACAAGACACAGACTTGCTAACTTAAACAAGACAGACTCATTTCTTTGA G
EST30935 9a	59 CG	---	---	AGCTATGTTAGAGCAAAATCCAGTGGTAAATCAAGAACTCTAAAGTTTCAGTAGAGA[C/G]AGGT GTTTGAATGTCAAGGAAATCACTGAGGTAGATTGGGATTACAATAAGACAGCTGCCCTGTGAGGT CATAAGAGCTTTTGTGAGG
EST32515 7	25 GA	---	---	CCGAATATAAGGAAAAAATGGTGGC[G/A]TGCTCTAAAAACCTGTTGAATAGATAATGGCCAAAT ATTACAGTTTCTCAGCTTCCCTATGAATAGTGGCAGCTGTTTATTTCATGTTTATGTGAGTTTCTATGC ATAAAAAATCCAGTAAGA
EST33274 4	27 TC	---	---	TGCTTTGTTCCCTCCAAATCCTAAAA[T/C]GTGTGCTTCAAGAAATTCGTGGAAGGACTTTGAA TACGAGTTTGACCATATTCAAGTATTCTTGAATACAGGTTTCAGATAACTATGGAGATGATACCAT GGACTAGGTA
EST33352 7b	75 CG	---	---	TACACATTATTCAAGAGACCACCTGACATGCAITCTCCTCCGCAAGATACATTCGTCTCTTAGAGA AGTTTAA[C/G]GCACATAGTATTATTACTAAGAAATATCTCTGGTGTCATATCTAGGGG
EST33424 1	126 AC	---	---	ATTTTCCCACAGCAGAGAAGTATATTATTGTGCTGAAATCAGGTAGCAGGGAATGAATAGCTCTTGG GAACCAGTACAGAATGTTTCAAAAAGATTTACAAATCTCAGTCATTACACACTGAGCAAC[C/A]JAA CAAAGGTGTTGAATCCTCTT
EST33488 7	90 AG	---	---	CCTTTGGGGGAGTTTTAAGCCAGAATGTGACAAAGTCACATTACAGGAAGACTGGAATGTAGCCATAG TTGAACTCTAACATCGTCTATAG[A/G]ACCATTTCCCGTCTCCAGTTAGGTTCTAGGCATATAAGCT GCTC
EST33508 1b	45 CT	---	---	AAAAACATGCTATTGAACAAACTTTTTTATAAAGATAAGTTGA[C/T]TGAAAAAGCAGTTTTAAAT AACATCAACTCACAAATGACITTTTAGAAGCCAAATAA



EST33508	36 A G ---			AAAAACATGCTATTGAAACAACTTTTATATAAGAA/GJTAAGTTGACTGAAAGGAGCTTTTAAAT AACATCAACTCACAATGACTTTTAGAGCCAAATAA
EST33863	77 C T ---			ACAACATAGGACTGGTTATCTTGTTTGAATAATATGTTGCCACTTCTTATGTTTAAAAATGA TCATTTAAAC/C/TTCTTGAACACTACAGCCTGAATCCCCC
EST34739	97 T A ---			GAAGTATCCTCCAGTGGCAGGAACAGAGCTCCAGATCAACAGGTGGACCTTTTGGTTGATGA GCTGATAGCTTCTAGGCTGTGGGAACTC/T/AJGGTGCTTACAACCTCACTGACAGAAATTTCT TGTTGTGCTCATAAACA
EST34792				ACCTGACTGCTTTAAAGCTCTTTGTAAGCTGACCGTAGCACAGATCAGTGGCATCCACTATCAATA CTCATAAGTCTAATTTATCCTCAGGATGTTCCCTGA/GJGATTCAGGAATTTCTTAGTCTATTACA
EST34835	104 A G ---			AAGATTTGTGCTGIG
EST34835	93 T G ---			GGAAATGTTCCCTTTGCAAAACAAAGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTTGTGCTTCTGCTTCTGGT/GJGGCCTTAAAGAAACAGACAAATTTGTGTAAGAT
EST34835	82 G A ---			GGAAATGTTCCCTTTGCAAAACAAAGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTT/GJGCTTCTGTTGGCTTAAAGAAACAGACAAATTTGTGCTAAAGAT
EST35230	93 G T ---			CACAAAGTCCACTTTACTTACATGAAGGAACATAAAGGCATGAGAAACAGTCATCTCAATAAATG CAAGACATGAGCATAAAAGAGTTCTC/GJGGCTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337	33 C T ---			TCCTTTCAAATTTTGTAGGCATTTAATG/C/TTATAAATTTCTGCTTAGGAATGTATCTGCT ATATCTCAGAAGTTGGGCATGTTGTGTTCCATTTTACTTACTAGTTCAGAACITTTTCAATTTTCATCT
EST35708	32 C T ---			CTGCCCCAAATTAACITTTAGGCAATGGAAC/C/JAGACTTACTGTATGGGGACATTTTAAAAAG ACAGCTTAGTAATATGTTTCATATGACGCGTGTGCTCCCTCTCTGAGGTTGGCACCTTCTCCTGTTGTG ATGTGCAAGTGTGGCT
EST35747	51 C G ---			ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAACCCACAAAGGCTCCA/C/GJATGTTAAACGT TTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTGCCCCCTCCAGTAGGGTTGAGATT G
EST35751	89 C A ---			TGGTCCATTATATAAACTGAGGGAACAAACGGTGTGACATGGCAGACATTTATTCAATGGAGA AGTTCCTCCCATGAACCAAGA/C/AJCTTGCTCTCATGATAAAGTGGAGACAATAAGAAAGCCAGGT ATATAATTAAGGCCTGTGA
EST36301	93 C T ---			CACCTGTTCAITGGTTCACCTGGGCTGCTATCTGTGGGCTGATGCTCTACCAAGTGTGACGCTACAGC AGTCAGGAGGACGACCATGGCCCTG/C/JGCTGATGGAGCTTGTAATTTAGCCCCAAACTGATCTTCA GAAAGAGGTACAAACA
EST36519	33 G T ---			GCCATCAGCCACAAAGACATGACTACCAACGC/G/JGGCCCCCTTGACCCCATACTGGCCTCAGCAC CTAAGACTGGACAACITTTGACCTAATGACCGCCCCACCTGGCATATACTGGCTGGCCTCTTCTCTGT CACAGGGGTCTTAGTCGT

EST36620 6	50 G A ---				GAC TTT ATT AGA TAA GGG GTT CGG CTAC CCCTCAA AGCTCTCAG GACTGG[G]A]GCTAGGGTTTAAGG AAGGC TTA TTTAAATATGGGAAATAAAA TACAAAAGGGCCACACCCGATGCAAAAAGACTTT
EST36690 0a	89 C G ---				CCTGTGATGTCATGGGTGCTGAGCAGTCGTACTTACTATGCGTCAGACAGCTCAGCGTATGTCAGGA AAGGAAGCTCGGGGATTCCTA[C]G]AGGGGACATATCACACATATCTAAAGTCACCTGTGTGACTCGG CTTGAGCAAGTCATTTCA
EST36729 9	62 C T ---				GAGACAGAAGCCATCAGTTAAATGAGGTTAGGCTCTCCCTCTAATACTGATTGACAATG[C]T]A TATTAGCCAGGTAATGCAC TTTAGCTACCTGGACAATGCTATCAAGTGTGCTGGGAAGGGAG
EST36823 6	103 A T ---				ACTGTCTGCCGATGATTGGAGCTTGAAAAAAACTACCATGCCAGATCTCCACCCAGACCAATTAG GTCAGTATCTCTGGGGGTGCTATTCAAGCAACAATT[A]T]CTTTTATGTTCTTAAGCTCATCATGAG TTAA
EST36987 4	126 C G ---				ATGATCGCTTAIGTAA TTTGAGGGCGACATGGGTAATGGGAGATACCCACAGGACCTGTAAATATT TAAATAATATTTAACAGCTGATCAGAGGCTAAATTACAAC TGCATTTTGTGACGTTT[C]G]GTTA GGGAATTAAAGACAATGCAG
EST37054 3	88 T C ---				GGTCTCACTCTCTTGGCCAGGACGGTTTGAAACTCCTGAGCTCAAGTGACCTCCACCTTGGCTTCC GAAAGTGCTAGGATTACAGG[T]C]GTGAGCCACACACCTGGTCTTGGTTTAAAGTAACCACTGAA C
EST37269 3b	105 T G ---				AATAGTCTATGGCTACGGCCCGTGGGATGTTAAAAATGGGATTTTAAATTAAAGATTGTGAACATG CAAAACCCAGCAATTTCTCAGCTTATATTTTGAAGTCT[T]G]CAGGAGAAAAAATGGGGTCC
EST37284 2	93 G T ---				AAAAGACCTTTCTCAAGCAGTAAACTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCAAGAA GCTCTCTGGATAATGTCACTCTAGGA[G]T]AGTAAACAGGTGTTAAACCCCTGAGATAGCAACCCCT CTTGGCTTGCTGAGGAATA
EST37315 2a	90 A G ---				AGATGGGTCTTGCTAGCTTGCTCGGGCTGAACTAAAGATATCCTCTGCCTCAGCCTCCAGGTAGT TGGAAC TATAGTAGGAGTATCTT[A]G]CCCTGCCCTGCTAGAACTTCAAGTTTGTGAGGCAAAATCCA CCCCAGAGGACAGGACAA
EST37374 1	45 C T ---				CCTGCCATGATAATGTTAAACATATCAAGATCCCTCTCAAAC TTT[C]T]AAGGGTGAAGAAGCATACC ATTCATTTTAGTTGAAATATTCCTTCACATAGCCAAACACATTTTTC AAGGCAC TCTAGCTACTACA GGA
EST37376 8b	101 G C ---				GTGACATCATGCTCTTCAATGCCCTTTCAATTAAATAGTAGTGTGAGCGCTGGGGGGCTGAAGTCAGACT CTCTGGGTTCAAATCAGAGTGTGTGCTCCTGCA[G]C]GCTGTCTCAGGCAAGTTGCTGACTTCTCTG TGCCAGG
EST37376 8a	41 T C ---				GTGACATCATGCTCTTCAATGCCCTTTCAATTAAATAGTAGTGTGAGCGCTGGGGGGCTGAAGTCAG ACTCTCTGGGTTCAAATCAGAGTGTGTCTCCTGCAGGCTGTCTCAGGCAAGTTGCTGACTTCTCTGT GTCCAGG

EST37378	9	63	T G	---	---	---	ACACACAAAAAATGGTGGCAGAAAAATCTGGAAGATTCTAATAACCTCAATTCTGTGAAAAAC(T/G JAACATGCCTCAAAAAAGAGGGGAAAAAACCTTTAACAGAAACACTGTGCTGACATGATTAGCTT
EST37452	4	46	G A	---	---	---	AAGACATAAATCTGCAATGAAATCAGTTATGAAATATTAAACCTCT(G/A)CTTCTCAGGAGTGACAC TAATCATGGTCTGGAAGCTAGCCTATCGCATTTTAAAAACACCCTTAAATCAATGACGTAGAA
EST37613	6	34	A G	---	---	---	CTAGGCATGGGGCTTTACAGTCATTTATTACC(J/G)GTCATGAATTCATTTAAAAACCCACAGCGAT ATAGCAATGAGCAAAACAGAGCCCTCCCAAAATCACCCCTGCGTTTCATGGATCTTCCATTCTAA
EST38025	4	56	T G	---	---	---	TTATTGAGTAGCTACACTGTGGCCAGAACTAAGCTTTACATGTTTTATATCACTTA(T/G)TTATCTCA ACAATCTTGAAGGGTGGTATTATTTCCCGCTTATAGGTGAAGACTCTGAGGTTTCAGAA
EST38068	6	57	C T	---	---	---	TCTACCAAGTCCACAAAGTATCTGTATATGCTTTAAGTGGCATTTCATGTCACTTA(C/T)CGCATGG AAGAACGCTCTCCTTTAATTCCTTAACCTCTCTTCTCTGGGAAGACAGAACGTCACAA
EST38420	6a	100	T C	---	---	---	TAAATCAAGGCTCTTTTCATTACCAAAACAAAAACAAAAAGGGAACAAAAATACGATGGGAGAGG GAAGAGATGATGCCGAAGTGTCTCCTGACTGAC(T/G)GTCCTGCAGTGCCCATGGTCCCGTGCTT TATTCTCTCTCTCTCTCA
EST38950	5	25	T C	---	---	---	TTTATTGCAAAAGTAAGCAGCGGT(C/T)GGTCCCTGGATTGAGGCTGAGGAAGACATTACTTCCTG CTGGAATACTTGGGACTTACATTTGACACAGGCTAAAGTATGGGATGAGAGAGGAACAAAAAGCTT ACAAACAAAGAGCAGCCA
EST39053	6	90	T C	---	---	---	TTTTTGTACTCTGTAGCCAGTCATTAATCTGAAGGTTTTAATATATCATTTTATTGGGATGAGATCA TAGCTTTACACAAATGCTATG(T/C)AAACAAGTTACTGAATATTTTCACTCGTGGAGTTG
EST39331	1	70	G C	---	---	---	TCCTTCTGCTCTAGCACTCAGACCACCAAGAAAGCCCTGGAAGACCAGCCATGGAAGGAAAGTA TG(G/C)GTGTTTTAGGGAGAGCTGGCACCTGGCCTCTAATCTTCCCTCTGOCATTGACCAGATGGGT GCCTTTGGATACATCACT
EST40544	7	31	C A	---	---	---	GTCACCATTGACCTTACATAGTGCCTCTAGT(C/A)ACCTATGAGGCCTAGAACCTATTGTACTTCT CACTTTATCACAATTAGCTATCGAAGTTTGAAATTT
EST40548	4	37	T C	---	---	---	TTCTAATAGCATGCCCTGTGACAGGGAAACTAAGCTCT(T/C)TCAAAATAACTGAAACTAAATCTGTA AGATAAATGCTGGAATTTGAGAAGGCACATGCCCTTTGTAGTTTCTCCAGAAGGCTCAAGGTGTTG AATACTGTGGGACTCA
EST40549	1	42	A G	---	---	---	TGTTCTCTAGAGAACCCCTGTGTGATACACTACGCATGCAC(A/G)ATAAGTCACATCAAGACTAA TAATCTAAATGTTAGTTTGTACCCACATTTCTCATTGAACTAGCTCCCTGCAAGCACCTTCTA CCCTGCACTTTGGGGAG
EST40579	1	81	A C	---	---	---	TGTGAATTACACATCAGTAAGGCAGTTTACAGAATTTTCATTCTTACCTAAAGTCTGTCTATCTG AGCTGGTGGAA(A/G)GGACTTGGAGACAGCGATTATAACGGAACAAAGGCTTCCAGGAAG
EST40584	3	68	A G	---	---	---	TTGATGGTTGTAGGAATTTGGGAAGAAATTATCTGTGAAGGAAATTTGCCACTGTATGCACACCC A(A/G)TCTGTACTCCCAATATCCTATGTTTTAAGCT

EST51340	51 G A ---	---	GATCAAACTGTATTGCCAGGCAGCTCCTGAAGAACTGTGAACATATGAAC[G]ATJCTCAGCCTAGA AGGATAATGTGACCTTCAATTTGCACACCATCCATTGTCTCTTTCAAACCTAAGAGCCTCTCTAAGCTA GATAGGCCAAGGATTATT
J04162	134 T C ---	---	CATGGGAGTAATAAGAGCAGTGGCAGCAGCATCTCTGAACATTTCTCTGGATTTGCAACCCCATCAT CCTCAGGCCTCTCTACAAGCAGCAGGAAACATAGAACTCAGAGCCAGATCCTTTATCCAACCTCTCGA[ T/C]TTTCTCTGGTCTCCAGTGGAAAGGGAAAAGCCCATGATCTTCAAGCAGGGAAAGCCCAAGTGAGT AGCTG
K01506	63 T C ---	---	CTGAACCTCAGCTGCCCTACAAACTCCATCTCAGCTTTTCTCTCACITTCATGTGAAAACTAC[T/C] CAGTGGCTGACTGAATTGCTGACCCCTTCAAGCTCTGTCTTTATCCATTACCTCAAAGCAGTCATTCTCT TAGTAAAGTTTCCAACAATAGAAATTAATGACACTTTGGTAGCACATAATATGGAGATTATCCTTTTC ATTGAGCCTTTATCCT
L18877	69 T C ---	---	TGAGTCTGAGCAGGAGTTGCAGCCAGGGCCAGTGGGAGGGAGTCTGGGCCAGTGCACCTTCCAAAGGCO C[T/C]ATCCATTAGTTTCCACTGCCCTCGTGTGACATGAGGCCCATTTCACTCTTTGAAGAGAGCAG TCAGTATTGTAGTAGTGAGTTTCTGTTCTATTGGATGACTTTGAGATTTATCTTTTCTCTGTTGGA ATTGTTCAAATGTT
L31848	36 T C ---	---	GCTATTTACATATCCCAAGCCCTTAGGGCTACAG[T/C]CTCTGCTGGACCCTGTAGGGTGCCA TTTGGAGTTTACAGCCTAGAAGAAAGGCTTTGGCCCTGGTGGTGGCATAGGCCTGTAAATCGT AGCGCTTTGAGAGGCTGAGGCAGGAAGATAGCTTGAAGCTCAGGAAGTTTCGAGACAAACCTGGGCAAT GT
L38517	137 G C ---	---	GGGTCCAGAAAGCCTCTCAGCCAGGAGGAGCTGGCCCTGGAAGGGACCTGAGCTGGGGACACTGGC TCCTGCCATCTCCTCTGCCATGAAGATACACCATTTGAGACTTGACTGGGCAACACCAAGCCTCCCCAC CC[G/C]GCTCGTGTGTAGTATAGCTGCAAGCTGAGCTGGCGAGGGGATGGTTGTGACCCCTCT CTCCTAGAGACCTTGAG
L39059	123 T G ---	---	ACTTGAGAAGCAGAGCTCGCCACCTTCTGGAGGCCACTGTGATGATGAGCCAAAGCAATTTGGAGCCA AGTTGAAGGGACAGGGCAACAAATACAGTAGTAGTTCTTTTGTATTTTGTATATTTGJCGCCTGA AGATCATCCCGCAAGCAGGCTGGAGGTGCCGTGGGCTGTGTGCTGGGATTTTAGTCTGTGCTGG GAG
L41268d	173 G A ---	---	CAAAGTTGCTCTCTGCCCATGAGCACCACAGTCAGGCCCTTGAAGGGATCTTCTAGGGAGACAAACAGC CCTGTCTCAAACCTGGTTGCCAGCTCCAATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTGCAT CTTAGGGCATCGCTCTTCCCTCACACCACAAATCTGAAC[G]ATJGCTCTCTCCCTTGTCTTACAAATGTCT AAGGT

L48728b	111 T C ---	---	AAGTGAACAGAAAGCAAGATGGATTGTTCCCTATATAAAGCACATAGTATGTTTACTGGIATCGT AAGAAGCTGGGAAGAGAGCTCAAGTTTTTGGTTTACTTTTCAGAAATC/GAAGAACTTATTCAGAAAG CAGAAATAATCAATGAGCGATTTTAGCCCAATGCTCCAAAACATCATCCTGTACCTTGGAGATCCA GTC
M18079	52 G A ---	---	GCGCACAGTCCAAAATACAAATTGGACAGAAAGATCTATATTGTACAGAACT(G/A)TTTATTTACCC CCATCAAGTATAAGGTTACTGATTGTTGTCCTTTTATAAACATTGGTATATTTCCATTTCATGCCAA AGCAAAAGAAAGTAAAAGCTAA
M19169	113 T C ---	---	TAGGATCTGTGCCAGGCCATTGACACAGCCACCCACTCCACCCCTGTAGTGTCCACCCCC TGGACTGGTGGCCCCCACCCTGGGGGAGCCCTCCCATGTGCTGT/GJGCCAAGAGACAGACAGAG AAGGCTGCAGGAGTCTTTGTTGCTCAGCAGGGCGCTCCGCCCTCCTTCTCTCGCTTCTAATA GC
M21539	114 T G ---	---	TCACCTCGTTCCACAGCTCCACCTGCATCTTCATCAAGCCATCCAGGGATACACAGGGAGCTTCT TTCCCTTAGCCTGTGATCTGCCCATGATATCCCGACAGCAAAAT/GJGTTTCTTTCTGAGGCTG CCATGCTGCCACTGTCCAGGTGGAGACTGAGCAAGGAAGTCTCAGCTGTACCGGCCCTTCAGAGCT TCTCTTGGGTGC
M26041c	173 A G ---	---	CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCTCCAAATGTTTCTCTCTCACCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTGAATTAATTTCCCTGACTTC CTGATTTTCTCTTCTCA/GJGTTACCTACTAAG/GJGATGCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041b	157 A G ---	---	CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCTCCAAATGTTTCTCTCTCACCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTGAATTAATTTCCCTGACTTC CTGATTTTCTCTTCTCA/GJGTTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041a	45 C G ---	---	CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCTCCAAATGTTTCTCTCTCACCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTGAATTAATTTCCCTGACTTC TTCCTGATTTTCTCTTCTCAAGTGTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M63967	57 G C ---	---	TAGGCAGCTGTACGGAGGCCAGTCACAGTCCAGCAATCCACAACCACCTTGAC(G/C)AATGCT TGCCAAAGCTGTTTTAAGCCAAAGAACACCCCTTCTTTGTTCCAAATTAACCTTGAAGAAACCCCA CAATAAAGCAATTCATC
M81695	34 G A ---	---	ACTTACTTACCCTACCTGTACGGTGACGGGA/GA/GAACCACTGCACCACCGAGAGGCTGGG ATGGCCTGCTCTCTGCTTTGGGAGAAAACGCTGTGCTGGGAGGGCCCTTGTCTGCAAGGTTG CAACTGGAAACCCCTTAGGACAGGGTCCCTGCTGTGTCCCCCAAAAGGACTTGACTTGCAATTTCTACC T

U06641d	166 C T ---	---	---	CTCCTCCCTTTATTTCAGCATGGAGGTTTAAATGGAGGATCTCCTTTCTGTGACAAAACATCTTTC ACAACTTACCTTGTTAAGACAAATTTAAAAAGATCTTTTACAACTTACCTTGTTAAGACAAAAT TATTTCCAGGCTATTTAATACGTACTTAGC/TJTGAAATTATTCTATGTCAATGATTTTTAAGCTA TGAAAATACAAATGGGGGA
U09607	39 T C ---	---	---	GAGCCTTATGAGGGTCTCTACTTTCAGGAACACCCCAAT/CJGACATTGCATTTGGGGGGCTCCCG TGGCCTGTAGAATAGCCTGTGGCCTTTGCAATTTGTTAAGGTTCAAGACAGATGGGCATATGTGTGAG TGGGGCTCTGTAGTCTTGCCCAAGAAAGCAAGGAACCAAAATTTAAGACTCTCGCATCTTCCCAAC CCCTTA
U09608	82 T C ---	---	---	GAGCAGAAGGCAAGAGCGGCAAGATGAGTTTGAGGGTTGTATCCAAAGGCCATCATCTGGAGCCTC GGAAAGTCTGGTCT/CJACATCTGCCCGCCCTTCCAGCCCTCCCAAGCCCTCCTCTTGTCTTCTTC ATTCAATTCACAAAATTTGGC
U10694	20 C G ---	---	---	GTGACATGAGGCCCATCTTQ/GJGCTCTGTGTTTGAAGAGAGCAATCAGTGTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCACTCTGGGTCCTTGTCTATGGGTGATTTGGAGATTTATCCTT GCTCCCTTTTGGAAATGTTCAAAATGTTCTTTAATGGTCAGTTAATGAACCTTACCATTGAAAGTTAA TGAAATGACAGTA
U13877b	162 T C ---	---	---	AAAAAGGACTGGTTCAAATCCAGGTTCCTATTTTGTCTATCTTTGTGACCTTGCACAAAGTTGTTTAAAC CTCTTTGTTCAGAAATTTCTCCATGGAGTAACAATATCTAGTGTGGAGGATTAGTGAAGTTACATGT AAAGCACAGAGGAACAGCCAGAGAT/T/CJTACCGTGGTCTTACTAAAGTACATATCCTAACTTGG GGTTTACCTTCAGCA
U15555	187 T C ---	---	---	TTTCTGTCACCTTTACCTGGTTTTAATAGCCAGCCAGTCATAATAGTAGAGGAATCAGTCAAGCAA AAATGCTTTTGAAGAAATTAATTAAGCAATGCTGAACATCAGGAATTTGTAGATATCCGTACAGAGAT TCCAGTAAAATTTATGAGTCCAGCACCCTTTTCTAAGCAGTCTGGTCCATG/T/CJTGCTCTCATAC CTCATATGCAGGATTCATTCA
U17077	122 T C ---	---	---	TCCAAATATTGGTCCCCAAAGCAGCTTCCAAAGTTTGCCATCTGGATGACAAAACGGAAGATCCACT AAAACGTCCACGGATTAAACAGAACGTCCTTGCAGACTGAGCGATGACACCACAC/T/CJTGTGTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAGCTTTCTTTTCTGCGGAAACAACTGTCTCTTGG AATTA
U18543	58 T C ---	---	---	GCACATGCAGAAATAGACTCAGCCTATGTCCTGATTCAGCTGGGTAGTTCTAGAACTTT/CJAGAAG CTCCATCTTTTAATGTTTTTATTTGTTATGTCCCCCTCCCGGCTTCCACCTAAAATTTAGAGCTTTAA AGATGCACCTGCCAAATAGGACACACGATGGTGTAGCTGAAGTTTGATTAGCAATTAGGCACCTTCC AAGGCTTTAGTAGAGAGAGCC

U25975b	164	C A ---	---	TCAC TGTGTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCCTTTTAGTATATGAAAATTATT ACTCTTTTGGGGTTAAAGAAATGGTCTGCATAACCTGAATGAAGAAGCAAAATGACTATTCTCTG AAGACAACCAAGAGAAAATTGCAAAAAGAC/C/AAGATATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTTGTGGACTGA
U25975a	143	C G ---	---	TCAC TGTGTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCCTTTTAGTATATGAAAATTATT ACTCTTTTGGGGTTAAAGAAATGGTCTGCATAACCTGAATGAAGAAGCAAAATGACTATTCTCTG AAGACAAC/C/GAAGAGAAAATTGCAAAAAGACAAAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTTGTGGACTGA
U25997	61	A G ---	---	CAGGGAGAGGTTATTCACAACCTCACCAAACTAGTATCATTTTAGGGGTGTTGACACACCA/C/GJTT TTGAGTGTACTGTGCTGGTTTGATTTTTTAAAGTAGTTCCTATTTTCTATCCCCCTTAAAGAAAATT GCATGAAACTAGGCTTCTGTAATCAATATCCCAACATTCTGCAATGCGAGCATTCACCAACAAAA TCC
U28413	29	C T ---	---	ATTCTGACAGCTAAATTAGCCCTAAATG/C/TGGGTAATAATTTTCCTCATGTTTTTAAATGAGGTT AATATTGCAATAAAATCCTAAACACAGACTTCTGTATAGTTTATTAGTCAAAATGTGTTCCCTGATCC CAGATGTTGTGGCCTGGGAAGCCCTCAITGCTACAGTACAAAGTAACACAAGTCGTTGTACCTCAGTT G
U30884c	89	A G ---	---	TAGGGGTAGCATTTAAGATTACAGGAGTCATTAGCAGTGTGATGATTTTGGGACCTGCCGTATAATCTGT CTTCTATTTCCACGTTAGCCAATTGTTCTTGATGAATCTATATGATGATGATGATGATGATGATGATGAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCCAACAGTTGAACACAAGT GCTGTCA
U30884a	34	A G ---	---	TAGGGGTAGCATTTAAGATTACAGGAGTCATTAGC/C/GJTGATGATTTTGGGACCTGCCGTATAATCT GTTCTTCTATTTCCACGTTAGCCAATTGTTCTTGATGAATCTATATGATGATGATGATGATGATGATGAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCCAACAGTTGAACACAAGT GCTGTCA
U31216b	78	A G ---	---	GGGACAGCATATGTGGCACCGCCCTCTCTGTGCACGTGAAGACCAATGAGACGGCCCTGCAACCAACA GCCGTCAATCA/C/GJCCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGACCAAGACCCCTTACAACTAGAGGAGGAGGAGGATGCCAGCGGATTTCGCTTTAGCCCCGCC TGGTAGCCCTTCCAT
U31216a	70	G A ---	---	GGGACAGCATATGTGGCACCGCCCTCTCTGTGCACGTGAAGACCAATGAGACGGCCCTGCAACCAACA GCC/GA/JTCATCAAAACCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGACCAAGACCCCTTACAACTAGAGGAGGAGGAGGATGCCAGCGGATTTCGCTTTAGCCCCGCC TGGTAGCCCTTCCAT

U31416c	76 G A ---			AGTTGCCAGCTCCCATGTACACGAGCTGGAATCTGAAGGCTGAGTCTTCATCTAGGGCATCGCTC CTCCTCAC(G)ACACAAATCTGGTGCCTCTCTCTTGTACAAATGTAGTCCCACTGCCTGCT GGAAGAAACACACTCCTTTGCTTAGCCACAGTCTCCATTTCACTTGACCCCTGCCCACTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68 C T ---			AGTTGCCAGCTCCCATGTACACGAGCTGGAATCTGAAGGCTGAGTCTTCATCTAGGGCATCGCTC [C/TT]CCTCACGCCACAAATCTGGTGCCTCTCTCTTGTACAAATGTAGTCCCACTGCCTGCTG GAAAGAAACACACTCCTTTGCTTAGCCACAGTCTCCATTTCACTTGACCCCTGCCCACTCTCCA ACCTAACTGGCTTACTTCCT
U37519a	78 C T ---			ACGGGTCACACAGAGAAACCTGAGTCTAGCCATGAGGGGCTTATGCTCCCAACTCACATTGTTCTCTCC AGACCGCAGG[C/TT]CCCAAGCTCAGGTTGCTGAGAGCTGCATGACTGCATCCTGCCTGCCAGG GCTGCAAAAGCAAGGCTTGTCTATCTGGGGACGCTGCTCGAGAGAGCCGAGAGGCCGCGAAGC ATGCCAGGTGTCC
U37690	54 A G ---			GACCACGCTGAACCCACCCACCCGCTGTGCTGACCATGGCCCTGAGCGTCTA/GJCCCGGAATTC ACGAGGCTGAGGCATCCGGGAGCTGGCGTAATGCTGGCCGACGTGTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAAGGCTTT
V00540	39 T C ---			TGAACCGTTTCAACATGGAATGATCTGTATTGACTAA[TT]ACACCACTGCACACTTCTATGACT TCTGCCATTTCAAAGACTCAITTTCTCCTATAACCACTGAGTTGAATCAAAATTTTCAGATCTTT TCAGGAGTGTAGGAACATCATGTTTACCTGTGCAGGCACTAGTCTTTACAGATGACCATGCTGAT A
X15943	106 A T ---			TCAGAAGGTGACTGCCCTTGTATGATGGATGGGAAGATGAATGACTGGTTTTACTGGGGTGTA AACCACTCTGAGCCTCTCTGAGACCATGTGGTTTAA[AT]ATCCATAAGGGAAGGTACCCACAC CAGTATCTGAGTTCAGTAGCTAAGACCCCTAGAATTTGGATTCTCTGTTTTTTCATGTCCTCTT GTAACCCCTGAGATCATCAG
X52011b	148 C T ---			AGGAAGATCCACCGACCTTCTGACCTAATCCTTTAGATTAGGTCACATTACATTAACTTAGGA ACCCAGACCGAAAGTTGCTGAAGGGAAGGAGACACATTCAAAAGAAAGTTGGGAAATTTGGG AAATCTGTTGTGCA[CT]GCTCAATGAAAACGCCCTTCGGCTTTTATTTTTTTTGGAACTG CGAGTGGCTAGGCTAGCCT
X52011a	118 A/C ---			AGGAAGATCCACCGACCTTCTGACCTAATCCTTTAGATTAGGTCACATTACATTAACTTAGGA ACCCAGACCGAAAGTTGCTGAAGGGAAGGAGACACATTCAAAAGAA[AT]GTTGGGAAATTT GCGAAATCTGTTGTCACGCTCAATGAAAACGCCCTTCGGCTTTTATTTTTTTTGGAACTG CGAGTGGCTAGGCTAGCCT



X54741	24 A G ---	---		CAGGCCACCTGCTCTCTCCCAQAGJTGACACAGCTTCCTGAGTCACCCCTGTGCCAGCCAGCTCCT GCACAAATGGAATCCCGAGGGCTCCAGGACTGGGGCTTGGCAGGCTTGTCAATAGCAAGGCCAG GGCAGACTGGAGAGATCTTGCTGGCAGGGCTGGCCTTGTCGCCAGCCACCTGGGCCCTTCTCC
				AGCAAGCAGTGC
X54869	99 A G ---	---		AAGCATTGCGTTTACAGTGCATCAGATACATTTTATATTTCTTAAATAGAAATATTATGATTGCAT AAATCTGAAATGAATATGTTATTGCTCTAGJATACAAAAATTTCAATCAATTTATTGAAATAG GATGCACAAATTAAGTACAGACATCCTAGCATTGTGCGGGCTCATTTTGCTCAACATGGTA
X66924	147 G A ---	---		GCGTGTCTGACACCTCCAGAACGAGGTGCTGGCGCCCTTCTGCTGGGACCCGGGAACTCTC CTGGCGAAGCCGGAGCGGAGTGGGCCCACTTCGCCCTGCCACTTGACTTCACCAATCCCT TCCTGGAGACTTGAAACCTGGTCTCAGGAGCGAAGGACTGTGAACCTTGCGCTGAAGAGCCAGA
				GAAATGTGAAGAAATGTACAAAGCCCTTAAAGCGTTGTACACCTTGATTGTATAAGATAATGJTGJ CATACTGGAGAAACTCCAGAGTGTGACAAATGTGACAAACATTTAATTAATCTCATACCTTA TTGCACAGGAAGCATTTATCTTGAGAAAAATGTATAAGAAATGGAAAAATCATTAAATATCTGCT CATATCTTAACATCAGCGAGTT
X78932	62 T G ---	---		CTCAACCCATAAGCTCAACACATCTTCTCTCCTCAGCCACATCCACACATCCACCTCCATCC CCAAACCATCTCATCCCAACTACAGCCCCAACCCAGCCCCAGACTAATCCACAGCCATCCCCAA CTCATCTCATCCCAACTGCAGCCCCAACCCAGCCAGGCCATCCCCAACCCATCCCCAAGCC AACTCAACACCATCC
X80026	25 T C ---	---		ACCCAACTCAAGTCCAGGCCCCAGGCACTTTCTGCGCTGCTTGTGGCCCATCCAGTCCAGG CGCTGGAGCAAGTGTGCTAGCTACTTCTCTGJGJACCTTGAAGACCCCTCCCACTCCTGGCCTCA CATTTCTGTGTATCCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCTAGAAAG
X80197b	99 G C ---	---		ACCCAACTCAAGTCCAGGCCCCAGGCAAGJTGJCTTTCTGCGCTGCTTGTGGCCCATCCAGTCC AGGCGCTGGAGCAAGTGTGCTAGCTACTTCTCTGCACTTTGAAGACCCCTCCCACTCCTGGCCTCA CATTTCTGTGTATCCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCTAGAAAG
X80197a	28 A G ---	---		GGCACGAGTGAACAAAGTCCAGAGGAGGCGCGCGCTGCGGTGTCGGTGTCTTTCTTTT CAGCCCGGAGAGGCTGCTGACTGGGGCTTCTGAGCCTGCTGCGCAAGCTCCCGCGCGCTCT CTTTCTCCCAAGCGAAACCAATGCGCCCTTCACTCGCGTGGCGTGGAGGCGGGGGCTT CTTTCAGAGC
X85106	150 G A ---	---		ACCAACGCCATGGTCTAAGGACATGGATCGGGTGGCCCCCAGACGTGTGCACAGGGGACCTCTGCC CACTCTGGGCTTTTCAGATACTCTGACCAAAAGCCTGCTTTAAACCGCAAGATGGGGCTTGTGGGG ATGCGCAGGAGGAGCCATCGGGTACTACGACGCAACACTCACAACTGTCCAGGCTGAGATAAATCCC GGGA
X87160	128 T G ---	---		

[illegible]

1282	130 C T	---	---	GTGGATCACCACCTACAGTCTAATTTTCAGATGTTTTCATACCCCTAAAGAAATCTTTGTACCCATTAGCAATTCTCTCTGCTCCCTACCCCGAGCCCTACTCTTTATCGCTATAGATTGGCCTGACTTGACATATCATACACATGGAGCCATACATATGTGCGCCCTTCATGATTTGGCTCTTTCACTGAGATAATGTTTTCAAGGT
6810	68 C T	---	---	AGTATCACACATACCTAATAATATTAGATATACACATAATAAATCACCTCCCTACCTTGAAACCTTTA/C/TAAGAGCATTTTAAATTTACAACAAAGCTCAACGAACCTACAATAAGTCTAGTAGCTGTACGTGCCAAGGGATAAGGCTGAACAATAAATTAACCCCTTAAATGCTCTATGAACAAGTACAAATTTCTTTTGAGTCTGCAGAGCAATGACCCTAAGAAATATTTTTAAAGGC
6817	118 A C	---	---	CCAAATACATTGGGTGAACGATGAGCTAGCTGTTCTAGTATTTGCTTTTGTATCCAGTTAAGACCA TCAGCATATACAACATCATCACTAACTCAACAATGTAGCTGCAGGGTAAC/C/CTGTGGATACCCCTG TGTCTCTACTGGCTCCAAAGGCATTGAGGGATCATCAAGAGATTTGGACACCTTTGTGTTCAAATC TTGTTGAGGTGGGCTGTGCAGATCGGCTTTTGGTTGGTGTCTAG
6819b	212 C	---	---	CCATTTATTTTCTCTAAATTTTAAATAGAGAGCTTTAATGGAAACATTTAGTACCATCATGTCA CCGTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAAGCCCTAGTAAAGCCCCGTCAGTAGT ACACATTTCTCTATGGTCTTCAACAGTTTTCATATACAAAATTTTCTGCTATTTTGTCTTAGCAAA CAGCAATAACTTTTGTGTTCTCTATATGACACCTAATATCCA
6819a	166 G T	---	---	CCATTTATTTTCTCTAAATTTTAAATAGAGAGCTTTAATGGAAACATTTAGTACCATCATGTCA CCGTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAAGCCCTAGTAAAGCCCCGTCAGTAGT ACACATTTCTCTATGGTCTTCAACAGTTTTCATATACAAAATTTTCTGCTATTTTGTCTTAGC TTAACAGCAATAACTTTTGTGTTCTCTATATGACACCTAATATCCA
681xx	39 A G	---	---	CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATTG/TTATACTATGCGACCATTTGGGACA CAGATTATATATGTCAGACACCAAGCAATGTCTTTAAGATATGCGCAAGCAAAATCTGTCATGGT TTAACAAAAGAAATGAACGCTAGG
6972b	149 G T	---	---	AGGATCCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCTCTCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCTCTGGACTCTTTTGGTTGGTAACTATTGATTATGTC CACAAATTCAGAG/GTCCCTGTTATGGTCTATTCAGAGATTCAACTTCTCTCTGGTTAGTCTTGGGA GAGTGTATGTGCGAGGAAT
6972a	122 A G	---	---	AGGATCCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCTCTCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCTCTGGACTCTTTTGGTTGGTAA/GTCTATTGATTA TTGCCACAAATTCAGAGCCGTGTTATGGTCTATTGAGAGATTCAACTTCTCTCTGGTTAGTCTTGGGA GAGTGTATGTGCGAGGAAT

7598k	210 A C	---	---	AAAGGTAATCAAAAGTTCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTAATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCTGATATGTTATCTTATATATTTTCCCGTATTTTCCCT CAATGCAG[A/C]
7598j	208 A T	---	---	AAAGGTAATCAAAAGTTCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTAATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCTGATATGTTATCTTATATATTTTCCCGTATTTTCCCT CAATGC[A/T]GA
7598i	192 G T	---	---	AAAGGTAATCAAAAGTTCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTAATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCTGATATGTTATCTTATATATTTTCCCGTATTTTCCCT CCTCAATGCAGA
7598h	144 C T	---	---	AAAGGTAATCAAAAGTTCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTAATTTCTTGAGGATGCCCTTTTA ATATTTGATCC[C/T]ATATGTGAGAGATTTTCTGATATGTTATCTTATATATTTTCCCGTATTTTCCCT CCTCAATGCAGA
7598g	142 C T	---	---	AAAGGTAATCAAAAGTTCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTAATTTCTTGAGGATGCCCTTTTA ATATTTGAT[C/T]CCATTATGTGAGAGATTTTCTGATATGTTATCTTATATATTTTCCCGTATTTTCCCT CCTCAATGCAGA
7598f	120 A G	---	---	AAAGGTAATCAAAAGTTCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTAATTTCTTG[A/G]GATGCCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCTGATATGTTATCTTATATATTTTCCCGTATTTTCCCT CCTCAATGCAGA
7598e	83 C T	---	---	AAAGGTAATCAAAAGTTCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAA[C/T]CAGATTTTACCTTGGAGAAATGAAAATTAATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCTGATATGTTATCTTATATATTTTCCCGTATTTTCCCT CCTCAATGCAGA
7598d	77 C T	---	---	AAAGGTAATCAAAAGTTCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGC[C/T]GCTAACCCAGATTTTACCTTGGAGAAATGAAAATTAATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCTGATATGTTATCTTATATATTTTCCCGTATTTTCCCT CCTCAATGCAGA

7598c	56 A G ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTACAAAAGACACCCAAAGCCA/JG/AGGAAC TCAATGAAATAAGCCGTAACCCAGATTTACCTTGGAGAAATGAAAATATTCTTGAGGATGCCTT TTAATATTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTATATTTCCCGTATTTT CCTCAATGCAGA
7598b	47 C G ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTACAAAAGACAC/JC/CAAGCCAAAGGAAC TCAATGAAATAAGCCGTAACCCAGATTTACCTTGGAGAAATGAAAATATTCTTGAGGATGCCTT TTAATATTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTATTTCCCGTATTTT CCTCAATGCAGA
7598a	30 A G ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTJ/JG/JGATTTACAAAAGACACCCAAAGCCAAGGAAC TCAATGAAATAAGCCGTAACCCAGATTTACCTTGGAGAAATGAAAATATTCTTGAGGATGCCTT TTAATATTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTATTTCCCGTATTTT CCTCAATGCAGA
7998c	116 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGAGCTGTTCTATTTCAGACATCTTGCCAGCTCTCCTGTA ATACCTTAAATGAATGGGTAGTCTATCTCTCAAGGTCCCAATA/JT/CCTTGAGGTTCCCT
7998b	94 A C ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGAGCTGTTCTATTTCAGACATCTTGCCAGCTCTCCTGTA ATACCTTAAATGAATGGGTAGTCTT/JC/TCTCAAGGTCCCAATAACCTTGAGGTTCCCT
7998a	75 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGAGCTGTTCTATTTCAGACATCTTGCCAGCTCTCCTGTA ATACCTTJ/JATGAATGGGTAGTCTATCTCTCAAGGTCCCAATAACCTTGAGGTTCCCT
8071	119 A G ---	---	AAATACAGAAATTTTATTAGAACTGTTTAAAGTAGAAAAAACCCCTGTCAAGAAAGACCAGGTGG AAAAATGGGTTCCCAATAAATGGAATTTTAGGGCAACAAGCTTAAAGGCC/JG/JCAAAAAGAGA AATAGCACCACTGTCAATTTGAACAATGGCTAGTTACTTGCATTTTGGCATTGTTAATCACTGAATC TGGGTTTTCCTCTGAATTCACACAGAGCATGCAGTACACACATTTTTCAT
8467b	93 C T ---	---	AAGGCTTTCCTCTAAACATCAGTCCCTACGGAGAACTGGGAAATCTCGGATATTGGCTTATCATT TGACGCAAAATCCACTTTGCTGTAA/JC/JGGTCATCCGAACCTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAGGAAAAATTACTG
8467a	70 A G ---	---	AAGGCTTTCCTCTAAACATCAGTCCCTACGGAGAACTGGGAAATCTCGGATATTGGCTTATCATT TG/JG/JGCAAAATCCACTTTGCTGTAACTGTAACGGTCATCCGAACCTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAGGAAAAATTACTG
8498	84 C T ---	---	AAGGCTTCAGGGTTGGTTTAAATCAGGCTGCACACTTTCAAATCAATCTGACATCTCTCTATGTCA AACTGGCTTCAGTAG/JC/JAATACTTCATTAAATCGAAAGAAAAAATGCTTTAAGGAAAAAA AATCCAGTTTAAAGAACAAATTAACATTAGTCTTTAAATAAAGGAGGGCTAATGTTTCTATGTTGCT TTATACATCTCTCTCTCAATACAGAACCCAGGAATGTAATTTTCTTAACCTCAG

WI-18562	29	G A ---	CTAAGGAAAAATTTAATGATGGAATAATC[G/A]ACAAAATATTCAACATCATTTAAAAACAAGTAG CTTCTCTATTTCACATAGCTTAGTTGGGATAGAAATAGAACTAATGTTTACAATGATTCATTACATT TAGCATTAATCAGAAACGA
WI-18618	51	A C ---	ATAGCAGACTTTTAAATCAATGCCAGAGACAAAAGTGAGGCCGAGCTAAGAA[C/A]CGCTCAGCTTCG TTACAATGAAGAAATGGTTTCTTCGATGCCAAAGTAAATTTGTAACCCACAGTGCTCGCACAGTTC AC
WI-18683	22	C T ---	TAAGCTGTTGAGGACTGGACTC[G/T]GGTCCCCTTTATTGAGACTGACAGGCCAGTGGGTCCACCCAAA CAAAAATAAATTTCTCTCCCAAGCCTGCCTGCAGT
WI-18520	75	G A ---	GACTTTGGTGATTAAATTGCTTTTCCCTTAAATATGAGAAATAGGTGTAATTTCTCCTTTTGTCTTTT ACTACA[G/A]CCGGAGTGGTAAATACTACCTACTGCCAACAAACACGGGCATCCACTCTGTCTTCAA TGCCTCTCCGTGAGAC
WI-18563	94	A G ---	AAATAAGTTTTATTGGCACACAGCCAAAGCCCACTGGATGACACATTTGCCACGGCTCATCTTGCAG TACAATAGCAGGGTTCACTAATGTAC[A/G]GACATGGTGTGGCTCACAAAGCCAAAGATAATT
WI-18582b	69	T A ---	GTCTATTTCAAATTTAGCTAGACCCATTTCACTCTGTTTAATGGCTACATTTGTTTTCATTGTGAGAC T[A/GTGCCATAATTTATTAATCAGTGCATATTGAAAGACATTTGGATCGTTTCCAG
WI-18723f	94	G A ---	AACCTTATTGATCTGACGATCAGGATTAGTTCTCTCATCCACATTGACTGTCTGTAGATTTTGAAG TGGTAACAGGTACATAGGTAACCAA[G/A]TATATAGCTTATTGGTGAATCTTCATCCT
WI-18723e	71	T C ---	AACCTTATTGATCTGACGATCAGGATTAGTTCTCTCATCCACATTGACTGTCTGTAGATTTTGAAG TGGT[C/AA]CAGGTACATAGGTAACCAAAGTATATAGCTTATTGGTGAATCTTCATCCT
WI-18723c	96	A G ---	AACCTTATTGATCTGACGATCAGGATTAGTTCTCTCATCCACATTGACTGTCTGTAGATTTTGAAG TGGTAACAGGTACATAGGTAACCAAAGT[A/G]TATAGCTTATTGGTGAATCTTCATCCT
WI-18619	44	G A ---	TTTATTACAATATTAGGTGGCACAAATAAACAAGCTTCTGA[G/A]ACAGGAGGTAAACATTCTCA TAGACTTTGCAACTCAGCCAGAAGTAAACCTCGAAATA
WI-18715	76	G A ---	TTATTACAAAAAGTGATATTGCAGAGGTTCTGGGGCTGTACATGGGCAGGGCTTGGTGAGCTTTG TACATGG[G/A]CTGGGAGACAAGGGAGCCTCCAGGTGAAGGGTATTTTTTAATAAAAAATAA TGGAGCTACAACACACCC
WI-18535	107	G A ---	GTAAATAAAGTTTTATTGGCACAGCACGCTCGTTTCTCATATGCCATTGACATCTGCTGTGCCCT ACACAGCAGGTGGGACCTGCTCTTCACGGGAGAGCTA[G/A]TTGTTTAAAGCAGTGGTCCCAAC CTTCTGTGGTCCCOGTG
D17525	107	C T ---	AGAGTGGTCAGAACACAGGCCGAATCCAGGCTCTATCACTTAGTTCAGTTCTGGCAGGTGAC TTTATCTCTTCGAACCTCAGTTTCTTCATAAGATGGAA[C/T]GCTATACCTTACCTACCTCGTAAAA GTCTGATGAGAAAAAGATTAACTAATAGATGCATAGCACTTAACAGAGTGCATAGCATACACTGTTT TCAATAAATGCACCTTAGCAGAAGGTGATGTGCTCTACCAGGCAGACGAAG

DWU-133c	313	A G ---	---	TAATTGGCCCACTGCCCTTATTATTACAAACAGAAATGTCTCATGACTTTTATGTTACCATCCT TTAATAGATCTCATACACCAGAAATCAGATCATGAATGACTGACAGATAATTTGTTGGGCAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTTGAGTTTGAATTTAATAGTAACCTC AATTCAGTAAATGGTATCACTCGTTACCCCTTTAAAGATATGATTAGACT
DWU-133b	236	T C ---	---	TAATTGGCCCACTGCCCTTATTATTACAAACAGAAATGTCTCATGACTTTTATGTTACCATCCT TTAATAGATCTCATACACCAGAAATCAGATCATGAATGACTGACAGATAATTTGTTGGGCAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTTGAGTTTGAATTTAATAGTAACCTC AATTCAGTAAATGGTATCACTCGTTACCCCTTTAAAGATATGATTAGACT
DWU-133a	199	C T ---	---	TAATTGGCCCACTGCCCTTATTATTACAAACAGAAATGTCTCATGACTTTTATGTTACCATCCT TTAATAGATCTCATACACCAGAAATCAGATCATGAATGACTGACAGATAATTTGTTGGGCAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTTGAGTTTGAATTTAATAGTAACCTC ITCCAATTCAGTAAATGGTATCACTCGTTACCCCTTTAAAGATATGATTAGACT
DWU-36	102	C T ---	---	ATGAGATCCTTTAAATCCTTCATGAACGTTTGTGGTGGCACCTCCTACGTCAACATGAAGTG TGTTCCCTCAGTGCACTGGGAAGATTCTACCCCTGACCAACAGTTCCTCAGCTCCATTTCGCC CCTCATTTATCCCTCAACCCCGCCAGGCTTTTATACAGCTCAGCTTTTGTCTTTCTGAGGAG AAACAAATAAGACCATAAAGGGAAAGGATTCATGTGGAATATAAAGAT
DWU-387	169	G T ---	---	GTGTATAAATGCAACTGTTGATTCTCAACATGGCTCACAATTTCTATCCCAATCTTTCTGAA GATGAAGAGTTAGTTTAAACTGCACCTGCCAACAAGTTCATTCATATATAAAGCATTATTTTA CTCTTTGAGGTGAATATAATTTATATTAACAATGCTGTAAGAGCTTCTTAATACTAAGTATTTTCA GGTCTTCAACCAAGTATCAAAAGTAATAACACAAATGAAGTGCATTATTCAA
DWU-447b	172	--- --- ---	---	ATTTTAGTGCTTTGGTTAAATAATCATGCAAAAGTATTCGAACTGTCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAAATCACTGTAAATTAATAGTTGATTAGAGCACAAAGCTTAGCTAATCAA CCATTATTTTTCATTTTGTGTTCTAAGAGGATTGANAATCAGTTAGTTAAATGCTTTCTGTAG GCCCTTCTTCTTACAATGAAGAGATGATTCTTCTAGTTATGGTTA
DWU-447	85	A G ---	---	ATTTTAGTGCTTTGGTTAAATAATCATGCAAAAGTATTCGAACTGTCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAAAGTACACTGTAAATTAATAGTTGATTAGAGCACAAAGCTTAGCTAAT CAACCATTTATTTTCATTTTGTGTTCTAAGAGGATTGANAATCAGTTAGTTAAATGCTTTCTG TTAGGCCCTTCTTCTTACAATGAAGAGATGATTCTTCTAGTTATGGTTA
DWU-476	63	C G ---	---	GTAAATTCAGTTTTCAGTTCCTCTTTGTGCTGCTTCTCAATAGCGTTTAAAGTGAGTCGAT AATCAACTGTCCATCAGGTGAGGTGCTCCATACCCAGCGGTTCTTCATGAGTAGTGGGCTATGCA GGAGCTTCTGGGAGATTTTTT

DWU-505	67 A T ---	---	TCATACTAGGGCAGTATCTCCTCTAGCTAGTGGCCCATACAGAAAAATTCATACCATACAAAAATTA  A/TJGCGAGTATTTATGTTTAAAGCACAGGTGTACCGAAAACTGTGAAAAAGTCTGAATTTATGGGTT CTATGCGATGCAATTTTGCTAACCTAGAGAAAGAGTTTGATAAATTTTACCAGCTTTGAAGATGGAT TAACTTTTGACTTTGAGCTTTAACTTTTAA
DWU-512	131 A G ---	---	AAAAATCCAGGCATTTCGAATCTGTTTTCATGATTTATAGAGGGTTTACACAAAGTGCCACTTATTA AGAGCTTCCACAGTGAAGATGGAGAGGTGAACCTTGTGTTTGAATATCCAGATGTTTGGTC A/G  TGCGTATGGCAGTGAGCAGGTATGTTGCTTTTGTCTGCACTGAAAAATTAATTTGCTATCAAGAGC AAACTATGAACCGGTTTATTCAGATGTCTCCAGATGAAGATGCCGAG
DWU-525	97 A C ---	---	AACTGCATATAGATAATTATCCAGATGTGGCTCATCTTTTCAGCTTGTCTTCTATACTGTTTGT ATATACAGTTTGTAAACCATATGATTGA A/C AAGAGAGAAAGTCTATGCTTAGGCCAGTCAGTACA CCCAATTTTAAAAAATAACATATTCCTGCTTTCACAAATATAGTTGAACAAGATTTCCCTAAAAAT CCACCAGGATTAATCTCTAAAAATCTAGTCTCTGATTTCG
DWU-59	94 C T ---	---	CATTTCTTTGTAAAGGTAATGGACTCACAGGGGAGAAACATGCTGAGAAATGGAAGTCTACCGG CCCTTCTTTGTGAACGTACATTGGC C/T GAGCCGTGTTCAAGTCCACAGGTGGCAGACTCGTTTGT GTAGTTTGTTTTAACTTCCAAAGTGGTTTACTTCTGATAGCCGGTATTTCCCTCTAGCAGACATG CCACACCGGGTAAGAGCTCTGAGTCTTAGTGGTTAAGC
EST11	68 C ---	---	CTTGATCATGGGGTGGAAATTTTGTGATCTGGGCTTCATGGGATGCATAAAAAATTTTCCAGTTGGTAAG CAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGGCA
WI-19856b	63 C T ---	---	CACACTGGCATCTAGGCCCTTCGCTGCATTGCAGAAAGGAGAGCCAGGTCCTCCCTCGGAGAA C/T G CTGCGTTCCCGAGCCCCACACCGGCTTGCACACACAGGCTGTTGAGGCGAGGAGGTGGGTAAGCGT AGCTGTAGACCCAAAGCAACCAACCGCCTGGGACCCCTGCGGGAGAGGAGCACTTTAGAACATGGAA AAGTGTGGTCACTCCATCATTAGACAAGACACATCCTACATAATAAAAAAGT
WI-18014	40 A G ---	---	TCCATTTACATTTGGTGGCATTTGTTGAATAGCTACAGAA A/G GAATGAAAGTGCACCATCAGAGT GTAATTAGGTCTGTGTGACCCAGGAAGTGTCTGTTAAACAGAGATTTCTCAAGGGCAAGTGGCTTCT A
WI-18036b	97 T A ---	---	TTCCAATGTAAGAGTCAAGTACCAAGTTAACTTCTAGAAATACAAAGAGAACATGATAAAATCTG ATCACAGTGGAAAAATTTTAAATCTTTTCTAAT T/A CTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18036a	27 T C ---	---	TTCCAATGTAAGAGTCAAGTACCAAGTT C AAACTTCTAGAAATACAAAGAGAACATGATAAAAT CTGATCACAGTGGAAAAATTTTAAATCTTTTCTAATATCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18046	72 C T ---	---	TGTAAGGTGACTTCTATAGCTTCCCTAAACTGCAAACTTTTCAATTTACTGAGATTTATTTCCAGGCCAAT GTG C/T TTGGGTCTGAGATTTGATTATCAGCTGGGTAAGTTAACCTGTTCTCTGTTTCA





WI-18299b	52	G A	---			TCACAAGTCAATCTCCCATCCAAATGACAGTTTGCTAAGATCATTAACTTG[G/A]TTGCCAAATTTT TTTATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAATCTTTTGCCAAATATTGACATATTCCTG CAG
WI-18299a	48	C T	---			TCACAAGTCAATCTCCCATCCAAATGACAGTTTGCTAAGATCATTAA[C/]TTGGTTTGCCAAATTTT TTTATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAATCTTTTGCCAAATATTGACATATTCCTG CAG
WI-18307	76	G A	---			TCAACTTGACCAAGTTAGCAGCAAGAGGATACCTTCTTAGAGACTTTTCAGTGGACTTAAACTCAG TTTCCGCTG[G/A]TGCTATGTAAAGCATCCACGATGGTTTATTGTACTCTGCAATCTGCTTGGTCAC
WI-18324	72	C T	---			TTTGGTATGAATCTTTCTCTGACATTTACCAATCATCACTTAAACTCCGGGGGTGGGGTACTGATT TAT[C/]JTAGATCCAAATAAAGCATGCAGAAAGTG
WI-18350	48	T C	---			ATGAAAGTCACCTTCAATCATAGGGTCAAGAGAAAGAAATGTTTTCAGA[T/C]TAAATCTATGAAAA GGTGTATCTGCTTGCAATTTAAGAAACAACACAAGTCA
WI-18395	77	G C	---			TCTTGACATGATCTGTGAATAACGTGATTGTGGTTGAATTTCTCGAAAAATTTGAAGAAATAAAATTG ATTATTCAAAG[G/C]JTGTCATTGGTTTATACATATCTCTCTCTCTTAATGCAAGCTATG
WI-18398	62	G T	---			TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAGAAAAAGAAAAAACAACACTCAAGGGTT[G/T] GATTAACATTGCCAGTATAACCATATTCAAAACAAGCAGCAGAAATTTGGAGGATAATTTGTT
WI-18396	21	C A	---			CTCGTTGGTATTCCTCATCC[C/A]TTCCCTTTTCGCTCTTTCTAAATTAAGAAAAAGCAATGGAATT TTAAAGATCATCTAAGAAATAAGAACTTACATATGTAACATTTAACTTATCAACTTGTACAAAAGTC AATGAAAA
WI-18409a	20	C A	---			AAGATGGGAAAGAGGAAATC[C/A]TTTTTCTTACTAGAGATTTTTTTCCCTTTTAAATCTTTTCAAAAT TCAAAGGATCATCAAAGGAGCAGGTGCAGAAAGCTCTGGGGCCAGAGGCCCCCAAGTGCTA
WI-18442	62	C T	---			AAAAAGGAAAAAGAAAGGATGGAGTAAGAGAGAGACAGAGAGGAACAAAAATAAGTTTCTGG[C/T] JTTGGCTGATCTGGGTGATCAGGTGGACACTATTATCCCAGAAAGGGAAACACAAAGAGAAAAAAGG TTTATAGGTGGGAGAGAGGA
WI-18452	38	G A	---			TTGATGTTAATACTGTCTGAGATCGGCTAAAAT[G/A]AAGCATAGTTATTATTAGCTTTGG TATAITCTCGACAGATTTAAACAAGTAAGACATATATCAACCCTCATATTTTCCAAACCA
WI-18489	102	A C	---			ATATAAGCTGGAGACTGTGGAGGTGAGAGGCGAGTGGGACTAGCTGTTGAAAGAGAGAAATGTAGC AGTAGTAAAGATGAAGAACTGCAAGGATTCAAACA[A/C]GGTTATGGCAATAGAGGTGAAAAAGAAA AGGCCATATAAA
EST5b	93	A	---			CTGGTGGGAGGAAACAAATTGTGGTATATTCATACAATGGAAAACTCTTCAGAAATAAGAAAGGAA CAAAACCACTGAATCACACACATGGACAAATCTCAAATCATATTGCTGATGGAAAGAAACCAATTC TAAGAATACACAGTACAT

EST5	93 A	---			CTGGTGGGAGGAAACAAATTGGTGATATTCATACAAATGGAAACTCTTCAGAAATAAGAGGAA CAAACCACTGAATCACACAAACATGGACAAATCTCAAATCATATTGCTGATGGAAAGAAACCAATCA TAAGAATACACAGTACAT
EST6	48 C	---			TTAGCTACTTTTCAGAAATGAAGGAGAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGCTCT GAACAAAGCTTTCTTCCCTTTTCAACAAGACAAAGCAAGCCACATTTTGCATTAGACAGAT
EST8	158 A	---			GGACAGGACCTCTATCCCGCTGGTGCAGCAGCGGTGATGGACTGAGGCCCGCCAGGGATCTGGGCC CTCTCTCAGGGGGCTCCAGGACCCAGAGCTGTCCTGCTTTGAGTTCCCTAGAGCTGTGCGGCCA GATAGCTGTTCTGAGTTGCAAGCAGCATGGAGATTTGGACACTGTGTGCTTTGGTGGGT
WI- 18740c	104 G	T	---		TCCTCATTTGTTGGGATGATGAGAAGAAATGATTTGGGAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAACTCTCATTTACCATCATGTATC[G]ATAGTGGATAATTCATTTGATGGCTTCTATTTT TGGCCA
WI- 18740b	96 C	G	---		TCCTCATTTGTTGGGATGATGAGAAGAAATGATTTGGGAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAACTCTCATTTACCATCATGTATC[G]ATAGTGGATAATTCATTTGATGGCTTCTATTTT TGGCCA
WI- 18985a	105 C	T	---		CCAAAGTCTCTGTTGGTCTATAAAGAGTTTGGGATGGGAGAGATCCAGACCATCTTGGGGCA GCCAGGCCCTTGCCCTTCAATTTACAGAGGTAGCACAA[C]TTGATTCCAAACAAACCCCTTCCCC TTTTTAAATGATTCTGTCTTAATGCCATAGATCAAAAGGCTCAGAAACCATTTGTGTTTCCCTCTT TGAAGCAATGACAAGCACITTTACITTCACGGTGGTTTGTGTTTCTTAT
WI-18746	114 G	A	---		GCCAGCAGCTGAAGTCTCTTTCTCTCTCGGCTGGAGAACATCAAGATACCTTTGCGTGGATCA AGCTTGTAAGTCTGACCGTTTATATTACTTTTGTAAATATCTT[G]ATCCACATTTCTAGTTCAAGCT TTGGATGTGGTTACCG
WI-19112j	212 G	A	---		CCGTGTTACACACACACAATGGCAAGCATAGTCGCCTGGTTACGGCCCGAGGGGAATATGCCAAGG GACCCCTTAATGGAAACACAGATCAGTAGTGTCTATCTCATGACAAACCAAGAAACCGGACGACAA TCTTTTGGAGATTTTCTAGTGGCTTAGAAACATGGCTTTTAAAGAAACACGGTGATATCTTTGAG GGTGACAAGGC[G]ATCTCTTCAACAGTTCCATACCAACTGCTTTGCTCTAG
WI-19092	232 A	C	---		TGGTGGCTGGCTAGCTAGTTCTACAGAACATAATTTGCCTCTATAGAAGGCTATTTCTAGATCATGT CTCAATGGAAACACTCTCTTTCTAGCCTTACTTGAATCTTGCTATAATAAAGTAGAGCAACACAC ATTGAAAGCTTCTGATCAACGGTCTGAAATTTTCATCTTGAATGCTTTGTTTAAACTGAATTTTC TTTTAAGCTAACAAAGATCAATTTTC[A]C]ATGATTAGCCGTGTAAC
WI-19057i	175 G	A	---		CCCATTTATTATAGCCAGTGTCTCAAAGAGTAGAGGCGTCTACTGGTCTTTCAACTCTTCA GTCTCTGACGGCGGACTTTACCGTGACAGCGGAAGTGGTATTGACGTCCAGGCCAGCCGACTG TCTTCATGCAAGAACACAGTGGCCAGATCCCCACAGCT[G]ATCTCTTTCATCTTGGTTTGGCCACA

WI-20103	168	C T	---			TGGGACTTCCAACTCAGAGGATGTGGGAATCCCAAGCTCAAATGATACAGGATAAACTGGGATGGGCT AGGATGGACAGGCTGTGGATATGGGAGTCATGGGTCAAAGTCTTATCCAGATGGCTCCAGGTACAG TGGGCTTCTCTGGGCTGGAAGCTGGTCTCCCA[C/T]TTCATTCTGCTCAAAGCTTCTTGAAGGAGC TGGTTTGACTTCAACTTGTAGAGCCTAGCCTCATCTTTCAGTCAACTGGGA
WI-20441	111	G A	---			GCCTTACCCATTTGCACATATATACATATGCACCACCTTTGCAGTGGCAACATATATATCCACACTA TAAACATACCACATTTATAATCTTGAAGGACAGAAATGGA[G/A]TTGAATAAGTACCCCCCAA CATATACAAGAAAGTTAGCATACTTACCCCGTTTTCACATACATCAGAGGCAAAATAAGAAATCTTT TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGGG
WI-19911b	116	A G	---			TGGTTACAAAACCTAAGCCCATATACAAAATTAGGAACACATTTAGATGCCCTCTTTTGAAGAACGT TTTAGTCTTTTAACTGAGTTTAAAAAATAAACAATGCAATTTT[A/G]ACACTGTTTGTGAAA ACTTAAAGTGCAGCAATA
WI-20613c	165	A G	---			GTCTCAAGGGGGAGAAAACCTGGTTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGGCAGTTAGAAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAGTTGGAA[G/A]GAAAGGGAGTTTCCACGCAGCCAGTGGTGAGC TGC
WI-20613b	156	A C	---			GTCTCAAGGGGGAGAAAACCTGGTTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGGCAGTTAGAAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATA[G/C]AGTTGGAAAAAAGGGAGTTTCCACGCAGCCAGTGGTGAGC TGC
WI-19984	47	A G	---			CAGTAAAGAGTGATTCAAGTTGCAGTAATACACTGCAGGTAATA[G/T]TATAACATTAGAAAA GCAAAATTCCTTTAACTTAAGGACAGACTGAACCATCAGGTATGGGTCTGAGATCAAGTAATACAGG TAGGCAAGAGTTTTCACACTGGAAATGAAGGCAGTTTCCAAATACTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135	T C	---			GCCAGTTGGAATATGGCCTATACGAACCAAGAGTGATACAAAATGGAAGTGGTCATCAGGCAATA ATTGTTTCCTTGGAACCTGCAACGACTGTCCATGCTCTGTGGGGACTTACACATTCAAGTTTGACAG T[C]TGAAAAACCAACTGGAGTGTCTTCCAAAGAATGTCTGTGCTTCAAAATAGGAATCCATG TTATTTCTTCTTGGCTTAAAGCTTTATATCTTTTCAAAATGACCTAAGCTGA
WI-18846a	49	G A	---			GAGTGCCATACCTTCTCCAGGCTCTGCCCAAGAGCAGGAGGTGCT[G/A]AAAAGCTGGGAGCGT GGGCTCAGCAGGGGCTGGTCACCTCCCATCCCGTAAGACCTCTTCCCTTCTCAGCAGGCCAAACATG GCCAGACTCCTT
WI-18959	123	G A	---			AGCAGTGGCCTTATTGCATCCCAAAACACGCCCTCTTGACCAGGCTGCCCTTGTGGCAGCAACGGC ACAGCTAATTCCTACTCAGTGTCTTTTAAAGTAAAAATGGTCGAGAAAGAGGCAC[C/G/A]GGAGCCG TCTGGCGCCTGCCAGTCCGTGGGACGGGATGGTTCTGGCTGTTTGGATTCTCAAGGAGCGGAGCAT GTCGTGGACACACACAGACTATTTTAGATTTTCTTTTGGCTTTTGAACC

WI-20146	31	T C ---			---	TGAGTCTTCTGTGAATTCATTGAGCAGTTAGCTGCATTTGAGATAAAGTCAAAATGCCAAACACTAGCTCTGTATTAATCCCATCACTACTGGTAAAGCCTCAITTTGAATGTGGAATTCATACAGGC
WI-18922	74	G A ---			---	TAGGAATTGGTTTACGCGTGAAGCAATTAGACACTTTGGAAGATGGCATAACCTGTCTCACCTGGACTTAAGCIGATCTGGCTCTAATTCACAGTGCCTCTTTCTCCTCACTGTATCCAGGTTCCCTCCACAGAGAGCCACCAAGTTCTC
WI-18763b	53	A G ---			---	TTCTGTGTGTGGGTCAACCGTACAAATGGTGTGGGAATGACGATGATGTGAJGJTATTTAGAATGTACCATATTTTGTAAATTTATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA
WI-18763a	38	A G ---			---	TGTGTTTGGCAA
WI-18771b	75	G A ---			---	TTCTGTGTGTGGGTCAACCGTACAAATGGTGTGGGAJGJTGACGATGATGTGAATTTAGAATGTACCATATTTTGTAAATTTATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA
WI-18771a	57	A G ---			---	TGTGTTTGGCAA
WI-18820	70	T C ---			---	CTCATTTCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGATGCCCTAGAAGATGTTGGGAAACAGAAJG/AJAAATAAACTGAGTTAAGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18742b	51	C T ---			---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGATGCCCTAGAAGATGTTGGGAAACAGAAJG/AJAAATAAACTGAGTTAAGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18882	94	C T ---			---	GGGAACAGAAJG/AJAAATAAACTGAGTTAAGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-19970b	167	G A ---			---	GGGAAAAATTTGAGACGCAATACCAATAGTTAGGATTTGGTCTGGTGTGATGAAATTCGTGAGGCCCTGTGATTAATCTTTCAATGATTGTGATTTCCCTTTTAGGTATATTGCGCTAAGTGAAACTTGTCA
WI-19970a	126	T C ---			---	GTCA
						ACAAAGTCCTGTAGCCCCCTCACCTTTCTCTGTTTTCACITTTGCCAATGTATC/JATCGGGTTTGGTTTCTTGTATTATTTAAACGGTTGTGGTTTCCCTTTTCCACGGAGGTTCAAGTAAAGCCGCTGCAGGAGA
						GTITTTACC
						GTGTGTCAAAAATGGGGTCTGCTCTGCTACCTTGACCTTCCCTTTCCCTCTCTCTCTCTCATCA
						TCAATCCCAACAACATCCTCTGCCA/C/JACACAACAAAAACGTAAGTTTCATTTGGGCAAAAAATTGA
						GC
						TATAAGCCGAGTCAACAGGACGGCTGTCTGGCCACAGACAGGGGCTGCCTGTGGAGCCTGCCACCCGGCCCCGGCAGTGCAGTCCAGCGGGGAGGAGGCTGCCCTTCTCTCCAGTTCCCTACTGCGGGGAOC
						AGCAAAAGCCCTTCTCACTGGGTGGTCAAAGJG/AJATGTCACCTTGGCCTGGTGCATCCACAGAGGA
						TGTTGTTCAAACCCAGAAATCTTTTAAACGACTGACCTTCCCTTAAAAACAGA
						TATAAGCCGAGTCAACAGGACGGCTGTCTGGCCACAGACAGGGGCTGCCTGTGGAGCCTGCCACCCGGCCCCGGCAGTGCAGTCCAGCGGGGAGGAGGCTGCCCTTCTCTCCAGTTCTCACTGCGGGG
						ACAGCAAAAGGCTTCTCACTGGGTGGTCAAAGGTAGTACCTTGGCTGGTGCATCCACAGAGGAT
						GTGTTCAAACCCAGAAATCTTTTAAACGACTGACCTTCCCTTAAAAACAGA

WI-19067d	202 T G ---	---	TATTGCTGCTGTCACTGCCTGACATTCACGGCAGGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCCTGCTCCCCAGAGACTGCCTCGGCATCCACAGATGATGGATCTTCAGTGGGTCTC TTGGGCTCTAGGCTCGGAGATGTTGTAGGGGTTATTTTTTAATAGTGTTCATAAAGAAA[7] GACATAGTATTCCTCTCAAGACGCTGGGGGAAATATCTCATTATC
WI-19067c	153 G C ---	---	TATTGCTGCTGTCACTGCCTGACATTCACGGCAGGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCCTGCTCCCCAGAGACTGCCTCGGCATCCACAGATGATGGATCTTCAGTGGGTCTC TTGGGCTCTAGGCTCG[6]CJAGAAATGTTGTAGGGGTTATTTTTTAATAGTGTTCATAAAGAA ATACATAGTATTCCTCTCAAGACGCTGGGGGAAATATCTCATTATC
WI-19067b	151 T C ---	---	TATTGCTGCTGTCACTGCCTGACATTCACGGCAGGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCCTGCTCCCCAGAGACTGCCTCGGCATCCACAGATGATGGATCTTCAGTGGGTCTC TTGGGCTCTAGGCTCG[7]CJGGAGAAATGTTGTAGGGGTTATTTTTTAATAGTGTTCATAAAGAA ATACATAGTATTCCTCTCAAGACGCTGGGGGAAATATCTCATTATC
WI-19067a	57 C G ---	---	TATTGCTGCTGTCACTGCCTGACATTCACGGCAGGGCAAGGCTGCTGCAGCCTCC[6]CJGTGGCTG TGCATATTCCTCCTGCTCCCCAGAGACTGCCTCGGCATCCACAGATGATGGATCTTCAGTGGGT CTCTGGGCTCTAGGCTCGGAGAAATGTTGTAGGGGTTATTTTTTAATAGTGTTCATAAAGAA ATACATAGTATTCCTCTCAAGACGCTGGGGGAAATATCTCATTATC
WI-19106	247 T C ---	---	TTAATCCAGCCCTACCTTGTTAGTTATTTAGGAGACAGTCTCAAGCACTAAAAGTGGCTAATTC AATTTATGGGGTATAGTGGCAATAGCACATCTCCAAACGTTAAAGACAGTGGATCATGAAAAGT GCTGTTTGTCTTTGAGAAAGAAATATGTTTGAGCGCAGAGTAAATAAGGCTCCTTCATGTGGC GTATTGGCCCATAGCCTATAATTGGTTAGAACCTCCTATTTTAA[7]CJTG
WI-18944	147 A G ---	---	CAAGGCAAAATATCAGGAGCTTTTACACACCTACTAAAAGTTATTAAGTGTGAAACAAA AATGCCAGAGGATAATATGATTCCTCACATCTTTAACTTAGTATTTACCTAGCATTTCAAACCC AAATGGCTAGAAC[6]GJTGTTTAAATTAATTCACAATATAAAGTCTACAGTTAATTATGTGCATA TTAAACAATGGCCTGGTTCAATTCCTTTCTTTCCCTTAATAAATTTAAGTTT
WI-18952	232 G A ---	---	CCCATCCCTGTGAAGGAGTAGGCCACTCTTAAAGTGAAGGATGGATGTTTCATAATACATAAA GTTCTCTGTAATACAACTAAATATATGCCCTCTCTCACAGTCAAAAGGAACTGGGTGGTTGGT TTTTGTTGCTTTTATAGATTTATGTCCTATGGGATGAGTTTAAATGCCACAAGACATAAATTA AAATAAATAAATTTGGGAAAAGGTAA[6]GJACAGTAGCCCCATCACAT
WI-18932d	177 C T ---	---	CACACCTCATGCTAGCCTCACGAACTGGAATAAGCCTTCGAAAAGAAATGCTTGAAGCTTGTA TCTGATATCAGCACTGGATTGTAGAACTTGTGCTGATTTTGACCTTGATTCAGGTTAACTGTTCCC CTTGGTATTTGTTAATACCTGTACATACTTTGAGTTCAAC[7]CTTTAGTACGTGTGGCTTGGTCA CTTCGTGGCTGAGGTAGAACGTGCTGTGGGAAGACAAAGTCTGTGGCTTG

WI-19042	193	A C ---			TTTGTACGTGTGCTCTGCAATGCCTCAGTAGCATCTCAGTGTGTGAAGTTGGAGATAGATG GATAAGGGAATAAGGCCACAGAGGTGAATTTGTGCTTCAAGGACATTTGGTGAAGATCCCAACAG ACACAATTTATCTGCGACAGAACTTCAGCATTTGTAATATGTAATAACTCTAACCA[AC]GGCTG TGTTAGATTGATTAACATATCTTCTTGGACTTCTGAAGAGACCACCTCAAT
WI-18984	208	A C ---			ATTGGCCCTGTACAGTTGCTTATTTATAAATTCATTAACACACTACAGGTGTGAATGGTTAAAA TGTAGGCCCTCCAGTTCAITTTTCAGTTATTTCTGAGTGCAGACAGCTATTTGCGACTGTATTAAT GTAACCTATTAAATGAAATCAGAAGCAGTAGACAGATGTTGGTGCAATACAAATATTGTGATGCATT TATCTT[AC]ATAAAATGCTAAATGCTCAATTTATCACTGCGCATGTTTGACT
WI-18851	90	T A ---			GCITCAATTTGGCGATTGATTCAGTGCACCAATGTAACAGGGTTGGTAGTTGTACTCATTTTGAAT ATACCTTTTCCCTTATTGATTCTT[AG]TAATATAGGATCCTGGAAATGAGACCTGGTGGAA
WI-18821b	76	T C ---			TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC ACAGAGGCT[AC]GGGGGTAGCCATTGTGCAGTCAATGGCCCGGGGGAACCTTGCCAACCTTCGTGTCAG GTGCTGTGT
WI-18821a	69	C T ---			TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC AC[AC]TAGAGGCTGGGGGTAGCCATTGTGCAGTCAATGGCCCGGGGGAACCTTGCCAACCTTCGTGTCAG GTGCTGTGT
WI-19021a	20	C G ---			ACTCCTCTGCTGTCCAT[AC]GACTGTCTTTGAACAGGAAAAGTCACAGAGTTTAAAGAGAA GCAAAATTAACATCCTGAATCGGGAACAAAGGGTTTATCTAATAAGTGTCTTCCATCAGCTTG CTACCTTACCCACACTTCCCTCTGATTTGCGTGAGGACGTGGCATCTTACTTACGTACGTGGCATAAC ACATCGTGTGAGCCCATGTATGCTGGGGTAGAGCAAGTAGCCCTCCCTGTC
WI-18908	70	G C ---			TGGAAATTCCTTTCATCTGGAACCATCAGAAACCCCTCACACTGGGACTTGCAAAAAGGGTCAGTA TGG[AC]TTAGGGAAACATTCATCCTTGAGTCAAAAAATCTCAATTCCTCCCTATCTTTGCCACCC TCATGCTGTGTGACT
WI-19037b	155	A G ---			CACGGTTCTCTGCATCGTTACCAGAGCCCTTCTGGTCTTAGCCACGCGCTGTATGACCGCGCAATA TCCCCAAAGCTTTGGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCAITTTCTGGAGAGGGTCT CCCTCCCTTACGAACACA[AC]AAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGCCAGGCACTGGGGGGTGAAGTGTGGTACACAGTGAATGGGAGGTGG
WI-19037a	47	C A ---			CACGGTTCTCTGCATCGTTACCAGAGCCCTTCTGGTCTTAGCCACG[AC]ACCTGTATGACCGCGCA ATATCCCCAAAGCTTTGGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCAITTTCTGGAGAGGG GTCCCTCCCTTACGAACACA[AC]AAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGCCAGGCACTGGGGGGTGAAGTGTGGTACACAGTGAATGGGAGGTGG
WI-19064	66	T C ---			TTGAGGAGGTGGGTGAACCTGCTCCTTGGCAGGGATTGTGACACTGCATTTGCTGGGCTGTTCCTT/ C[AC]GGGCTCTTCTGGACCTTGACCGTGGATACAGGGCAATGGTATTTGGTCTCTGGGAGGG TGGGTGAATAAAGGC

WI-18972a	112 A G ---			AGGCCTGTGGCTTATGTCACCAACAGAGGGTCTCTGAGAAGTCTGGCTGCCTGGGATGCCCTGCC CCCTCCTGGAAGGCTCTGACAGATGACTGGGCTGGGAAGCAGAGTCTGCTGGCCATGGAGCC TCATTGCAAGTTGTTCTTGAACACCTGAGGCTTCTGTGGCCACCGACCTACGGCTTCTCTCC AGATGTCTTTGCCTGAGCACAGACAGTCAGCATGGAATGCTCTTGGCCA
WI-19016b	184 C A ---			GTTTGCAACCAACATGTGCTCTTTTCAGTCATTCACTGTTTTAATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTTGTAATGTGATTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAACCTTAGATACATAGCCGACTGTATACAGAGGTTCACTCAAC/C/A/CTCAACACTATTGAC TTTTGGGCTGGATAGTCTCTGTGTGGGGGTTTTGTCTTGCACTGTAG
WI-19016a	161 C T ---			GTTTGCAACCAACATGTGCTCTTTTCAGTCATTCACTGTTTTAATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTTGTAATGTGATTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAACCTTAGATACATAGCCGAC/C/TTGTATACAGAGGTTCACTCAACCTCAACACTATTGAC TTTTGGGCTGGATAGTCTCTGTGTGGGGGTTTTGTCTTGCACTGTAG
WI-20096	21 T C ---			GGTTTGGGGCATTTATTCT/C/GATAGAGACTGGCACAAGCTTTGGGCTAAGGACACCGGCCCC ACCTCATCTAGAAACAATCTCTCGCCAGACTTG
WI-19591b	156 C A ---			TGGGGCAATTTTAAACAAACAGGCAAAATATCACATATACCTGAATATAAGGTAACCTCAAGCCATG AGTATAAGATTAGGCAGTTACTTTATTTGAACAAGGAAGTGGCATAAGCAACTCAGTGTGCC CTTAGGGTGGGAGCTCTCC/C/A/CTACCACTCCCAAGGCAATCTTTGGGAGAAAAA GTGCTCTATCTGCTAGCTGTGTTATCTAGGGATTGCACCTTCTTACACGG
WI-19591a	45 T A ---			TGGGGCAATTTTAAACAAACAGGCAAAATATCACATATACCTGAATATAAGGTAACCTCAAGC CATGAGTAAAGATTAGGCAGTTACTTTATTTGAACAAGGAAGTGGCATAAGCAACTCAGTGTGT GCCCTTAGGGTGGGAGCTCTCCCTACCACTCCCAAGGCAATCTTTGGGAGAAAAA GTGCTCTATCTGCTAGCTGTGTTATCTAGGGATTGCACCTTCTTACACGG
WI-20310	125 G A ---			TCCTCCAGCTCTGTATCCTTGTCTTGGGGTCTGTGTTACGGCCCTCCAGGCATGGTTCTTCAT TTAGGTAGGAACAAAGGCCAAAGAACATACAAAGCCAGCTCTAGAGGCTCA/C/A/TCAGAA CTGGACCTTTAACTACAAAGGAATCTTGGATGAATTTTTCGGGGCTTCAGGAGCAGGTAGC AGAGCCAAAGTGCACACTCAGGCCATCTTCTCCCAATGTCTCCCGGGGG
WI-20860	224 G A ---			CTCTCCCTAAGGAGCCTTGGCTTGCAGCCCCATTGAGGGATGGAAGTCACAAGACAATGAGT GGAGCTCATGCCCTCCCATGAGGAAGCCCTTAGTATTGCTGACATCTGCCCTTATCTGCTCTCCT CCCCAGTGTCTACACTTGGCAAGCAGAGTGGTGGCAGACCCAGCTTGAGAGCTCTTGAGACC GGAAGGAAGGGCGGTCA/T/G/A/GGTGATGGCTTCTGGCTCTCTGGCTT
WI-19359a	39 T C ---			GACGTGACAAAGGAGGTTAAATGAATCTTTGTTTGT/C/JCATGTTCAAAAAAGAGATTAAAT ATTTTGTGACTGCATCTGTGAATGAAGACACTCAAAAGCCATGTTTCCAACCTTAGGTTAATAAA GGCTATTTGTCCACCCACTCTTGGGCTTGTGCATATCTTGGGCTCAAGTGGAGGCCACGTG GGAACAAGGCTCTAGAAACAAGGACATGCAGCCTTCCCTGAGCCAGTTCTCT



WI-19766b	93 A G ---	---			TGGCTCAATGACTGGTACATTGGAGAAGCTGTGCAGCAGCATCCTTTCTGTGGTGGCAGGGCAGGAGATGAACCATAGGAGCCAAAAGTC/GJGACAAAACAGAAAGGCACACCAAGCCTGAAACCCCTCGGACAACAGCAGAGTTACCAGCTGAGGGATGTCCCTGGAGGTTCTGACCCATGAGAGGCCCCCTCACCTCCTTACCCCTCCTCTACCACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-19766a	31 G A ---	---			TGGCTCAATGACTGGTACATTGGAGAAGCT/GJGTGAGCAGCATCCTTTCTGTGGTGGCAGGGCAGGAGATGAACCATAGGAGCCAAAAGTCAGACAAACAGAAAGGCACACCAAGCCTGAAACCCCTCGGACAACAGCAGAGTTACCAGCTGAGGGATGTCCCTGGAGGTTCTGACCCATGAGAGGCCCCCTCACCTCCTTACCCCTCCTCTACCACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-20512d	126 C G ---	---			CTTCTCTGTTGGCTTGCATTGTGCGATTGGAAAACCATTGGAAGAGGACTTTCTGTGCAAACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGACTGAC/GJAAAGCTTAGAAAGGAACTGAATTGCTTCTTTGAATATGGATTTAGGCGGGCGTGGTGGGCTCACGGCTTATTAATCCAGGCACGTTGGGAGGGCCCAACGCGGGTGGGATCACCTGA
WI-20512c	59 T G ---	---			CTTCTCTGTTGGCTTGCATTGTGCGATTGGAAAACCATTGGAAGAGGACTT/GJTCCTGCAAAACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGACTGACAAAGCTTAGAAAGGAACTGAATTGCTTCTTTGAATATGGATTTAGGCGGGCGTGGTGGGCTCACGGCTTATTAATCCAGGCACGTTGGGAGGGCCCAACGCGGGTGGGATCACCTGA
WI-19599	230 C G ---	---			GGCTTAAATCCCTCTGTTGGGACTGGTCTCTCCAGTTACAGCAAGGATCGCACCCCTTTCCATAACCCCTTCTACATTGGAAGAGCAGCACACCTTGATACAGATGGTCCGTGAAGTCTTTTAAACGGACAAAGGTAATACACAGCTAACAAACCGTGATGTGGCTCACACGTAACCAACACCTCTTTTTCAGAACAGAGAGCGTTAAAAGTAAAGGGCA/C/GJTTCCAAGAGTAACACTGCTA
WI-20679	82 T C ---	---			TGTTGAAATAAAATTTCCATGGTCTTAATTGAAGTGTATGTTACTTTCTTTTGAATATCCTTTTTTTCATTAAAATAAT/GJCTAAACCACCTATGTTTCAACCTTCTGTTTAACTAAGATATGGGTTTTGGAAAAGGCCACAAAGTCACCAAGCTCCATGAAGTGGGCGAATGGTCTTTTGGAAAGCTCTCAGGGTGTCTCTCCAGAAA
WI-19909a	29 T C ---	---			CCAGAAATAAGCCTGAATATCTCTTTCT/GJTTAAAATAATAATTTTCTCTTTGCTCTTCCAAATAATCTTAAAATGAACCTGTCTAGTCTATTTTAACTAGGCAATTATAACACTACCTAGGCGGGTTTTTCTCTTATACCTTGTTCTGTACTGTGGAATCAACTAA
WI-20341	221 G C ---	---			TTGAGAGGCTGAGAGAAGGCTGTGAGACATTGTAATAAGTCTTAGGGGCATGAGACATTAGGAAGGCCACAATTATGAGTAATGAATGTGGAGGCTGATGAGAAGCTACTGCTCCCATTTGTTAGCAGGAGGCAGGAAAAGTGATCTGGGGTCTCTGGCAGCAAAAGCGTGGTGAATATTTGGGTGACGTCATGCATCCCCCATGCATTGGTTTTG/CJATGCTCCAGTGAGCTGTGGGCAAGTCT

WI-20113	60	T C	---	---	TTCTGGTACATGGTAAGTGCTCAGTATTACTGAGTGAATGAGCAAGACCTGAAATACTGTTCJGGA AACAGTAAAAGCAAAATTACCACACAATTAGGAGGAATATTTCAGACATAGGATATTTAAACAT CACTCAATACTGGAGCATGATTCAGCAATAATCTATTCCATAAACCAAGGTAGATAAATGTCCACA GCTTTAAATATAGTTAAGTACAGTTGATCCTCGTTATTCATGGATTCCGTATTT
WI-20895	107	G C	---	---	TGATGGCAAGTACAAAGGCTCTGAAGAACAGAGTAACAGAGCAGCGAGTGCAGCGTGTGGC CACTCCACAGGAGCAACACTGACTTCATTAAAGGCAAG/CJCTTACTCTGTACTTTTCCCTC CCACATAGTTTAAACCAATAGAAAGGCATTCTATTCTCACACTACTGCTCTCTAAGGTCCTAGGAA TATACTGGTACTATAGGCAACAGATGCA
WI-20721	72	T C	---	---	CCTGCAATCACAAAAGTGGAACTAGTTGATATTTTGAATCATACTTGATTAAACCACCTTCAGAAA TTCTATTCJAAAACACTAGCAACTTCCTTTTATCAGA
WI-19415c	161	A G	---	---	CTGGATTTTAATATTCTGGCCTAATAACCAATGTAAATTAATTAATTTGGTCAATATCTCCACCTC ATTCTGCTAACATGTTTTGCAAGATTCCCTAAGTAAGGATTTGACGACTGAGACTAGTCCGGCAAA GTCATGAGACCCCTTAGCTGATCTCATJA/GJAAGTCCACCTCATGAAGGAGATGATTCACATCTCAA GCTAAGGTATAAGTGTGGACATACAAAGGCTTACAAGTTTTACACTTCCTG
WI-19348c	103	C T	---	---	GCTGCTACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTTCG GCGGTCGATGAAGAGACTGTTGGTCATGGCGGAG/CJGTCTCTCCAGGCTCATATGGATGTCCT CGAGTTGCACAGGGAAGTCTGCTGTGTAGAAGCTTCCTC
WI-19348b	98	G A	---	---	GCTGCTACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTTCG GCGGTCGATGAAGAGACTGTTGGTCATGGC/GA/GTGAAGCTCTCTCCAGGCTCATATGGATGTCCT CGAGTTGCACAGGGAAGTCTGCTGTGTAGAAGCTTCCTC
WI-19635	98	A T	---	---	ATTAGTTCGTGTTGGCCACATTCAAAGCCATCCACACAGCTCTGTAGGCCATTGTAACACAATG TTAAAGGTACAGTAAATAACAGTATTATATCTTATTGTAGCAGCGGTGTGAGGCTCATTT GTTGAATGAAGCATCCTTAGGCAGCAGTGAAGTGCATGATGCTGCTGAAAGAACTTTGCGCTT
WI-19641a	46	A G	---	---	T TCCAATTTTCAGAAACATGTTCCATGTTTATTGTGATAAGCACTAGJA/GJATTATAGTCTCATGTTT TTAATTTATGAATAACGCTGATTCATTTGATTTTGTATTTACAGAAGATGTCAGGCTATCTCATTC AGTTATTAATAATGGATCAGAGTAGTAAGTCAAGAATAAGTGCATAATGTGGTTTAAATTTTAAAA AATACTCAGAAATGAGGTAGTATTTAATTTTAAATTCATCCACCCACCTTG
WI-19642b	52	C A	---	---	ATATAGATACCATCCATGGTTTCAAGCATGGCCTGGACACATTATCCCTTC/JA/GGGTAAACAG GACTATTGCATGAGCATTCCTTAAATACGATTTTGTATGGACACAAGTTTCATGTCTATTA
WI-19673b	180	C T	---	---	TCTGCCATGATCAGTGTGATGAAGAACATGATGGTCACTAGTAGGTAACCTTCTGTGTCATTGCCT TACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTTGCATCACCACCTGTAATCTAATAGT GAAAAGGCAAAATGATGCTCAGTATCACTGTGAAAACATTTTTC/JCTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGTCAAAAAACACAGCCC

WI-19673a	35 G A ---			TCTGCCATGATCACATTGTGATGAAGAACATGATG(G/A)TCACTAGTAGGTAACATTTCTGTGTCATTG CCTTACTCTCAGTGGTGTGATTTACCTACCTGATTTTGCATCACCAGCTGTAATCTAAT AGTGAAGGCAATGATGTCTCAGTATCAGTGTGAAAACATTTTCCCTTGGACCAGCTGAAAGAA TCTTGAGGAGCTGAAGGCTTCAAGGCTCAGGTCACACGTCGCAAAAACACAGCCC
WI-19724	35 A G ---			TTTATTTGGGAACAAAGGATTGTAATTTGGGTA(A/G)CTGAGTCACGGTGGCCCTGAGTAGTGTC CTAGAAAGCAACACGAGAGTTTGGTTTTTCTCTT
WI-19307	196 T C ---			TCCTCTCCCCCACTAGATGGTATTGATCACTCTGCCCAAAATGGTACCCCTTCAGCAAGAATG CAAGCCCTCTTGGATTGCTTCATGAGAAAATGGTGGCTTGGGATGGAGTGACATTCCTTGCTGT GGTGAACCTGCAAAAGAGGAAACAGGCAATGTATCCATAGAGGCCCTTAAAGAGACCCG(T/C)TGG AAATGGGCCATGGTCTAATTTGGTGTGAATAAATAACCTCTTTGGCTG
WI-19269	85 A T ---			CTTTCCCTCATCCCTCTTCCACCACACCATCCCGGAACAGTGTCCAGGATTCCTGCCCACTGGC CATTTTGGAGTGTGTC(A/T)TTGGGTAGCAATGTGGAAACACACAGGCCCTTTGTGGAGAAAATGG AGGGGTTGAGGGAGTCCAGGAGGGGCTTATTTAGGGCCCTTGCACCTGCTCATAGCGAGCTCG ATCTCTCATCATCTGGACAGGTGGAAGCGAATCTTCCCGGGCGTAGGCA
WI-19946	122 C T ---			CAATGGACTGAATGAGTGCCTGCTGGGTGGGTGGGGCACACACCTTCAATACAGTCAAGGTGG CTTCCAGTTTAGAAAACAGAAATCTGCATCTCAGCTCAGCTGACGACACAGAGAGG(T/C)TCTCCTG ACCCAGACGACTCAGGAGCCAGTCTGTTTTCAAAACATGCACTTAACCTGGCCAGAGAGTTCA CGTAGGCATCTTAAATAACTAATCCAGCAAAATGTTGGGTACGGTTACTAA
WI-19956	141 G A ---			CACAGCATGGTGAATAGCATCAGATTGAATGAAAGTTTGTAAATGCAACCATAAATAATTATA ATAATATACATCAAGTAACCTTACAGCACACATTTTAAAGGCCAAGTTTGGATCTGTGGACCT CAATG(T/G/A)CTCTCGGAGAGGAGCCAGCTTAGCAGCAGATACCTTACAGCTTGTCTACTCAA GTGATGGCCCAACAGAGCTTCTGAATCTCTCTGGGAGGTAGCTGACAAG
WI-19076	40 G A ---			TTGGTTGGATACTTGTGTAAGGCAAGGAGTTTAA(T/G/A)GTATTCAAAATACCTTTTAAAA GTATTTAGCACAAGATTTTCTGTAAACTAGATTATGTTGTAACATTTTCTAAATCTGTAGGAG TGTCGGTTGTTAAGAACTAGAGCTTATCTCTATCCAAATCTATCTTGGCTCTGAAAAACTGCAGA AAGGCATTTGAAGCTGTTCTTTAAGATAIGGGATTCTTTTATCTT
WI-20218	26 T C ---			CCACACACTCTGGTTTATAAGCTA(T/C)JAGGACAGAGCAGAGTGAACCTGAAAAACAGGGTAG AAAAATAACATAAATTGGAGGGGAACAGTGGGATGAGAAAGAATGACAAACAGCCACATGTGCCCA GTCAAAATACTTTTAGTCCCTGCAGCAGAAAGATGCCAACCAAGTCTCTATACTGGCTGGGATCCTGCC ATGGATGCAGGAGAAAAA
WI-20295g	154 T G ---			CAACCTTTTGGACAGGGGACGTGAATTTCTGATGAAAGTTATCTTACCAAGTTTAAATTCATAATTG GGAAATCCTCTTTTAAATATCTCCAGGCTTGAATGGGGAGGGCTGGCTCTACCCCTTCTCTTTCCA TCCAGTCTATTGCCAGAT(G/C)CAGAGAAAGCGGGAGGCCAGCTCTCCAGCATAGCCACTGTGG GTCCGGCTTCACTCTGTGCTGACTCTCTCATGCTGGGACTGTGCTTTGGGG

WI-20361a	192	G A	---	CTGGAGTGTGACCTAAGTGACATTTTTTTTAATGCCAAATACAGTAATCTCCAAAGCTTTTAATGG CTTATGCAAGATGACAGAATATGTGAATCTGATTGTCCCGAGTGTACACTCTGCACCTCCAAAGCTA CAACAGTCCACAGCTGAGAGGTTCCCTATACCTCTACTACTGTGACAATTTAGC[G/A]ATCCTTC AATGGGAAATTCCTAACTACGAGACAATGGTCTCTACAGTAGGCCGG
WI-20572	75	A G	---	GAGCCAAACCCAAACAAAAATAAAACAGAACTCTTTTTGTAAACTAAGTCATACCTACTTCTCTCT TCAGAAAT[G/G]TCATAAAACATCATCTTTACAACTGGAGAGCGAGGTAGGCCATAATTTGTTCA AATTCATCTTCTCAAAATTTAAATTTGTTTAAATCCCAAGGTGCCTATTGAATCTTCCAAAAATA AACTGCCTATCAGGTATCATACCTGCAAAATGCTTCTAATATCTCTTGATTAT
WI-20588	133	G A	---	CATGACAAAAGACAAAAGATCAAGGAGTAACATAAAATTAAGTTGAATAAATAGTATACAGCAATC TTCACTTTTTAAGAAAAATGTGAGATCCTTTGTTGGTTTTTATTTCCCTTAAGTACAAAATGCTAAAC[ G/A]GGAGCCGAGCTCTTCGCATTGAGG
WI-20593	79	A G	---	TGACCTCATACTGGGTCTGGTTAGAACACAGCCACTAGAACAAACTCCAGTCTTTTTCAGTCTGTTG CTGTACTTCAG[G/G]TTTAAATCTGGGAATGAGCATGCAGCAATGCTCCACCAGATGAGGAAGAAA AGCTGTTAAAGGAACCTCAGGATGTTGTTAGGAAGGGGAGTGATGCCAGGCCCTTCACCAGACTAT CCAGAAGCCATTCATGGGTAATTTGGTCTGCATCTGTGAGACACTGAGCT
WI-19765	57	T C	---	TTCTTTGCCAAGCCTGTTCTCAAGTTATCAGAACTGGGTGTATACCTTGCTCCTCAT[G/A]TGATCT TGTCCTCTGCTGTTTTAGGTTAGCAAGGTGTATGAATACITTTAAGTTTTGTTGTTCTTTCTCTCGT GGTATCAGTGAATACTGATCTATTCCTGGCTAGGGTCAATTTACAAAATTGCCATGGAAGTACGAGC AAAAGGCCACCGTGGATAAAATCACTCACCATCGAGGCCACCAGTATT
WI-19066f	239	A G	---	TGACAAGGGAGAGAAAGGGAAATTTCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCCAATCTCTACGAGGAAGTGG CATATGTTCTTGGTGGTCCACCCTGTAGCTGAATTAATCTCTCCATATTCGCGATGCTCAATTACAGT ACCATTCGAGGCAAACTTTTCTTAAACGCCCTTCAGT[G/G]TTCTTTTAA
WI-19066g	184	C T	---	TGACAAGGGAGAGAAAGGGAAATTTCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCCAATCTCTACGAGGAAGTGG CATATGTTCTTGGTGGTCCACCCTGTAGCTGAATTAATCTCTCCATATTCGCGATGCTCAATTAC AGTACCATTCGAGGCAAACTTTTCTTAAACGCCCTTCAGTATTCTTTTAA
WI-19066i	148	T C	---	TGACAAGGGAGAGAAAGGGAAATTTCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCCAATCTCTACGAGGAAGTGG CATATGTTCTTGGTGGTCCACCCTGTAGCTGAATTAATCTCTCCATATTCGCGATGCTCAATTAC AGTACCATTCGAGGCAAACTTTTCTTAAACGCCCTTCAGTATTCTTTTAA

WI-19066e	147	G C ---	---	TGACAAGGGGAGAGAAGGGAAATCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGCTTAGCCAGTCCAATCTCTACGAGGAAGCTGG CATATGTTCTTGCG/GC/JTTGGTCACCTGTAGCTGAATTACTTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTAA
WI-19066c	100	G A ---	---	TGACAAGGGGAGAGAAGGGAAATCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCTGTAGCTGAATTACTTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTAA
WI-19066b	87	C T ---	---	TGACAAGGGGAGAGAAGGGAAATCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCTGTAGCTGAATTACTTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTAA
WI-19066a	72	C T ---	---	TGACAAGGGGAGAGAAGGGAAATCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCTGTAGCTGAATTACTTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTAA
WI-20660	105	G C ---	---	TTTACAGCGAGTTTCCCGTCTCAATAAGTATGAATCTAAATAGATTAGGGTGAAAGAAAATGTG TGCTAAATAAATCTCCCTTTTGAATGTATATTG/GC/JTTAAAGGGAAGCATTAATATTA CAGACATATTTACAAGGTTCTGAACATGAGTGATTCCTACTGTTTCTGTACAAGATAGAACAAA AAGCTATCCACCGCCCCCAAAATACTGTTTAAACACTATGTTTAAAGA CTGCTGCCAGCTCTCTCTTGCGCTGCTCCAGATGGCGGTCTCCTGGCAGCCTCCCGCTCAGTCTCC TCCACCGCCTCTTCTCTCCAGCCTGCTGCATGCATGTGCACCTTGGT/C/JTTGCTCCATCGCC TTGAAAGCTCTGAA
WI-18768	120	C T ---	---	TTCCCCAGGGTTCTGTATTGCAGCTAAGCTCAAATG/JA/GJATTTAACTTCTAGTTGCTCTTGTG GTCTTCTTCCAAATGATGCTTACTACAGAAAGCAAATCAGACACAATTAGAGAAGCCTTTTCCATAAA GTGTAATTTTAAATGGCTGCAAAACGGCAACCTGTAACTGCCCTTTTAAATGGCATGACAAGGTGTGC AGTGGCCCCATCCAGCATGTGTGTGCTCTATCTTGCATCTACCTGCTCC
WI-18790	49	A T ---	---	GAAAGCCAGAGATTAGCCCCGCAATCCGCATCTGCAACCCAGGACAGAA/JTJGSCATGGACAAGGGA TGAGCTTTACAAAGATGATGCACCTTGGAGATCAGAAAAATTCATATTTAAGCAAAGTGATACAAACA CAGTGATTTGGGAATGCCT
WI-18987	35	G A ---	---	AGGAGGCTGTTCCAGGAGTCTGCCCCAGCAGCCTC/GA/JGTGGCCAGCCCCAGACACTACCCACCTT CCCCAGTGGCCCCGTGGATCCTGGTCTTAGGCTGGACACAGGATTGAGAAAGACACCCAGGCTGCACA GAAAGAGCCAGATGGACCTGAGTGTGGTTCACAGCCCCCTACACTCAAGGCTGAGAGGCCCTCAGGAA AGTCA

WI-18919	26	C T	---			TGGATGAAACCACAGGGATTCCGGA/C/TGGCAGACCCCAATTTTATACATTCACATTTCTCTACAGTGTGTTTTGTTGTTGGTTTTATTTTTTATACTTTGGCCATACCAGAGCTAGATTGCCAGGCTGGCTGAATAA
WI-18741c	64	G A	---			CTTTGGTCAAGGCTTTGGACATCTCTCAGTCATCAGACAGAGTATCTCTGCTAGACCTC[G/A]CTGGAGTCAAGCTTGAATTAATAIGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-18741b	38	G C	---			CTTTGGTCAAGGCTTTGGACATCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTCGCTGGAGTCAAGCTTGAATTAATAIGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-18741a	23	T G	---			CTTTGGTCAAGGCTTTGGACAT/GTCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTCGCTGGAGTCAAGCTTGAATTAATAIGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-19179a	170	G A	---			TCAGAACGACAGATGGCATCTGTTCCCTGCTTGGTTGGTTGGTGTGTAACCTTTACAGAGACCTGAATTTAGAAATGGCCAGTCTCTATGAGATGGGATATGAGATGGCCTATGGAATAAGATAGGCTATCTCAACTGCTGAGTGATTCATAAACATATCAACCA/GA/ATAGCATTAACCCATTTTATTTCTGTGCTCTAGTCTGAAGATGCTCACCAGTTTTCTGTGTACAGTAAGGACGATGCT
WI-19212	46	T A	---			CCAA GTTG CATCCATGTTTGATTTCTGATGAGACTAGAGTGACAGT/GA/GTTTCAGAACCCCAATGTCTCAGGTAGTTGGAGCATCTCTATGAGATGGGATATGAGATGGCCTATGGAATAAGATAGGCTGCAATAAATACACATTATCAAAAGTCTCTACAATTTATTTCCGAGCATGTGAGCTAAGTAGACCCATAAGGAGAGAAAAATGCCGTCTCTTCCCTCTTTCTGCACTGCCATAT
WI-19183	210	G C	---			CTGTTGAAGGCTTCTCAGGCAACCTCCAGCTTAAAGCCCTAGACAGGTAAAGACACACATTGGATGAGCATGGGTTCTCCCAATTTATGGGCATGAAATATGTGTTAGAATAAGGAACAAGCATTATTCCTTGCCAAACAGCCTCACCTAAGAGGCTTTTGTGTAGTCAAGCAACACACTTGCCTGCTCTGCCCTTGAG/GC/TGCAATTTGACCTGCTCTCACGTGTAAGGTGACTTGGTGGC
WI-20014b	214	T C	---			TTGAAATCCAGTCTCTGGCCCCCAGGCGGGTCTGTACCACATAGAATGCTCTCCTACTGGGGTGTTCTGGCTTTTGTAGAACTTGGCTGAGATGTTCTCCCTGTCCATACCATCGATGTTCTTTGTTCAGAGCAATGTTCTGTATTCTGAAACTGAAACTGAACAGATTTGCCCTTTCTCCTAGTCAACC AAGCATACT/T/C/TCTGGCTCCCAAGTACTTAAATGTTCTCATCTGT
WI-19041	198	T C	---			GTCTCCCCAGAGTGTCTGACCCCCAGCCCTGTCTGCCCTGTAAAGGGATACAGAGAAGCTCCCCGTCTCTGCATCCCTTCCCAGGGGGTGCCCTTAGTTTGGACATGCTGGTAGCAGACTCAAGGGCGTG CACGGTGAGCAGATGAGGCCCAAGCTCATCACACCAGGGGCCATCCTCTCTCAATACAGCCT/GC/GCCCTTGAGTCCCTATTTCAAAAATAAAATAGTGTGTCTTGGCTGTCTGT
WI-19135	20	G A	---			CAGTTACCCCTGCTTTGCCTC/G/A/AAAGTGCATCAATTTGTAAATTTAGTATTAACTCTGTAAGTGTCTGTAGGTACGTTTTATATATAAGGACAGACCAAAAAATCAACCTATCAAGCTTCAAAAACTTTGGGAAAGGGTGGGATTAAGTACAAGCACATTTGGCTACAGTAATGAACGTGATTTTTTATTAAGTGCCTTTGCCATATAAAATGCTGATATTACTGGAAACCTAGCCAGCTCAC

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WI-19236	54	G A	---			TACACAGAGGTGCGACCTTGACCTCTGAGGGTTGGGTGTGGAGGGGGGAAAGG[G/A]GATGGAGAC CTGCTCCCGACGCTTCTGTAGCCGGTTACATGGGAACAGGGTTAACATCTGTGTAGGGGAGGT CACCTTACCTTTTTCATAGGGGAAGAGTGTACACACTCTGGCTATCTCAGGGGAATGGGGAAAAG AATCTTTCAAGGGCAAAAGAACTCGTGGGAGGATGCTGTGTATGTATACT
						GTGCGAGTCTTCAGAAAGCAAGGACTGCCCTTCATTACGCTTGCTGACCTCCAGCCTTCTAAGG CTCAGCCCCACGGGACTCTGTGGCTGCCAGCTTGTAGCTATCTATATATTTCATAGCCAA ACAGGAGACCCCTTTGCAGGACTTGCACACAGGGAGGCTGTAGCAGGAAACCCCTTCTTCCCTGGT CTGGCTCTGCTGGAGCGG[G/C]TGGGAACCAACACCTTCAGTGTGGTG
WI-19144	222	G C	---			CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAAGACTGAACACGCTGATTTACACGAGGGTAGAC GGCAGATGCCCTGACAGAGAGTGGTTGGCAGACACACACTAG[C/A]ATTTTCACGGGTGGGCAC ATGGGTGTGGACCTGGAGCTGTGCAGCATGTGGCGTCTCTGTGGAAGCCACCGTCTTCTTTGG GGGCGCGGAGATCTAGCATCTCTGAATCCTGGCTGTGAGGCTTTGAAG
WI-19139b	110	C A	---			CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAAGACTGAACACGCTGATTTACACGAGGGTAGA C/TGGCAGATGCCCTGACAGAGAGTGGTTGGCAGACACACACTAGCATTTTCACGGGTGGGCAC ATGGGTGTGGACCTGGAGCTGTGCAGCATGTGGCGTCTCTGTGGAAGCCACCGTCTTCTTTGG GGGCGCGGAGATCTAGCATCTCTGAATCCTGGCTGTGAGGCTTTGAAG
WI-19139a	66	C T	---			GGCTGGGACCTTTAGGAAAGTGAATGCAGGTGAGAAGAACCTAAACATGAAGGAAAGGGTGCCT CATCCAGCAACCTGTCCTTGTGGGTGATGATCACTGTGCTGT[G/C]GGCTCATGGCAGAGCATT CAGTCCACCGTTTAGG
WI-18910	112	T C	---			TTCAGGAGGTGGAGTTCGTCAGCTCTCCTGCTGTGATGTGGAAGCTTCTGATATTTGAAGAAACA CGAATGTCTGTAGCTTCTCTCACTGCCCCAGTATTGCTCTGTATTATCAGCGATGCCCTCTGT CACTCATGCCCTTGCCTAATTGTTCAATGGTGGAA/GJGCTTCATGTATATGATCAGGACCCACC TCCAGTTCTTCTGAAAGTGTGACAGTGTCCAGCCGGTCTGCAGCACA
WI-19235	173	A G	---			CGTTTCCCTAACTACCCAGTTTAGTTTGGGATGATTTGATTTCTGTTGTTGATCCCATTTCTAA CTTGGAATTGTGAGCCTCTATGTTTCTGTAGGTGAGTGTGGGTTTTTCCCCCACCAGGAAAGT GGCAGCATCCCTCTCCTCCTAAAGGGACTCTGCGGAAC[C/T]TTTCACACCTCTTCTCAGGGAC GGGCGAGGTGTGTGTGGTACACTGAGTGTCCAGAGCAGCATT
WI-19222	179	C T	---			AAATAATGCAACGAGGAGGAGAAAGAAATGCATTAAGACAAGAACTTCTCATAGAACATTG ATCTGTTTACAGGAAACAACTTGCCTTGAAATTTACAGAGTGTACATATGCAATTTGCAATGAA A/GJTAGCTATTTTCCCTAAGACATTTTTCATTCATGAATATTTCAAGTTTTTCACTACTGTACA CATTTCTTAAACACATGATACCAGCAGCAACTGAAATGAATGCCGAATTG
WI-19117	134	A G	---			

WI-19134c	263 C T ---			CTCCTGTTGTCGACCTGACAGGGTGACACAGCCCCCTTCACACTCTGTCCTCCTATCTTCCTGGGTAGA TGCCCTGGTGTAGGGCTGAGTACTGAATGGTCTTCATCCCCAGCAAGGGGTGACAGCCAGGGTTCAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGAGCCAGCTGCACATATCCTTTTCAGAGCAC TTATCCACTTGCCTCCTCTACCTCGGCACCTGGGTGGAAAGGG
WI-19134a	162 T C ---			CTCCTGTTGTCGACCTGACAGGGTGACACAGCCCCCTTCACACTCTGTCCTCCTATCTTCCTGGGTAGA TGCCCTGGTGTAGGGCTGAGTACTGAATGGTCTTCATCCCCAGCAAGGGGTGACAGCCAGGGTTCAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGAGCCAGCTGCACATATCCTTTTCAGAG CACTTCATCCACTTGCCTCCTCTACCTCGGCACCTGGGTGGAA
WI-19224	112 C T ---			GGTTTCAACCAGTCTTTCCAGGGAACCTCCGATGAAGTGTCCAAACAAATGAGCGAGTGAACCAAGA AGAGGATGACATTAGATCCAGGAGATACAACAGAGGAGATAATCTCTTCAGGATGCCTGTGAAGA AAGATCCCTGGATCCAGGATGATTATAGGACAAGTTGTTCAATCCAGAGGCCAGAGACTTCC AGGGAACACTCATTTCAAGGAGGTGAAATGATGATGACTCCTCCCAAGATGAAAA
WI-19201	179 T C ---			GCAGCTCCTAAGGACCACCTGGCCATTAGCTCTTGCTTTTGATGGCATCTCTTCCACCTTGTCTCTC CTTGCTCCTCTGTGTAGTGGCAGGTATGACAACATCATCCAGTGGAAACACAGCCTCACACTGCC CTTCCGCCCCCCACACTTTGCCCTGCAGGTGCACCGAAAGGACCTCTGGGGGATAAAAATTCAAAAA GTGTGATGTGCTGCTCAGAAGGTACAGACTCCATGCTGCTGCTTGGCCTCAA
WI-19034	45 T C ---			GAATGGCTCCACTCAGAGCTACCCCGGTGATGAGGATAGGGGAATCTTCTTATACATTAAAG GCAACAGCAGTTAGTAAAGGTTTTACAGTGTCTGCTGTTTGAAGTGAATATAAATTTTTTG CTAGCCCATGATCAATCGACTTCTATTGTTGATATACACTTCAGCATTTAAGTCTGTCGAATTGAC ATTTGCTACTTATAAACTTAGTCCTTAAGTCTTCTTATGCTGTGCTATATA
WI-19102	25 C G ---			TGTTCTGAGTCACGCTGAGGAGAGCTGCTTCACTCAGGAGTTTCATGCTGAGATGATCATGAGTTCA TGCGACGTATATTTCTTTGGAAACAGAAATGAAGCAGAGGAAACTCTTAATACTTAAATCGTTCT TGATTAGTATCGTGAGTTTGAAGGCTAGAACTCTGTAAGTTTTTGAACCTCAAGGAGAGAGGTAT AGTGAATGAGTGTGAGCATCGGGCTTTGCAGTCCCATAGAACAGAAATGGG
WI-18548b	65 A G ---			AAAGGAGGGAGAATCTTTTTACATAAAATGCCCTTGCATCATCCTCCAGTCCCTCACTGGGGAA(A/ G)AAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18548a	62 G A ---			AAAGGAGGGAGAATCTTTTTACATAAAATGCCCTTGCATCATCCTCCAGTCCCTCACTGGGG(G/A) AAAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18700	97 T C ---			GGCAGCAGCTTTTTTAATTTGAACACTTTCTTCTTGAGGACACACCTTCAGTACAGTTTAAACAAATGGT TACACCTGAAATCTGCTGAGAGCAGAGCTTTCJAAGATCCACAAATGCAAAAGGCCACTGCTGGCTCA CTTCTCTACA
WI-18501	121 C T ---			CAGAGGGAAGGTTTATTGAGTCAGCCACAGAGGAACAGAGAAACAGACACAGAGGAGTTCTGTGT GCATGGAGGAATCAGGGGCCCGNACAGCTGAACCTCGGCAGGACAGAGGGGGGCTCTGGACAGCA GCGCATGCCACAAACATTCA



WI-18017	87 C A ---			ACAAAGAAATGGAATAGGTTGGAAAACTTATCTGCATGTACAAAGTAATCCCGTAGATAA GGAGAGGCAACCCNGGAACA/C/A/ACTGCTGGATAAATCGTTCAATTAATAATATATCTCTTGAT CAGAGCTGGTGGAAATCAT
WI-18148b	101 A G ---			TTATTGCGTTCCTTCGATAACCTC/CTTTGGGACTATGAGATCATACCAGATGTGAAACGAAAGCA GTGATTCAGAAACCCNTCGATTCGAATATCCC/A/G/JTGGCGCATATGCAAGGAAGATGA
WI-18254	64 T C ---			TATACGGATCATGTATTTGTGTACCACTACCAAGTCAATTTGTAGAGCAGTTAAATCACAT/C JGCCAAAATCCCTCTGCTTCCTTGTAGTCAGTCCTTCTCCCAACCCAGGNACTTGGCAACCTGTTT TCCGTTCCCTAGACATTT
WI-18265b	117 C A ---			CAATGGGTGGAGTGAATAAAGCATATTGAGAACAGACGGCCTTCTGGCCNCTCTGCGTCC AAGGCTGTAAAGTCTCAGGATTGCTGTAAGTGAGCCATGAACCTGGCTG/C/A/GTTTTCAACCTTTC CTTGGGTGGTTCTTCAG
WI-18295	40 C T ---			ACCACATTTTGTGAGAGCCTATTGTGGAGAACAAACAG/C/JTGGGAAGTAAGGTTGATTACT TCCTCTCCAAGGATGATGTTTAAATGAATCCCTTNCCTTAGCTTCAATTCATATATGCCAAA
WI-18459b	64 T C ---			GGCAAGAGACAGAGATTTAATTGAATAAAACTCCAGGCTGTACACGGGTGGGAGACACAAAT/ C/GAGTAATTAAACAATAATATTTANATGACAGTGCAATTAATTAACTCCTGGGTAAAGCCAGAG GGGAGAGGGCGTCTTCA
WI-22585	56 A G ---			TTATTTTAAATTTGCATCCTGAGATAATAAAATTTATCTGACAAAGTGAACAATG/A/G/CAGAAGC AGCAGTGAAGTTTCGGAGAGCGAGTATCCTTCATTTGGCACAGCTGTATATAGATTGA
WI-21155	36 A G ---			GGGCTGTGGAGTAACAGAACTTGAGAAATTTGGC/A/G/JCTGTGTAGAATGATTTCTAAAGCTTC AGACAAATGGCAGA
STS-F02766b	88 G A ---			GCCTTGCTCTTGTGCTCCTCAGAGGCTCAGATGGATACGAGCAACTTCCTTTTGAACCTTTTAT TTTCTGGCAGGAAGAAG/A/G/JGGATCCAGCAGTGAGATCAGCAGGTTCTGTGTGCACAGACAG GGAAACAGGC
WI-19888a	98 C T ---			GGCAGATTCAACCCATAACAGAGAAATAACTCCTTATTGGAACAAGGTTTTTTTGTATGATGATG AAAATATTTGGAACTAGAAAGTAGCAGTGA/C/JTGGACAACGTTGAAAGATATTAATGCCACT GAACGTTCATTTAAATGGTAATTTTCATGTTATGTGATTTTCACTCAATTAAAGATGGAACATGT CTTATAATTGTAATACATGAGANCATATTTATGTTGGAAAGTGAACACAAG
WI-21485	82 C T ---			TGAGACCATCCTCCTCAACAAAGATCAGTCAGTTTCAGCACCTAATTTCCACACTGAAGTCTACG CAATTTTCATGCAG/C/JTGTGCACACAGTACAGTGCACAAATCCAGAGGGCAACACATTGTAAAT CATATCATCCGTTTCCAAA
WI-20601a	125 T C ---			TCAGAAATGCTTCCACTGCCCAACCAAGAAATTAATGAATGCNCTTACAATTGAGATGACTT GAAGTTAAAGAAAGGTACCTTCCTGGAGGTTGCATGACAGGATTAGTCTCTGTTC/JCTTGGT GCAAGTTTGAACAGATGATTAAGTACCATGTCATCAGAGCATCTGTTTCCCTGTCAGATCCCCACTAG

WI-20561b	94 T C ---	---	---	CGTTGCTTATTTAAGATGGCTGTTTATAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCAATTATTGTACTTCAGATGAAAAATCCTTACATGTC/GGGAAATCAATGCTCTTTTAAATTTTCAGATAAAGAAATTTNCATTTGAGGAGACATACAAATGTAA
WI-20561a	25 A G ---	---	---	CGTTGCTTATTTAAGATGGCTGTTT/GAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCAATTAATGACTTCAGATGAAAAATCCTTACATGTGGAATCAATGCTCTTTTAAATTTTCAGATAAAGAAATTTNCATTTGAGGAGACATACAAATGTAA
WI-20116e	69 T A ---	---	---	GCTTTCATTTTCTGTACCCACCCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAACATAT/AATAAATCTATATCATATATTTATACACACAAAAACACATTCTACCAGCACTGTGAAGACACAGACTAGGCTTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA
WI-20116c	59 T A ---	---	---	GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAAGCTTTTCATTTCTGTACCCACCCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTATAGAA
WI-20116a	22 C G ---	---	---	CATATAAATCTATATCATATATTTATACACACAAAAACACATTCTACCAGCACTGTGAAGACACAGACTAGGCTTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA
WI-20466b	133 G A ---	---	---	GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAAGCTTTTCATTTCTGTACCCACCCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAA
WI-21034b	39 A G ---	---	---	CATATAAATCTATATCATATATTTATACACACAAAAACACATTCTACCAGCACTGTGAAGACACAGACTAGGCTTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA
WI-22091c	205 G A ---	---	---	GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAAGCTTTTCATTTCTGTACCCACCCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTATAGAA
WI-21444	39 A G ---	---	---	AAAGATTGCAGTCTGGGACACAGTTGGAAACACTATTTATAAGTTGCACATATTACAAACAGNTCCCAATGGTGAACCTGGTATCTAAGATGAAAGCTTAATGAACATAATGAAGTGAATAAACGGC/GATGTGAACATAATGTTTAAAAAGTTAGAGCTTGTCTCAAGTCAGTACAGCTCTTAAGATAATAAATACAGTAACACTACTTTTATCTTGTCTCTTTATCCCTTTTCAGGTTTCGATT
WI-21034b	148 T C ---	---	---	CTGGCAGCAAGTAACCAATTTAAAGAAATACCTCAAC/GAGTCTTTTTTTTATGGGGTATTTCA
WI-22091c	205 G A ---	---	---	GTTGTTAAACAAAGTTAAATACTTATTGGAACATAATCTTGTATTTTATTCGAGGAAGAAGAAATCTATAAGATTGACTTACTCAATTTGACTGGTTTTTTGAAGCCTTACTGGGG
WI-21034b	148 T C ---	---	---	AGAATGGACAATGATGCAGATGATTTGTGAGCATTTTGATGAGAAAGTGGTGATTAGAAGGATACAGCATAAATTTAATTTGAACATGCTTATCTAGCTAACCTAATCTGTTTCTGTAGAAATTAATCTGGTGAGATTGGATGAGAT/GCCCTAACCTATCTCAATTTTAAAGTAATGTGAGCAA
WI-22091c	205 G A ---	---	---	GGCGTGATTTGATGCAATGTCCAACAGTCAAGCTATCATGAAATCCAAATATTTCCAGTAGAGACATGCAGAGCAATGTCAATGTAAACATACAGCATATTAACCTCCCTTAAAGTACTCATAATTTCACTTGTGTGTAGCTTTTAAAGGTTTAAAAATGTTAGCATTAAGTGGTATTACTTGAGGGCAACA/GAATACGGCTTAAACAACACACTAAATCATGAGGCTCAGGGATTG

WI- 21805a	45 A T ---	---	CAACTGCTGAGGCTCTTCACTAGCTGATTTATATCCTATATT/AA/AAAAAAAAATCTATAGTCTG CAGCTTTTGACATCTCTCAAGGGTGGATATGTTGGGAATGCAGACTCCATCAATATGTTGGTT TTGTTGCTTTTGTAGCTTAAGTCTGTTAGNAATCCAGAGGAATATGATTGAGGCCAGAGTTA CATTGGTTCAATAAATCGAACAGTTGAAGGCTGTTTGTAAATTGCTG
WI- 21778b	155 T C ---	---	AAAAATCCATAATTATTGAACCCCAAGTTACAGAGAAAGTTCGTAACCTTTTATTGAATATTAGAC TCTGCCGGGTGTCGTTGTCGCTTTCAACTCCAGTCTGTCATGCCCCTGTAGGTGGGTGCCCCAG GTCGGGCTTCTGAGGTCCTT/C/GGTAGAAGGAGGGCAGGTGGT
WI-20907	241 A C ---	---	TGAGTCAGTGGTCAGATGGGCAGTTGCGCTCAGCTGCAGTCCCTGACTCCGGAAACACTGTGCTCT CAATGATCTAGAGCTCATCTTGGCGTACATGAGGGCAGTTGTTGTTCTAGTACCCATTAGCCC ATGGCTCTTCAAGCCAAATCACACTGGGAAACACACCCCTCACAGATGCCCTATCCATTGAGTTC ATACAGGTTTGTAGTGTAGCTAGACTAAAAAACATTTTAA/C/AAATTATCTA
WI- 21449b	222 C T ---	---	AACAGCAGCAGTCACCTCCAAATGCAAAAAAATTAACAATTTTAGAATAAAATTAATGTTTA TAATGCGGGTCAGAGANTTGAAGGTACACAGAAATCAATCAGCAGCTGGAGCGGTGGAG AAGCCAAAGCCCACTGTGTCAGGGTCCAAAGCTGACAAGAGTCCCAACCTGAGAGGTCTOCACACCC AAATCATACCCCTCAGCTTCCCA/C/TTGACAGAGCCAGTGTCTCTGGGTTAG
WI- 21558a	157 G A ---	---	GCCTACAAGGAAGCCTGTGGACAGCGAGNTGGGTGGAAACCGACTCCAGCTGGAAAACTGCCCTC CCATCCCCCTTAGCGCTTCTGGCTTCCGGCTGATTTCTCGACAGCAGTTCTGGCCAGGGCAAGG AGCTGTGGTGGGGGCGAGTATG/AJAGCCAGGGACTCCCTTCCACAGATGAGGCCCTAGGGCTGCAA AAGGGCCCCGTGAAAGAGAGATGTGGTCAAGGCTTTATGGGTCTCTCCACC
WI- 22187b	178 G A ---	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGCGGTGGCTAGCAGAGCTCATGNGACCA GTCTGGGCTGACCATGGGTGATTACATTTAAAAACCAACCAAAACAAAAATAACCAAGA ACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTG/AJAAATTTTCATGAAAAATTTCC CCTAAACCATAAACAAAAACTGTCTCTTACCCCAAAAGTGTGGAGGAAAG
WI- 22187a	110 C A ---	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGCGGTGGCTAGCAGAGCTCATGNGACCA GTCTGGGCTGACCAATGGGTGATTACATTTAAAAACCAAA[C/A]CAAAACAAAAATAACCA AGAACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTGAAATTTTCATGAAAAATTTCC CCTAAACCATAAACAAAAACTGTCTCTTACCCCAAAAGTGTGGAGGAAAG
WI- 21609b	146 G A ---	---	TCATGAATATGCAGCTCCATAATCTTCTCCCTTTACAAACGTGCAGTCCGTTACAAAGCTGTAAA AACAAAGCCCAACCCCAAGACATCACAGAGCAAGCAGTGGCAGTGAGAGGGAGCCTGTAAAG GATGTTTCAAAG/G/AJAGGGTCCGGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG

WI- 21609a	42 C T ---	---	TCATGAATATGCAGCCTCCATAATCTCTCCCTTGTAACAA[C/T]GTGCAGTCCGTTACAAAGCTGT AAAAAAGCCCAACCCAAAGACATCACAAGAGGAAGAGCAGTGGCAGTGAGAAAGGAGCCCTGTA AAGGATGTTTCAAAGGAGGTCCTGGCTATGTGGCCACTGGATGTAGGCAGTGAAGTCCAGGC TTTCSGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG
WI- 22512a	104 T G ---	---	ACATTCGGAGCCAGTTTTTCCATATTGCTCCACTGCCTAAATCCCTTGGTGCTCCCTAGGGCTTCA GGGTAGCCCTGACATCATGGTCTTTGTGATCTGTG/JACCTCACCCATGTCTCCACCTNAGTTCC CACATTTCCCCACGCTAAGGGCAGGCAGCTACACTTGACTGCA
WI- 21028b	139 A G ---	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGTCCCTTTTAAAGGGCTCA CAACACTAAAGATTTCACATGAAGGGTCGTGATTGATTGAGCAATCTAGGGGATGTGACAGGGG TTTC/JGTGCACTGGTACAGAACACACAGGGAGTTTACAAATTTTTTATACAATGCTTGGGAAT CTACGG
WI- 21028a	121 A C ---	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGTCCCTTTTAAAGGGCTCA CAACACTAAAGATTTCACATGAAGGGTCGTGATTGATTGAGCAATCTAGGGGATGTGACAGGG GGGTTTCATGCACTGGTACAGAACACACAGGGAGTTTACAAATTTTTTATACAATGCTTGGGAATC TACGG
WI- 18829d	58 A G ---	---	ACAACATGCCTGTTACAGGGGGAAAAATCCTAGGNAATACTTATGTACTTCTTG/JGTTCAT TCATACAAGACAAGCACAAAAGCACCACCCATGCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI- 18829b	35 T A ---	---	ACAACATGCCTGTTACAGGGGGAAAAATCCTAGG/JAATAACTTATGTACTTCTTGATTTCAT TCATACAAGACAAGCACAAAAGCACCACCCATGCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI-20964	87 G A ---	---	AGCCAACTCAAGGCCAAAAAATTTCTTAATATAGTATTATGCGAGGGGAGGGAAGCAAGGA GCACAGGTAGTCCACAGAATA/G/JGACACAAAGAAACCTCAAGCTGTGAGGTCAATTTGTAAATTA AAGAACTACTAAGATTAGATGAACACACACTCAGAAATCTCTAGGAGAGCTGAAAAGAAAGGAAC AGATGTTAACAAAAACAAATTAAGGCTGCTGGGGAACCTGAGTCCATGTTAAGCTTG
WI- 20059a	59 T A ---	---	CTCTGAACATAAGGGCCGTGAAGGCATGATTGGTTTGGCACACAGAGTGGATAACCAAT/JACAT TGGCTGGAATGAGGTGTCAGGAAATAAANTGCAACAATCTAACACCATTGTTGAAATCATGTCTGA GTTCTGGAGAAAGTTAAAGTGTAAATAATTACAAGAGCTGACATGCAACTCTTTACCTTACATTATT CATCTACAGACTATTTTCTCCCTAGGAGATGAGGAGTATGGCCCTTAGGT
WI- 22130b	165 C T ---	---	TGTTTTGAGGGCTGTAGCAGACTACATAATGAGCGGTGAAGGGCTGCCCTTCCCTCTCCTGACAC CAGCAAGGGGGAGGCACCATCACCGGCCCTGCCCATCATGCATCCATGATTACTAGCAGTAGGAA GCCAAGGGAANAGGACCCCGCGCTTGCTC/JGTGTTTAAATCCAGGTTAAGCTATACACGTTTAA ATACATGTCGGAGGTTACATGGTCTCATGCACTCCCTGTGATGGGAATGAC

WI-21661	117 G C ---	---	---	GCCTTAGTCTCCACCCCTTTAAATGTACTCTAGGTACAAAATAAACATTATACACATATAAGATCAGT CTTTCCAACCTTTAGAAATGTATAAATAAGAAATGACATTTTAAATAAAATAAG/CJTTAGTCACAGTC ACACAAAACCTACCTTCTAAGGAAAACCTGCCAGTGAAGCCGTAAATTTGTCTTCAGCTATGAAG GA
WI-21980a	25 T C ---	---	---	TCAGTTAAACACATTCATCAAGGAT/CJAGATTAAATTAATGTGAGGTGAGCATAAAAGGGAGATTAA TAAACCAGAAAATGTGTTTCTGGGAACCAAGTTTCAAGTGACTCAGGATAAGTTTATTAAATTCAT GGGTGAAGCCCTGGGATAAAG
WI-21636	71 A G ---	---	---	TGCTTGATTAAATGTGGTGTACATTATCCTATTTCACAGATGGAACAGAAAATACCAGCTTTTTT AAA/A/GJTAGCAATATCTATTATTAATAAATAATTGAAATAACACCATATAATATCATAAGGA AGTAATCTAATGTGTGATTTCAGAGGGGAGAAAACATTACCTCTAGAGCTGAGGCTATTGTGC TCATGCAAACTCCAATCTGAAGGTGGTAGAACTAGGAAGGGACAGGGATTTC
WI-22457a	112 G A ---	---	---	TTGCTATAATTTCTTAAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAAATCAGCTCATTAGA CAAAACAGTAAACATCTGGACACGGTTTCAGGCATGAAGGATACAG/AJGAGTTAATTAACATAAG GAACAGAGTCCCTGCATTCTGAAGCATAGGATGGGAAACAGTAATGCAGATTAAATACCTGGGGCC AAAACCCACTGAACCTACCCAGCTGAAACACACTGAAGGATAGGGTAAGGA
WI-21524b	97 C T ---	---	---	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATAGCCTGATGACGACCTTCGCGTCATACCTAT AATGGTTAATAACAGCATTCCTGTCTACCC/CJTGATGATGCTTCTCTGCAAAATGGACTATTTGCC CAGTTGCAACAGGGCTAAGATTGTGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTCAGAAAAGATTCTTGACTTTCTCCAAGTTACTTCCTCCAGGGGATG
WI-21524a	35 A C ---	---	---	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATG/CJGCTGATGACGACCTTCGCGTCATACCT TATAATGGTTAATAACAGCATTCCTGTCTACCCGATGCTTCTCTGCAAAATGGACTATTTGCC CAGTTGCAACAGGGCTAAGATTGTGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTCAGAAAAGATTCTTGACTTTCTCCAAGTTACTTCCTCCAGGGGATG
WI-22552a	32 G T ---	---	---	TTACCTTCCAAAACCCAGGCCACTTTGGAGAAAAG/GJGAGAGAAATGCTATTAAATCAATAAGCCAAGAC AATAGGGACTACCTGGGGTAGACCAAGATGGGAGTCACCATACACCATCTCTGCCACAGAACCC TTTGACATGCTGCCCTCCCTACTCCGCACTCACCTGTCTAATTGGGACCTGAAGCTTCAGCATCCCTT CTTTAGGG
WI-21703d	197 A G ---	---	---	CAACAGGCTCATGGAACAGAGCCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGGAGGGCTC TGCAATCCCTTTCTCAGCAGACAGCACCATTCTCACCTCTCTGGGAAAGCAGCATTGGAGCCTACACCA CTTGCTGCTTTCTCACCAGGGTAAGAAATGCAGGATTTGCAGAGGGGAGTGAGTCTGGGA/A/GJG TGGGCAGAGCAGACTAGGGCAAGGACTTAAGGGAACCTTGTTGGGGGAAGAG

WI-21703c	134 A G ---	---	CAACAGGCTCATGGAACAGAGCCTAGGATCCAGGATCAGGAGCATAGGAGGTGGTGGTCTGGGGCAGGGCTCTGTCATCCCTTCTCAGCAGCAGCACATCTTCAACCTCTCTGGGAAAGCAGCATTTGGAGCCCTACACCTGAGCTTGGCTGGCTTTCTCACCAGGTAAGAAATGCAGGTATTTGCAGAGGGGAGTGAGTCTGGGAAAGTGGCAGAGCAGCAGCTAGGGGCAAGGACTTAAGGAACTTGTGGGGGAAGAG
WI-22663c	139 G A ---	---	CCCTTGTCAGTGTGCTCGGCTTCTACTGCTGCGAGGTGAGCCGGCGCTCGCTAACTTATTTCACAGTCTCGGTGAACATGGGTGAGTCTCTCCGGCTCAGTGTGGGTTTGCACCTGGTGCACCTTACAGGC/GA/GAAGAGCTTCTCATTTGCTGAGGGCTTTCTCGAATCCGCTGTGAATGTGGGT
WI-22663b	55 C T ---	---	CCCTTGTCAGTGTGCTCGGCTTCTACTGCTGCGAGGTGAGCCGGCGCTC/GTGCATAATCTTATTCACAGTCTCGGTGAACATGGGTGAGTCTCTCCGGCTCAGTGTGGGTTGCACTGGTGCACCTTACAGGGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTCTCGAATCCGCTGTGAATGTGGGT
WI-22663a	38 C T ---	---	CCCTTGTCAGTGTGCTCGGCTTCTACTGCTGCGAGGTGAGCCGGCGCTCGCTAACTTATTCACAGTCTCGGTGAACATGGGTGAGTCTCTCCGGCTCAGTGTGGGTTGCACTGGTGCACCTTACAGGGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTCTCGAATCCGCTGTGAATGTGGGT
WI-22668	99 A G ---	---	TCCTTTATCTGCTGCCTGCCTGAGTATCTGGGAATCCTACAGGATTTGAGGAGCCCTTGGGATCCAACTTAACAAATAGTTTTCTGTAATATTA/GJTCTAGTCCATTTAGATTGTGTAATGATCTAAATGNGTAAACCATTTAATATCAAAAGTATAACAGCATTTAAGTCAGCTTTTCGAAAGAACTTTTATTTAAGATATAGTGGCAGGACAAGATTGGTCACGAAATCTGGCTTCAGTGTGAT/GJAGCACCAATTTCAAGTTTTAGGCAAGGATTTAACCTCTCAGGCTCATTTCTCTTTTGTAAAAATTTGTGATAATGGACCTATGTACCATCATAGGGGTACTTGGACAAATCAACTGAAATTTTT
WI-22631a	52 T C ---	---	AATCCACACTTTCACGGAGGGGGACCGCTGCCATGTCTGCCAGGCTCACAGAGCGGGCGGTACTCTGCTGGTGGTTTGGTGGCAGGTGGAGATGGTGACGGCGCATGGAAACCGTAAGGCATGACAACGGAGGCCGCGGGGTGTTTCAG/GTJCGGTGACGAGGTGATGGCTGGCAGGGCGCTCTACAGAAGGAGGAGCGCAATTCACAGCCTCTTGACGTAGTTTCCGGGGAAAGTACC
WI-20258	157 G T ---	---	ACTACACATATGCTGATTTTCAACAGTAAAAATAACATTTTACATTTGTAGAAAAATCTAGGGTCTACTAAATAATCTAGTACTGTTTCCACTCTCCTGCTAACTGTACAGGAGTGTGTGGGAAACGGAAGTCTGAAAAGGATTCAAAGGGGCTAGGATTTGCCACAGATCTCTGTAAGGAAAGGATGAGGTGAGCTTACCAACCCCA/CJAJTGAGTAGGGGCCAAACATCCTTAACAAGCTAGTTGCT
WI-22714	212 C A ---	---	TGGGGCTACTTTAGATGGGATGGCGTCAAGGCTCTGGGAAGGCCT/GAJTCTTAGAAGACATTACCCAATATGATGAGAGCAGCCAGTCTGTCGAAGCCATAGTTTGGATGGCGAGACTTTTCCGGCAGAGGAAATAGCAAGTGCAAAGGGCCTGAGGGAGAAATGAACCTTGGGCTTGTCTCTACAGGTTGAAGGGCGCCGTTGGCTGAGGTTTAGTGGATG
WI-22734a	44 G A ---	---	

WI-22724	117	A G ---				TGATATGATGTCTGAGATTGCTTCCAAATATGCCTAGGAAGGGAAAGTGTTTAGAGATATAGGA CAAATCAAGATTGTCAAAATGTATAGTAAGTGTAAAGCTTGCTAAGGGT[A/G]GTTATTCTATTTT TGGGATATGTTGGGAAT
WI-22750	48	G A ---				TGTAACCTGTGTTTCTGAAAGTTGAGGGAAAGCTGAGGCAGCTAAT[G/A]GGCTCATACAAAGGT TTGGAAGACCAATCTGACTACCTAAAGGAGAGTCAGCATTTCTGACCATTCTGACTGTGCT
WI-22775a	60	A G ---				TGCTGTTTCTTTAGTTTCATGACGTTTATCACAAATGTGCTACTGTTCCTCATTTTACATC[A/G]TAGTA GGAAAGGGAAATAAATCCCTAAGGGCAGCAATAATTTCTGCTTTTGAATCCTTCATTTCAGGCCAAA TATTTGTTGAGCACCAAGGGCCAGATGGGAAGTGGGTATGTAGGTGTTGGGAGCCAGGAAGGAAG GGT
WI-22808	143	C T ---				CTTAGCTAATGAAACTGGCTATGTGGACTATGATAGACCAAGAAAGCTACCCAAAGTCCTGAGGGAG CCTAGTCTCTCTAAATGCAGACAATGTACCCATGACAAGGGCTACAGCTTGGCTTTAGCAACCCAGGA GGATGAAGA[C/T]AGCAAACTGATTAAAGAGAGTAGGTATAAGAAACGAGGAGAGTGGGGTCCAAAT ATC
WI-21016	207	G A ---				TCTCTGTGTTGAGCCCTCATCCCAACCCCTCCAAAGCCCTCATGCCCAACACACCCGTGTCACCAATT CCTCATCTCCCTGTCTGCTCCCATCTCAAGTCCAATTCGAAGCCAGAGCCCTGGAGCTTTTCTG GGACACAGCATGAAAGAGGGGAGTGAGATGGCAGAGATGGGTGGAGCCAGTGCCTGTGGGTC CT[G/A]TTGGCGTGGTATGTGGGGGCCAATCCTGAGGCCAGAGGTCA
WI-21031	31	C T ---				TTGAACACCTGACCTGACCTCTGACATGTGG[C/T]CTCTGGTCCCAATTTGTCTCCAAACGGTGGCACA TCTTCATCTTTGTTATATATCTGCAGGAACACTCAGTCTCTTCAGAGCCGAGAAAACACACACA
WI-21314	122	A T ---				CCATATCCAGTCTCTTTGAAGCTTTCTATTGACTTTATGGGTTCAAGTTATATATATCCTTTATCACTAT GACTTTCATTGATTTTATTTATTTGTTTCTCCATTTCTCTGCAAACTTTTC[A/T]TTTGTATTATAA ACTGTTTCTAACTTCACCTTAATCTCTATCTGTTTCTGTTAGTTCCTGAACTTCTTTAGAGG
WI-21186	95	G A ---				AGCGAGCATCAGAAATCACCTAGAGGGTTGACTAAACAGACTTCTGGACCCCAACCCCAAGAGCTTCT GATTTCAGTAGGCTGAGGTGGGGCTTAC[G/A]AATTAGTATTCGAAGACCTTCCTAAGTGTTCGAG ATGCTGCTTGTCCCGGGGAACACACTTTGAGAACTATTTCTTAAATGTTCTCTCTCTCTCTTTTAA GGAGAGACAGGAATCCAGAGAACTGCTAATTTAAGCATATGATTGAAT
WI-21187a	94	A G ---				CCACGATAACTATAAAGCAGAAAATTAGCTTTGAAAATCAAAATACATATTTAGTAACACACACATT CATTTTATAAACACACATAAAGACACC[A/G]GGNTCTCAGTAATGCTCTAGTCCAGGGTTCTCAA AGTATGGCTTCAGACAAGCCCAATTTGCATCACCTAGGGGAATTTGCTAAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAAACTCTGAGGGTGAGACCAGCAACCTGT

WI-21190	39 T C ---	---	TTTTCCCCACATACCAATGCACCTGTTTGATATAAACTATTT/CJGTGGGTAAAGCCCTCTTTGGAGAC CAGTGACATAGACATGATCCCATTTATTTATAACAAATAATTTAATAATCTGTACTATTACTGC TTTAGTTATCTAGTTTATTGAGAAAGGAGAAGTCAGCATAGTTTATTTCCATGTAATAAAGCTT AACACA
WI-19937d	186 GA ---	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAAACTTTGGAAGGAAA GAACTATTGCACAACCAAAACATTGTACATACTGATTTAGACAAGCAAAAGCACTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTCTCCTCAGCAAGTC/GATGCCAAACCTTC CAAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-19937c	185 CT ---	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAAACTTTGGAAGGAAA GAACTATTGCACAACCAAAACATTGTACATACTGATTTAGACAAGCAAAAGCACTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTCTCCTCAGCAAGTC/GATGCCAAACCTTC CAAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-21117b	227 CT ---	---	GAAAACGGGGTGCTAAACAAGAAAGTCTCAGATCCCACCTGAAATCTGTTTCAGTTTCACAGGCTC TCTCCAGAAAAATGCATATGTACCAATTTGCATGTACAAATTCAGAGCCTTCAAATACATTCCTGGGG TCCAATCACATACCTCAGGTTCCAGCTCCTAGCTCCCAATATTCCTACAGTTCTGAAGANITAGCAGT CCTCTCATTTCTACAGTCTGTATTTCTTCTACTGAATCTTGGTGGGAG
WI-21122a	42 CT ---	---	TCACCTTTGATCATAATCCCTGTAAAGCTAAAGTTATTCATC/TJTTAACAGGAACTCTGTTTTCC TTATTCAAATGTCACAAGCCTGACGCTTACTGTACATATTGCTAGCAGGACAACTGGAAATACT AAACAATACTGGAAATTCACATTACAGACAGACGAAACCAACATGGGATGCCACACATAACTTCCT TTGTAGGTTTCACAGAGAGCCTATTTGTGGTTGCT
WI-21254	53 A G ---	---	CAGTTTGTACAGGAAGGGCCCATGAATGTGGGCGGAACCTATCCACAGGAG/GJCAAGGAGAAG CTGTTCTCTGG
WI-21054	23 GT ---	---	AAGGAACTGCATGGGTACAAATG/TJCCAATTCATACTTAAACAGGTGGGAAACGGGTCACTCT TGGCTGCTCCAGAACAAAGGGCGAGTCTATGCACCTCTG
WI-21059b	181 TC ---	---	GGGACCAGGGTAACACCATAGCAATATCCGTTATCAGCCCTTATCTTCCCACTGAGCCTGGCTGAA CTACAGCTGCCAGCATTCCTGGGCTTGCAATTTCCCACTTCGTCACATCTTAATTCAGCTGAAA AATCCTGGGGAAGAGACATACCTCACTGAAGTCAATTCCTATTC/TJATTTAGCCAGGGGCAAAA TGAGATTAGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT
WI-21059a	63 CT ---	---	GGGACCAGGGTAACACCATAGCAATATCCGTTATCAGCCCTTATCTTCCCACTGAGCCTGGCTG/TJ GAACTACAGCTGCCAGCATTCCTGGGCTTGCAATTTCCCACTTCGTCACATCTTAATTCAGGCTG AAAAATCCTGGGGAAGAGACATACCTCACTGAAGTCAATTCCTATTCATTTAGCCAGGGCAAAA TGAGATTAGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT



WI-20442	37 T C ---	---	---	TCCACGTGAAGGAAGAAAAAANGGGGGGGGCTT/CJTAAGGTGGCACAATTTTAAGAAAAAT ACCATCCATTTTCTCAGTCTAATCTGAATCCATACATTAACAAAAAGTCAAGTGATGAGACGAA CA
WI-21235	43 T C ---	---	---	GTGACAAGAGGTGAAGCAAGGGACAGGGGCAGCGAGTC/CJCTCGGGCCGATGTTCCAGGG CAAGCTACGTA
WI-22012a	57 T C ---	---	---	ATCAGAACTGCAATCTGCACATGAAAGACCTGGGGGAATGCCTACATCTGGAATTT/CJCATTA ATCAACGTTAAATTTTGCCGACCAGTTCTTCATTGCTGATCACTTTTGATAATGACAGATCCAACAT GAAACTCCTGAAGCAAAATGAATTTACCTTGCTTTGCTTTCATGCAAAATTTAGGGACCAAACTCAAAAGG TTTCATCCATGCTGGGACACCAAGATCTAAGGAATTTGACAGGGATCTCT
WI-21149a	167 G A ---	---	---	AGGACCTGCTCTCACACGTTCCCTCACCCACCAGCTTTTGGCAAGATAGTTGACTAAATACCCT AAATAGTGGCTTTTCTTTTAAACAATGACCTTATTTATCTTTTAACTTAACTGAGTCTTATATA CAGACCTGCCCACTGGAAGCTTTTACACGATGCTTCAGAAATGCGGCAGTATTGCACAATGGTT TGGGGCAGGTTCTGTGTTAAACATGGGATGGAACCCAGGCTCTACCTG
WI-21376b	188 A G ---	---	---	GGTGCAACTGGAAATAATGGTTTAAAAACAGGATAAGCATTAAAGAAAAACACTTTCAATGTGTC TTCCATTTGATGAATTTGTTTCTCTCTTTATCCCCGCAAGTGGAGTTTCATGTCCTCGGTGAACCA GACAGTGTGAATCTGTTCCAGCCCAAACTGACAGCAATAGGGATGAGTTCTC/WGJGAAGTGATTCT GAACTGAGCACGCACTCATGCTGCTGAGGGGAAGTCTGGGGAGAAAGAGCCT
WI-21382d	125 C G ---	---	---	CCATTGCAGTCCAGAGATGAGAACTGGACCAGAGGCAATCATGAACAGAGGGAGTCAAGAGA AGGGGTTTCTAAGATGGAGAAGTGGGGGGGGTTTGGATCCAGTGGGATNTGGCTTCOC/CJGAGGTT GCAACCCCAAGGAAGTCTCTGGAAGCAGCACCACTGCTGATGGGGAGAGAGCTGCCATCCTC AGTCAGGGTCCGAGTCAGGGTCCGAGGAGAGCTGCTGCTCCATAGTCTCGCAC
WI-21437a	201 G A ---	---	---	TCCCTGAGGTTGGAGTCTAGCATAGCTCCCTCCCTCAAGAGGGACAAGGGGTCAGGGGSCAGAGC AAAAATCCAGTCTGCTTCAACCACGGAGACTGCCCTTTGGGATGGAAGTTTCTGGAGCTCCCTCCATT CTATTCTGTGGGGCAGGAACATGCCAGGGCTGCTGTTAAATGGCAGGGGTACCTTTACAGGGGCG /AJCAGGCATAGTGTGGCCCTGNCCTGCCCTGGGGGCCACCCCTGGGAACAGT
WI-21202b	156 A C ---	---	---	CAAAATAGAAATCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTTGATCT GTTTATGAACATGATTTTATAAAATGGTCACAATATATTTTAACTTAACTGATTATTGAGGG AGGAGGAGAGAGTTGACCAAJ/CJGTCTACATGCATAGACAGTCTCTAAAGCGTATCTCAAAACATG A
WI-21202a	61 T C ---	---	---	CAAAATAGAAATCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTTGATGA TCTGTTTATGAACATGATTTTATAAAATGGTCACAATATATTTTAACTTAACTGATTATTGA GGGAGGAGGAGAGATTGACCAAAAGTCTACATGCATAGACAGTCTCTAAAGCGTATCTCAAAACATG A

WI-21627b	153 A G ---	---	GCATGAAAGAACTCCAATCAGACTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTCATTATGGATATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAA[A/G]TCCAAAGTCATCTAATAATTAACCATAATTTACATAAATTTGTAGG GACAGTACTAATACTCTACAATAAATAAGGGTTTAAAAATGTGTGCTTA
WI-21627a	106 A G ---	---	GCATGAAAGAACTCCAATCAGACTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTC[A/G]TTATGGATATTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAAATCCAAAGTCATCTAATAATTAACCATAATTTACATAAATTTGTAGG GACAGTACTAATACTCTACAATAAATAAGGGTTTAAAAATGTGTGCTTA
WI-21399a	75 C T ---	---	GGATTGAGTCCCAACTGATCTCAAAATTCACCTTCTTGCAATGTAACAAGCTCATTCCTCTCTAAAGTT TCAGTT[C/T]TTCACCAAGTAAAGGAAAGGTTGGACCAGACATGTTGGACCGTAATGCTTGGTAA CTGCCCTCTGCATTTGCTCTGAGGTTGTGTCCCTAGGACTAGGTAGGATCTCTCTTCTTCTGCC TTACCTAGGCATAGTGCCTGATAGCAGGCTGAAGCCCAATTCATCTGT
WI-20328a	68 G A ---	---	CGATGCTGCTAAGATAGGAGGTTAATCTTTACATGGTGAGTGGGTCACAGACACAAGACATCAAT C[G/A]TCTGTAGCAGCGAGAGAGACACTTTAAGTTGCCCAAGAGTACAAATCCCACATCTATGAGAC AGCAGTGTGGCTTCTTAAAAACAGTAAACCAATCAAAAGAAAGATTAGAGGTTTCAGACATT AGGAACAANTGTGGCCAGAGATACCACAGAGCCCTTGAAAGGAAAGGCCCTCACT
WI-21249	155 T C ---	---	TTCTGGCATTCAAATGTACATGTAATAATCCAAATTTAACAGATCAAAATGTTACACTAAGTTTCACCT TAGTATCTAAGTATCCAATCACAATGTATCTAAGTTTTCACTTTAAAGAAACATTATAAAGGTAATT AAAACTCTAGGTGTATACCTTA[T/C]ATGGAACCTAGTTTATTTCCNATTTAACTACTGTTTCATTGGGTA AAGTATGTTGTCCCAATTTTCAGCTGTTTTAAGGAATTATAAACATTGAGA
WI-21504	147 C T ---	---	TGACACAGCATCAATTTTCATGAATACCTTTGAAAGGGGCCATTAGAAAAATAAGAGCCAATTTGGGTC ATTTGAGAAACATTTTCAGCACAATTAACAGTGGGGCAGCGGCCGTTCCGCTCCAGCTGGGTTTCCCC AGATGCAACAAT[C/T]GCGGTTCTGGCTTCTCCACTGGTGGGATCGCGGCTCGGAGCTCT CAGGG
WI-21242	115 G A ---	---	CTGCACCGGGAGGACAGCTGCTGGCAGGGACTAATAAACCTTCCACCTGGCCATGGTGGTGTGTT CTCTATGGACCGAGGCCCTGAACCGCGGCGAGGGAGGGGCAGAGAA[C/G/A]CACTAGCTTGGGGGTG GGCACAGCTTCAGACCCCTT
WI-21475c	181 A G ---	---	TAGCCCTTCTGCCAACATCTGGCAATNTAGGCTGGGGTGGAGCTTGGCCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCAGGCTTCTCACCTTGCCTACTAAGCACAG CAGTCTGAAGCTTGGGACCTGGGACCTGGGCTTCTTGGAGAAGGCA[A/G]AAAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTTCCCGTTCTCCACCCTATTTCCTCCCTGAAG

WI- 21475b	117 A T ---				TAGCCCTCTGCCAACATCTGGCAATNTGAGGCTGGGGTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGCTCCAAACCCAGGCTTC[AT]CTTGTCTACTAAGCA CAGCAGTCTGAAGCTTGGACCTGGCAGTGGCTTTGGAGAGGCAAAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTCCCGTTCTCCACCCCTATTTCCTCCCTGAAG
WI- 20893d	207 A G ---				TGTTTGTGTTCCAGCCACATCTTCCAAAGGAACCCACCAAGCCCGTGTGCAGGCTTGCTGCAGGG CTGCTTCCGGCGTTAAAGTGTACTGAGGAATACAATCATTTGTCACGTAAGTTCATCACCGCACTCC AGCGTCAGGCCAAACCTTCCGTGGACCTGGGNAACCTGCCATTTCCTCTCTTTTACAAATGCAGT TTC[AG]ACATAACATTGGTAGAGTAACAACAACCAAGCCCAAGCCCTAAATG
WI- 20893c	179 T C ---				TGTTTGTGTTCCAGCCACATCTTCCAAAGGAACCCACCAAGCCCGTGTGCAGGCTTGCTGCAGGG CTGCTTCCGGCGTTAAAGTGTACTGAGGAATACAATCATTTGTCACGTAAGTTCATCACCGCACTCC AGCGTCAGGCCAAACCTTCCGTGGACCTGGGNAACCTGCCATTTCCTCTCTTTTACAAATGC AGTTTCAACATAACATTGGTAGAGTAACAACAACCAAGCCCTAAATG
WI- 19941c	71 C G ---				GAGCTCAAGGGAAGACCCCTTACCAGATAGGACTAACTGGAGGGGTGGAAGGAACAAGGTGAAA GGTAT[C]GJGTCCTGTTGAGACAAGGAGGGGGCCCTGAGAACACAGAGCAAGGTGGTTTGAG GGAGCACAGCAGGGTGCAGGAAGGAGATGGGGGACATTTCTATTCCAGTGCATGCCCTTAAAT AACTGGGTACAGGAGCATTTGGAAGGAGAGAACCAAGGACAGAGACAAGCG
WI- 21552b	166 C A ---				TGGGTACATGGACAGATGATATGTTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAATCGCATCTCTTCACCTCAAGCATTATCCATAGTGTACAAAGAA TCCAAGTATACTCTTGATTATTTAAAAATGTA[C/A]AATTTAAATTTATTTAGTATTAGTTACCCC ATTGTGCTATCAAAATATTCATCTTATTCTTTTGTAACTATTATTGTGA
WI- 21552a	66 G A ---				TGGGTACATGGACAGATGATATGTTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG [A]TAATAATTACTTCAGAGTAATCGCATCTCTTCACCTCAAGCATTATCCATAGTGTACAAAG AATCCAAGTATACTCTTGATTATTTAAAAATGTAACAATTTAAATTTATTTAGTATTAGTTACCCCA TTGTGCTATCAAAATATTCATCTTATTCTTTTGTAACTATTATTGTGA
WI-21512	54 C G ---				TCCTCGTACTTCATGCTCCCTCCCTGCCCAAGACCTTACAAAATATTTCTGT[C/G]TAGAGAGGGA AAGAGCTGGTCCCTGCTCTGGAGGCAACGTCAGGTCGGGGAAGGCACTCGTGGTCTGTGATCTGTC TCAGTGATGGGAGGTCTCCACTCGCCCCACAGGCAGCCTCGGGGCCAGAGATGAGATATGCTGTAA TCCAGTACAGGGGCTCGTGGGGTCCCAACAGCTCTCTTTGGGGG
WI- 21513b	192 G A ---				CACATAGTTTCTAAGAAGAGGATGAACCTGAAAACCTCCTTAAGGCAGGACAAAAGCAACTTTCATT ATCTTAGTTTAGACCAGAACTTTAATTTATATTCCTCTTTAACTGTCAAAATACACCAAATA CTTAGAGGAAAATATTCACAGTATACCAAAACATTTAAGATAAAGAGGCGAGTGA[C/G/A]AGTAG TATTCCTACATACCACAGTATACAATGATGCCTTCTGTCAGGTTTAGGAAC

WI- 21514b	133	C T ---	---	TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAAACCCCAATCTTCAAGGAAGAGGACACATTACCATGGAGC[C /TACAGGACTCGAAAGGACCTCAGAAAGCATTAGCCAAATCTCCTTATGCAGGAAATAAATGAGG ANTTTAAGGCTCAGATGGGTTAAGGGTGAATTTGCAAGGGTCATAAGGAACT
WI- 21514a	100	A G ---	---	TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAAACCCCA/AGTCTTCAAGGAAGGAGGACACATTACCATGGA GCCACAGGACTCGAAAGGACCTCAGAAAGCATTAGCCAAATCTCCTTATGCAGGAAATAAATGAGG ANTTTAAGGCTCAGATGGGTTAAGGGTGAATTTGCAAGGGTCATAAGGAACT
WI-22020	27	C G ---	---	ATGAAACATGTTGCAGTGGGATGAAT[C/G]TTATCATGATGCTAAGTGAATAAGCCAGACACAAA AATCCAAATGATATCTTCTACCTGTATGAGGGTACTT
WI- 19576a	113	A G ---	---	TTTCATCGGTTCTTAATACAGTACAATCCTTTTGTGAACAAAAGTCACACTGGCAATGATTATTTACA GATCCAAAATAGACTCAGGCTTCAGACATAAAAAATTAACATTC[AGTCTAGTTCAGTGATTAGT CACAGAAATTAACATCTGCCAGATGTACACAATTTGGTAAAAACTACAGCTTCTCTCCACGGGA G
WI- 21695a	141	A C ---	---	ATACACAGGCCACAATTGCAGGATGGAAGGCAGTGGCACTTGGAAAGTCACTACACATGGCAATA AGCAGCCTATCTCTTACCAACAGAGTTCTTGGGSCATGTGATGGTAGGCCAGACCCCTTTCCAA GGGAATA[WC]TACTACACTAAGCCTACACTGTACTGTGAGAGTCTAGTGGAACAAGGCCACAGGC AGTGGAGGAAATGTGATGACTTCACTGTGTTCAAGNTTCTAAGGCCCAGCAT
WI- 21574a	235	C T ---	---	AAACCCAGAAATTTAGGTACTTTTGTATTATGAGGAACTCACTATACTAGGAAGCAACTTATGAGTG TGTAATATTTGATCTAGCAGCAACTTTCCACTGATCCTGGCAGGTGACAGCTCTCAGTGAACAGCGC TCATCACCTAAAGTGAGAGGCTGTCTATTCTCATTTGTAATGTCCCTCAGAGTCACTAGGGAGCCATT GGCAGGCCAGGGAACCTTACTGCCTACTTCC[TC]TGTCTCAGGTGGGA
WI- 21644c	151	T A ---	---	TGACTGCCAAGATTTAGGCCCAACTTAGGAGCAAGGTCACCTCTAACCTTTAGGAAGTCTTGGGT GTGACCCACTGCATAAATGGATTTTCCACCATANTATTTAACAGACTCAAAGTGATACATAACAAGCTTG TTTCATAAATAAGGGAT[TA]TTCAATCAAGATCCATGGAATGATGCAGTTTAAACATGTGTTCTCAGC TTGCCTACTGACCACCTTTCTCTTCTAAATATGGCAACAGCAGCAAGTC
WI- 21614b	55	G A ---	---	TGCTTTAACCTCAAAAGTCCAAATAACATATAGACATTTTGANTATAGCTATC[G/A]TTTTAACA AACCTATTATGATCACTGTTGCAATTTTCAGTCACCTAAATACGGAACCATGACTATTATAAACA TTTACTGTGTGGGTTTGTGGGACTGAACATTAACCATACGTGTATTCTAAGGTACTAGGGAGTT GGAACAGCTACTACGGGTCAATGGTATTTTGGGCAAGTTGGCTGTGTGGG
WI- 21615b	151	C T ---	---	GACCGAGAAAAAAGTGCAGGCAATGATGTTTGTGGAAGTACATGACTATTTCAGCTTATAGA GAACTTGCAAAAAAGTACAAAGATGGCTATTTTAAATTCATACATATAAGATAAGGATGGACT CTTTCAGTGAGTATT[C/T]AGGACACAATCGACGGATGTAATCTATTTGANTTATACCATAGGCC TATTCTATATTGGGCCAAAGGGAAGGTAGGATGGGTACTGTGGAAACGGA

WI-21981	61 T A ---	---	TGTCATCTCATTCTGGAGAAATCATAGATGTGGCAGAAATACATATTTCTTGAAGAAAAAAATTA[AGT CTCCCTTATGGTACTGTGATTTCATAGGGTGTGGGTAAGTACATGACAACATGCATGGGATAGA CACTCTGTTCTCTACAGATCCGTCTTTGGGAAATTACAGGAACATAAAGGATATAATGGATGGGTT ATTACTTTTACATGTGGACAATCTAGTTGTAGGCGTTTAAGGTTAAATTTGG
WI-21660	120 C T ---	---	TCCCAACTAGCCCTCTCAGTATTTAGATGAGGATAGAACAGATAGCGGTGTAACAGCCCTCTCCACTGCT TACTGTGTGTACCAAGAGGCGAGAAAGCAGCTACCCCAAGCCTAACCTGGCC[C/T]GTCTTTTCAG GCTTCTCAGGATGCCACAGACATACTGGGGAACCTGGGATGCAGGGAGAGCCAGGGTCTGTCTTC AGGAGGGTACAGC
WI-19105c	211 C T ---	---	TGGAAAGTAGCCCTTCTGGACAGAAAGAAATATTTGTGTCCATGTGGTTGAGTCTGTTAAGAAGGA CACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGAACCTCCTCTT GTCTGAGGTTTCCAGGGCTGGGCACAGAGGTGAGGGCAGAAATTTGGGGTCCAGTGGATCTCCCC ACAACTTC[CT]TCCAGGGGCAGGATTTCCACCCAGGGCCCAAGGGTCCCCG
WI-19105a	33 T C ---	---	TGGAAAGTAGCCCTTCTGGACAGAAAGAAATATTT[CT]GTGTCCATGTGGTTGAGTCTGTTAAGAA GGACACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGAACCTCCTC CTTGTCTGAGGTTTCCAGGGCTGGGCACAGAGGTGAGGGCAGAAATTTGGGGTCCAGTGGATCTC CCCACAACTTCTCTCCAGGGGCAGGATTTCCACCCAGGGCCCAAGGGTCCCCG
WI-21760c	81 C A ---	---	CAAACTAGTCACTCTACTGATGCAAAATGATTGGAGGTGTCTTCTAGCTTTACAATAAGNGGAGG GACCTCTGACTGCA[CT]CCTCTGTCTCAGTTTCAGGGCA
WI-21760a	35 A G ---	---	CAAACTAGTCACTCTACTGATGCAAAATGATTGG[AG]GGGTCTTCTAGCTTTACAATAAGNGG AGGGACCTCTGACTGACCCCTCTGTCTCAGTTTCAGGGCA
WI-21569b	198 T C ---	---	TCTGCCATATTGTTCCAGCACCACTATTACTGTTATTTCTCTTTGAGGAAACCAGGNATTAAG AAATCTGTTTGAATTTCCATGATGCTTAACTATGTTTAAATCCTTTTCTTACCAAAAAGGA ACTTCTTAATCACCAGAGAAACAGAGGGAAGACTGAGATATGTTGCAGAAATTTATCTCTACT[CT] AGAGACAATTCATAGTTTCAATATCTTTCAGGGTTGTCTTACTTGGGGGGC
WI-20934a	72 T G ---	---	CCAAATGCAACATAGTCTTCTATTCTTAAAGTACATAGTAAGGTATGAAAAACATTTGTATTCA GAGAA[TT]GTCTAAGACAATGTGCAAAATTTCAATGGCCTGGCACTAGTGGTAATTCAGCAGAC AAACAGCATGAGAAAAGGCCGGGAGACAGTAATAAATACGTGCCCAATTGCAATGAGTTACCCAATC AAGCCCTTTTACCTCTTAAGATGGCAGATTAGAAGACCCCTTTCACAGGAGA
WI-21561	55 T G ---	---	TTTCCATTTTATTCAGCCGGGCCATCAGAACAAATAGCATCTATACCTTCGAACCTT/GICCTCTTAAC CTCTCCAGGCAAGAAAGGAAAGTATGATCATATTGATTCCTCAGAAATGGTGGATCTCAAGACTT TTTAGAAAGTGCTTATTAAGTATAAGAGGCTTGAATATATGATGATAAATGGTAGCCCTTTCTGGA AATAATTTTGTGTAATCTGTTTAAAGATTTTGGATGCATTTGTCCCCA

WI- 21961c	200 T G ---				AGCTTGGCTTGAAATTTGGGTACTTACTACCTTTGCAATTCTCTTTATTTATTTATTTATTTATTTATTTATTTATTT TTCCGTAAGTATTGGGTACAGAGGATTTTGGTTATAAAGTCITTAGTGGCGATTTGTGTGATTT TTGGTGACCCCATACCCAAGGAGTATACACTGCACCATACTCGGTCTTTTATCCCTCGCCCC[T/G/C] TCCCACITTTCCCTCAAGTCCCAAAAGTCCATTGTATCATTTCTTATGC
WI- 21961b	73 G A ---				AGCTTTGCTTGAAATTTGGTACTTACTACCTTTGCAATTCTCTTTATTTATTTATTTATTTATTTATTTATTT TTCC[G/A]TAAGTATTGGGTACAGGAGTATTGGTTATAAAGTCITTAGTGGCGATTTGTGTG ATTTGGTGACCCCATACCCAAGGAGTATACACTGCACCATACTCGGTCTTTTATCCCTCGCCCCCTC TCCCACITTTCCCTCAAGTCCCAAAAGTCCATTGTATCATTTCTTATGC
WI-21956	26 T G ---				CCCACTGGGCTCTTCAAGTGAAT[ ]G/TTCCTTCGTCTGTTCTAAAGCCCTTTTAAAAAGAACIT TCCATTCCTGTCTGAAACTTGCCTTAGTCTGTTTTCTGCTTCATGCCCTCAGTCGAATCTTCTCTT CTGAGCGGCAAGBACTGAAGTCTGTGGACCTGTAGGGGTTCGACGCCGTAACTCAGGGTAACTC CTATCTCTCCACCSTAACAGAGGGGTACATTATGGGGTCCAGGTT
WI-21966	148 G A ---				C AAACATACATTATGGCTGCCCTTTATTTAAGAAATGTTTACTGAGAACTCTGTACTGTAACAACATAT TTTTGTAGAAGCATGAGTGAGAGTGTGTGTGTGTCGCGCGCGGCACGGCATGGCACATGAGG GGATTGCAATGGG[G/A]ACAGGATAAAAAGGTATAAAAACTTGGTCCGAAATCTTTGCTTATTAAAC CTTGGCCCTGCTCCTCACAATGTTTCTACACTTAATTCTAAGAGAGGAGTAGA
WI- 21930c	146 G C ---				TATACTGGTTTTTGGTTACATGGATGAATTGTCTAATGGTGAAGTCTGAGATTTTAGTGTACCCATCA CCTGAGTAGTGTACATTTGTACCCAACCTGTAGGCTTTTATCCCTTACCTACCTCCACCTCCCAT TTT'GAGTCT[G/C]CATAGTCCATTATACACTGTATGCTTTGCATACCCATAGCTTAACTCCC
WI- 21139a	165 T C ---				GCTCTAGTGAAGAAATTCAGGACGGGTCTTCAAGACAGAGGGCTTGGTTCAAGTCCCTGTTCTGCGCA CTTACTAACTGCATGACCTTGAGCAAGCCACTTAATTTCTCTGCTCCTTCTCTGTGAAATGGGTACAA TGTGGGTGACGAGTAAAGGAACATAACAT[C/G]TACAGCACCTTCAGCACAAAAGCCTGGGCACACAG CACTGCGATGGAATACACAGGTAAACATTTTAAACAGTGGGACAAAATTTTAAAGTACGTGGCGAGC TGTTGGTTGCTTTGTGGTCATTAAAGACAAATGTTAAGANTCAGGAGTACTTAAGTCTAGTGGTTACA AATTTGTTCTCTTCAGTTTTTTCATTAAGTAAATCTTAATAGATGATATACATATTTACTGCAGATAAA ACCATCATCAGAAA[G/T]TATTAAATTAATTGCATATTTTGAGGCTACTCT
WI- 20317b	217 G T ---				CAGGACTTGGTTTGTGTCGCCCACTGCACATAAATGTCCTTTTTTGTGTGAGTATTGGTTGTGTGCG TTTTCTCTTTTGCATAAGAAATATGTCCATTTAGTCCAGAGGCTCTTGTCTTTATCCGGATGACGGAGG GTACACGGGGCGTCCGTCAGTTCGCCGGAAGGACGTATTC[G/A]CTGAACCTGGGACGAGTCTACTCT CTCCCCACAGGAGCCACGATTCAAATCCTCTTTTGTGTCGAACCTCT
WI- 22082e	179 G A ---				

WI- 22082b	67	CT ---	---	CAGGACTTGGTTGCTGTCCCAACTGCACATAAATGTCCCTTTTGTGTTAGTTATGGTTGTGTGIC /TGTTTTCTTTTGCATAAGAAATATGTCATTTAGTCCAGAGGCTCTTGCCTTATCCGGATGACGG AGGTACACGGGGCTCGCTAGTCCCGCCGAGGAGGTATTCGCTGAAGTGGGACGAGTCTACTC CTCCCCACAGGAGCCACGATTCAAAATCCTCTTTGCTGCAACCTCT
WI-20993	139	A G ---	---	AACACAAACTCCATGCTTCAAGATTCCACACCCAGATACTAAGACATATTAAAAATTACAGCAAT TAAACAGTGTAGTTGGTACAATAACACATATAGCAATGATACAAATTAGGGGAAAAAACCCCTGG GCTTCT/A/GTAAACAGTGAGTATACATTAAGACAGTATTGCAAGATGGCTTCAGGATTAAATTTGA TTAATTTAGAGAGAGCCATTTCAAGGTCTCCTAGCTCATCCACACACATCACC
WI- 21723b	125	A G ---	---	AAGCGATTTTATTAAATTGATTGGACATAGTGGTCAAAATAATTTTCTGAAGATAACAATTA TGGACTTTAAAGCTCGACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTTCCCA/A/GJCAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAACCTCGGAAATC ATT
WI- 21723a	82	G A ---	---	AAGCGATTTTATTAAATTGATTGGACATAGTGGTCAAAATAATTTTCTGAAGATAACAATTA TGGACTTTAAAGCTG/AJACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTTCCCAACAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAACCTCGGAAATC ATT
WI-22132	99	T G ---	---	CAACAGATGCTTGAGCCAAAAAGCAACATAGGCAGAAATACAATTGAGAATATCTTCATGTTTC AACCTTTAATCTGACTTGCCTTTTACTATCCTTT/GJCCCCATTTCTCTAATCTCTTTGCCCTTACAA TATATTACCTTCTAGGTATCACTCATCTATAGGAATGCCCTCTAGTTTAAATGCTCCTGCCCAACA ATACTAACCCATTGAAGGATAACTATGGAACCTTTAAATGGGACAGTGGG
WI- 21006a	106	A G ---	---	TGACAGATCACACCACATTTTGTGTAACCTTTTCTCCTTCAAGAGTCACTTAGCTTAAGCCAGAA GATTCTCTTAAAGAACACATACACATGTGCACACACI/AJAGAGGCAAGTACAAAAATGTAACC CCACAAAGTGCATGTGAATGAAGTGCAAAAAGGCTTCATTTGCAAACTCTGAGGATCATCTCT CTGCTTCAGGAAAATAACAGAAAGGTCCTAACTGCCCTAGGCCT
WI- 21761b	138	C G ---	---	CTGAGGCCTGCTCTAACTTCATNTGACGGAGCGAGTTTCCCTGGCTTGGAAATAACTGAAAGATTCTAT TTTCTCTTTGTGTACAAAGGATTCAAAATATTTACATCTTCTCTGCCAGTTAAACGTGCCGTGG CTC/GJCAATACACACCAAGCCAAAGCGTAACCTTGGCTGCCCTCAGGAAGGCTGGGAGGAAGTGCCAG ATGGTA
WI- 21079c	166	G A ---	---	AATGAAATGCCACCAGAGGTTAACAGCTTGCCATGTCATGCAACTGTGTGCGCAAAATCAAGTTGT TTTAATACCAGTGTGAGCTTTGATTCCTCCATGAAATTAAGCTGTGTTGCTCACCTGTTTACATAA CTCAGGCCACCTGAAATATCTGTAGTGGG/G/A/AAITTAACCACTGACCATCTCAGCTCAAA GCCAGATGACTATACCTACACATCTGCCAGGGTAATAGGCATGGGCAAT

WI-21079a	50	G A ---	---	AATGAAATGCCACCCAGAGGTTAACAGCTTGCCATGCACTGTGTG[A]JGCAAAATCAAGT TGTTTAAATACCAAGTGTGCAGCTTTGATTCTCTCCATGAAATTAAGCTGTGTGCTCACTTGTTTACA TAACTAGGCCACCTGAAATATCTGCTAGTGGGAATTTACAACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACCTACACATCTGCCAGGTAATAGGATGGCAAT
WI-22129a	45	T G ---	---	TCGTAGATTTTAGCCATGCCATATATTTAACTTTTAAAGGAAAGT[G]JTATATAACAGTCATTGCT TGGTAGAATCCAGTCTGCAATAAGTTAGCTCTAACAGTTAAACATTGAAGCTTATACCTTATATTTA AATGTTTAGCAATCTCTACTACATTTTCAAATATAATAATTTGGTGCAAATCCAGNAAAGGCA TTAACCAACATGGGACTGATCCTGGGGCTTCCACCTGACTAAGTTTAA
WI-21941	79	A G ---	---	TGGAGTTAAGTGGGCTCTGCTATTTCCCAAGAGGACTCGGAAGATGTTGATTCAGGGCAGAGT GAGGGCAGAC[A/G]GGATGAGGCTCTTCTGTAAAGTCCAAACAGACGCTCACAGTGTGGAGGCT GGGACTGCCAGGTTGGAGCTCAACAGAGAGGCTCACTGCATTTGACCCCAACCCACCTCACC CAGCACACAGGCACACGAGGGCACACGCACACAGNTGCACCTCACCACGC
WI-18916b	42	C T ---	---	AATGGCATCCCTGTCGATACCAACATCTTCAGCAGCTCAGC[G]TGGCTTCCCACCTTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTCGCCACTACTGCACCTGGACACAGCCTCACC AATGCCACCTTCATA
WI-18916a	35	G C ---	---	AATGGCATCCCTGTCGATACCAACATCTTCAGCAG[G/C]CTCAGCCGGCTTCCCACCTTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTCGCCACTACTGCACCTGGACACAGCCTCACC AATGCCACCTTCATA
WI-19828c	200	A G ---	---	TTCCCTTCTCCCCAAGAGTGGGCAGAAAAGCTTTGTTAACCTCCTTTTACAGATGAAGAAAAACAA GATCAGAGGTGCTAAGTGTAGCTGTAGCTAGTCCAGGCTTCTGGCCCCAATTTCTGGGTTCTCCCCAAG CCCATGCTTCTCCACTTCTCACAATCTTTACTTCTCTGACCTCACCACCCACCCAAAAT[A/G] [C]TTTAACTCTGGAAGAAACCCAGCTGCACACTGGGCACACTTGACCT
WI-21863b	47	C T ---	---	CACAAGTCTGTACAACCTTAGGGACACCAGCCCTGGCCCTGCCCC[C/TA]GCTGCATGCCACCCCTC ATATCCACCCCATCCCCAGCCTCTGCCCCGACACCCCGAGGCTCCCTGCTGTTGAAGTATTTT CTCCAAGGCAGGAATGATCCTTGATCCAACCACAGCATCT
WI-19860	51	C G ---	---	TTGACCTAAGCCCTAGCATAAAATAGCTAAGTAAATGTTTCCAAAGATG[C/G]CTGCATCAGTAT CTCCCATCCACATAATTTCTGTTGATTTGCCATCACCATAAAATGGTGGGATCTACCTCCCCCT CCTTGCAAAATTTGAGCTGNNCCTCTGATCCTGCTAAGGATCTGAAGCC
WI-19889b	80	C T ---	---	ACCCAGCTCCTTTACCCCTGCTGCTTTCAGTAGGCTTTGGCTAATGGCCANTGAACACTGCAGGGCAAG AGGAGTGAGGGG[C/TA]CAGCAATTTATTTCCCTCTTTCACCTCCCTGTTAGCTTTGGTAGTGGCTGTAT TTCTCTACTGATAGTTCCCTTGCCCAACAGTCGTAACTATTCG



WI-19891c	172 C G ---	---	TGTTGGTCTGAGAAATTCACAGCTTACTACAAAGGAAGCTGAGAATTCGTTGGTGGCCCCCTCCCCCGG ACTCCTCTGTCCTGGGAAACGTGGCTTTGNCCTCCAGACACAGTGTGAGATGCCAGCTCTCCTCAGCGG AGCTCCCGATCCCTCAATTTGCCATCTGCTGACTC/GC/GCTCTCCCGGGCGTGGGGCGTGTCTGT
WI-20155a	81 C T ---	---	GCACCTGTAGGGGTGTAGCTTCCATGGTTCTCCAAGCACGGGTGTACATTACCCCTTAGGCTGACCAT TCCCTTGGGGGGG/C/TGCAAAACTGCTTTGAGGAAATNCCCCAGGAGGAATAAAGTAGAAGACGC ACCTGCTATTTACCATACTATGGAGAAATACAGCTAATGAAGTGGTGGCAGAAAGCTTGGCCGTGTGA GTGCCCCAGGGTAAAGTCTCTCTCTCCAGTCCAGACAGAGACTTCTC
WI-20270b	91 T G ---	---	AGCCATACAATGCATTGCAAAAGAAACAAAGCAGCTGTACAGGAGTGGGGACGGCTCAGTGTACAAT ACATTATGTCAGGATAAGGAGCA/T/GJACACCAGGATTTATACACGGTGGCAGCGCTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGGTGGGAAAGGATGCT GGGTGATCTTGTTCOCOCAGAGGGCTGGGAGGCGAGGNGGGTGGGAA
WI-20270a	53 G A ---	---	AGCCATACAATGCATTGCAAAAGAAACAAAGCAGCTGTACAGGAGTGGGGACGG/C/JTCAGTGTAC AATACATTGATGTCAGGATAAGGAGCAT/GJACACCAGGATTTATACACGGTGGCAGCGCTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGGTGGGAAAGGATGCT GGGTGATCTTGTTCOCOCAGAGGGCTGGGAGGCGAGGNGGGTGGGAA
WI-20622	130 T C ---	---	CCACTTTCATAATTTTACAAAATGCTCAGCGAGCAAAATATGAAAAGCTTCAACACTTTCCTTTGTGTA ACTTGTGCAATAAATGCAACTTTAACAAACATACAAAATTTCTCTGTATCTTAAAGTTGAA/T/C/ TACTAAATTTTATGATGTTACTCATATTTTATTCATATACATCTTTAATGACATCATTGCCAATACATA CATTATTTCTNTAACTTTATTTTACAATAAGCCAAACATCTGTCATGCAG
WI-20768b	190 C T ---	---	TCCCCACTCAAAACTCCCAACCTTCTCTGGAAGGCGAGGCTAACAGGACCTCTGCCTGCCTGC TCACGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCAATTCGTATATCACCACTTA CAGGAGAGGTCTATTTCTGGGCAACCCAGAGNTCAGCACACATACTGCTGGGA/C/TJACGGGACTC GTAATTCGCCCTTGGTCCAACTCCTTCTATGGGGTTTAGCTGCCCTCATTC
WI-20768a	71 C T ---	---	TCCCCACTCAAAACTCCCAACCTTCTCTGGAAGGCGAGGCTAACAGGACCTCTGCCTGCCTGC TCA/C/TJGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGCAAACTCAATTCGTATATCACCACT CTACAGGAGAGGTCTATTTCTGGGCAACCCAGAGNTCAGCACACATACTGCTGGGACAGGACTC GTAATTCGCCCTTGGTCCAACTCCTTCTATGGGGTTTAGCTGCCCTCATTC
WI-21909	153 A T ---	---	TGTTTGTCTTGTGCCAGGTACTCTACTGCTTTACATAAATATCTCATTCTGTACATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGCACCTAAAATAAGGATATTTGTTGGTCATCTTTAAAGAAA TGCTTTAACATACCAAAG/A/TJAGTGGAAATCAATAGAATAAATAATTTAAGTCTTACAAAGCGTAC GACACTAAAGTAATAGGATACCCTAAATTTATTTCTATGTATGGAAAG

WI-22202	128	A G ---	---		TGTTGCTTTGGTTGTTGCTTTCTGGAACATATTGGAACACTTGTCTTTCATTAAGCTGTCTGACAGT GGCACAATCCCATCCATCTTCAGGCCTTTTAAATAGGTCATTATGAATCTGAATTTCTT[A/G]TTAAT ACTCTGGTGCAATTCATTATCATCTGCAAAAGCAACTGGCACAACACTCTCTTCCCGGTGCAGCTCTCGG AGAACATCTAAATTTGAGTCTAGTTCTGTGGGAACCTTCTCCAGCTCAC
WI-22189	70	C T ---	---		CCAAGGATGAAATTTCCACATTTATTTTNCITTTTATGTGAATAGAAATGGCAGTGAAGTGTCTATG AACTGAGGCGAGGAATGGCATGGGCTGGGCTGGGTACCGCTGGACGTTGTCTTCCAAAGTACAC TATGTGTGGTGAGACAAAGGGT
WI-22283	109	T C ---	---		GGGAGGATCATAGAAAAAACCCTCAGCCAGAAGTTAGGACATTGTGATTTCTCAGCCACTAACGA GCTGTATGACCTTGGTCACTAGGCCTCTGCAGGCTCTGGTTGT[C]TTTCATTTGCAAAATAAAACCCA GACCGGTCATCTTTGAGTTCCCTTCCAGCTCTATTTTATGATTTGCTCTTAGTCTTTATGAGCCA TGATGATTTATCAGTCTCCCTGATGCACCTCAACTCCAATGATGCAAAAG
WI-22290a	136	C T ---	---		GACGTATCTGTAGGGCTCTGCCAGTGGATTAGGTGAAGAGAGGTTTTATGGCCCTCTAAGCACCG GCCAGTAGTGGGAATGCCACATGCATGGGTGAGTGGGATCTGGGGGGTGCAGGACCTTGTCTTT [C/T]TCCAATCTCTCTTCTTAGCCAGAACTTTGCGAGAGCCCTTTNATTTCTCTTCCCTCTATTCC CTCTCTTTCCCAAATGTGTAAGGTCCCAATCCAGACCCCTCCAG
WI-22292	53	A G ---	---		CCAGTGAAGGGTTACAGCCATAGTGAAGTTCCCTTCTCAGTACCAGA[A/G]GTTTGTAGTAC GGTCGTTTAAAAAATACTTATCTGACCACAGTGGAA
WI-22387	186	C T ---	---		ACCTTGCACACCTGCCATCCGGTGCCATCTCTGGCTGGCACATCTATACCCACTCTGGCTCGAAAG GCTTGTCAACCAAAATGGCAGCTGGGCTAAGGCTAAGGCTATTTAAACAAGGCTCCAAAGGACCCCTT TCACTTGGGTCTAGCATCCAGCTCTCTCTCAGCAAGGCGAGGATTGTGGT[C/T]CCTTGTGTTTCTG AACAGGGCCCGAGGCGAGCAAGGCATGCCATCAGTGCAGCACTCAAGCCT
WI-22395b	127	A G ---	---		GCCGTTCCAGTATTGATAATAATTTGTGTTTAAATTTCTATACAGAAATGGTTCTTTCTTGAATATTT GTAGGGATGGATGAATTGAAAGTGAATTAAGTCAAGATAAGGGGGCAACTCTTTAAT[A/G]AAG GAAATGTTACCAATCCATAGTGAAGAGTAGAATATGTTCTTTTAGAGTAGNTAGAAAGTCCCCAGG CTCCT
WI-22405	90	A C ---	---		TTTATGGCTCCTGAGTGCCTTACCCAGCTACACTTTACCTTGTATCTATAAAAGTGAATTTAGAGT AAATACATTGGCTGTAAGTCG[A/C]GATCAGGTGCTCTCCACCAAAAGCAAAACAAACTGCTGA AATGTGCAAGGTTTCTCAGTG
WI-22419b	67	T C ---	---		CCCTTCTGGACAGTTTGTCTTATGTGTTACAGACAATCAAGGNTCCCTTCCAGGCACAGCCCAGTGT [C]CTGGATGGCATCAGCACAGGCTCCCTGCCCGGCTTGAAGCATGGCTGTGTGCACGAT
WI-21342d	59	T C ---	---		ATTTTCCCTTTCTGTGTTGTTATTTCCCTTTTGTGAGTAAATNAGCAATACACTGAT[C]TGGAA ATCTGCATGATTAATAACATTAAAGTTTCAATACACACCCCATATCAGAGTATAAAGCAAGAG GTTGAAAAATATCCCTAACCGAATGCAAAATAGGTATCCCTCAAAATGCACATTTCTCCTCTAGTT T

WI- 21763b	154 A G ---	---	CATACCCCTTTAGGTGCCACATTTGATCTTAGTTAACAGTCTTGTAGTCCCTCTTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACCTTCCAAGTGGAGCCAGGCCTCAGACTGTTCTCAGTCACT GCTCTCCACAGCTGATTGAGCAGACATTTGCTGTGCTTCTACCCAGCAGCTGCTAGTGCACTT GA
WI- 21763a	135 T C ---	---	CATACCCCTTTAGGTGCCACATTTGATCTTAGTTAACAGTCTTGTAGTCCCTCTTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACCTTCCAAGTGGAGCCAGGCCTCAGACTGTTCTCAGTCACT T/CJGCTCTCCACAGCTGATTACAGACATTTGCTGTGCTTCTACCCAGCAGCTGCTAGTGCACTT GA
WI-22440	64 A C ---	---	CAGTCCATTTGAGTCCCAAGTGGAGGGTGCATTTCTTATCTTGCTTAAGCCACTTGGGTAA[AC] TCCATTCAGCTCTGCACCTTCTCCAGTTTCTCATGTCAAGATCCTGAGGGAGGAGGCTTTCTGG AAAT
WI-22449	74 T C ---	---	CAATGAATGTTGTGGCATATGATTTNCCATTTGTGTGACAAATTTATTAGCTGGCATCCGGAATACAGTAG TTCTTTT/CJGAAAAAATACACAATGGGAACGTGACA
WI- 21965a	112 A G ---	---	CAGGTTCCACCAGAGGCTTTATTTACGCCACTCAGGACCCCTGGCTTCTGCTCCAAAGGCACCTGAACA CAGTCAGGCTCTTCTAAACACTGGCAGGGACCTCCCCACAGCCJAGJCCCCACAGGGTCTCTGT TCCCAAGTCTGATGATTAGGCAAGACCTTACACATTCACCCACTACCTGCTGGAGAGGAGGCTC ATGAGGCAGCCTGTGGTGCOCAGCTCAGTGTGACACACTGCCAATGTGC
WI- 21687c	115 C G ---	---	CACCTGGCAGTTGAGTCAGATTGTAGGAAAATTAACCAGATGGGTCTACATTTTNTCAAGTTCA AACCACATGGTTTCTAGTCAGAAAGTCTCATGGACTTCTCCTAAG[CJGJTTCTATGATCAGAC CACCTCCTAAATGTGGCTTTACCCATTACAGGCTACAGTTGAATCAGGCAGGAGCAGCTGCTGGAG AG
WI- 22374a	149 T C ---	---	AGCTTTTACAACAAAGCGAGGGTTTAAGGAGCCTGAGAAGAAATTTCAACAATATTGACTATACAGAG TCTTCAATTCGAAAAACAGTTAATAGTAACCTTGGTGGCACATACAACATGCATTGAATCTGTAT TATTCAGTAACTAAAT/CJAGGNTCCTGCATCATTTCTCTTACA
WI- 22250b	132 C T ---	---	ACTTGTCTTCAGGCAGGCAATTTCTGGGATCTAAACTAGAAATCCTTGAAAAACAATAGTACCAGCCA CTTTGAGGAATGTGCATTCACCTGATGGGTTATTATGGGTCCTGCTCCTGGCTGTTATG[CJ] GGANCCAGGAGTGGAGGAGAGCCGTGGAAATAGACAGGGGAG
WI- 22250a	89 G A ---	---	ACTTGTCTTCAGGCAGGCAATTTCTGGGATCTAAACTAGAAATCCTTGAAAAACAATAGTACCAGCCA CTTTGAGGAATGTGCATTCACCTGATGGGTTATTATGGGTCCTGCTCCTGGCTGTTATG GGANCCAGGAGTGGAGGAGAGCCGTGGAAATAGACAGGGGAG
UTR- 04932-2b	192 G C ---	---	GCAGCCATCCTCTCTCCAACACCTCCAGGCCACCCCTGGGGCCAGAGCACCTCATGCCAGCAGCAC CTAGTGGCCCGAGTACGGACCCGCTGGCCCCAGGTTCTCGGCTCTCAGGACGTCOCAGCAAGTGA GCCAGAGGTTTCTGTGGGACTCCAGCCAGGGGATGAGGCCAGCCCCAGAACCTG[CJGJAGTCTTC TTTGACGGGGCCGCGTGTCTCAGCTGCTCTGAGGAGGTGAGGAAGGAGGT

UTR- 04932-2a	149	C T ---	---	GCAGCATCTCTCTCAACACCTCCAGGCCACCCCTGGGCCAGAGCACCTCATGCCCCAGCAGCAC CTAGTGGCCCCAGTACGACCCCGCTGGCCCCAGGTTCTGGCTCTCAGGACGTCCAGCAAGTGA GCCAGAGGTTTC/TTGGGACTCCAGCCAGGGGATAGGCCAGCCCGAGAACCTGGAGTGCTTC TTTGACGGGGCCCGTGCTCAGCTGCTCTGGAGGTGAGGAAGGAGGT
sIFIBb	412	G C ---	---	GTAGGAAGATGGAACCTGGACAGACAGTCACTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACAGGCCCTTGCACCTGTCTCTGGCCCTCTCTGATCATGCCAGG TTTGACACCGCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAGATGCAGCCAGGAGCCTCTCTGA AGGACCATCTGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGT
sIFIBa	341	T C ---	---	GTAGGAAGATGGAACCTGGACAGACAGTCACTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACAGGCCCTTGCACCTGTCTCTGGCCCTCTCTGATCATGCCAGG TTTGACACCGCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAGATGCAGCCAGGAGCCTCTCTGA AGGACCATCTGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGT
sIGLV2	61	T C ---	---	GTACAAGAGGACGGCTCTGGGACGTCTCCACCATGGCTGGCTGCTGCTCCTCAC/CTCTC CTACTCAGGACACAGGTGACGCCCTCCAGGGAAGGGTCTTGGGACCTCTGGGCTGATCCTTGGTC TCCTGCTCCTAGGCTCACCGGGGCCAGCACTGACTCACTGGCATGT
sISG1001 7c	70	T C ---	---	GTTACGGCTCATCTTGAACCTCTGGTGTCAAGCGATCTCCACCTCGACCTCCAGGGTCTGGGAT TA/TCJAGGCATGAGCCCCACACCTGGACACAAAATACATTATATCTCTAAAGTATAGGATTACT TTAAGAGAAGGAACTAAAAGTATGATGGCTTACTTTCTTAATCC
sISG1001 7a	33	G A ---	---	GTTACGGCTCATCTTGAACCTCTGGTGTCAAGC/TAATCTCCACCTCGACCTCCAGGGTGTGG GATTATAGGCATGAGCCCCACACCTGGACACAAAATACATTATATCTCTAAAGTATAGGATTACT TTAAGAGAAGGAACTAAAAGTATGATGGCTTACTTTCTTAATCC
sISG1002 3	63	A T ---	---	TAATGATAATTAGGCACTTCTCCACACGAAGATGACACAATTGACCCCAATATCATTTGAGGC/A/T AACAGTTTGGGCTGTTTCTCAGTAGTATGACAGTGA
sISG1009 6	36	G C ---	---	GTGGAGAAAGATCGTCTTCTCTCCCTCCCATGACC/GCJGGCTTCCCGGGGCACTGTGCGTTTCC ACCCGAGACGGCCTTGTAGGGACCCACTGCCACTCCGCTGTGCGCTGGTTOGGCCTCCTAG GGCTCGAGTGTTAAG
sISG1011 8	107	C A ---	---	TAGGCTTAACCTGGAATCTACAAGCCAAAAGTCCCTCCCTGGCTGAGGGCAGTACCCTCCATTGGGC ACAGTCCAGACCCCAAGTCAAGATGCCCATTCCTTGGC/TAJCTAGCCCTCAGTTCCTTCAATTC ACCAGCCGCTGCTTGTGAGTTTCTCCAGTGA
sISG1012 0	89	T C ---	---	TAGTAGTAAGAAAGCAAGGAGGATTGCTTATGCGATGACTGTTTACAGTGGTGTGACACTATGC CGTGTTCAGAACACATTAA/AT/TCJGTTGTGTAATCTGATTTATCCTGCTTACAAATG
sISG1017 8	42	C T ---	---	TTGAAGCAATATTGCTAGCACTCTGCTGGACATTAAGTCCG/CTGGGAGGAGAAAGTGAACAGGAA TCGATCTTGTCTTTAACTGCCCTTAGTATAGGAGATGTTAAAATACTTGGC

siSG1019 3	136 GA ---	---	---	GGAAACAATACTACCTAAGGACAAAATACTATTATTAATAAAAAAGCTTCTAGTGTATATTGTTGTAACACATTTCTGGAGCTGGTAGGAATAACCATTTTATTTTCTGTAGTGCCATCTATACAAACATTTTAC T/GA/JTTGAAACTGAGATTTAAGTTGCAAACT
siSG1020 2c	143 GT ---	---	---	AAGCTAACTTAGGTGAATGGTGCCTCAAGGCTCTTCGAGGGGAAGCTCAGTCCTGGCTTGGGAGAGTCAGCCCTGGTCACTCATACACGGGCTCCAAAGCTAAGGCGTCAAGGAAGAGTCCCACTGCTTCTCGCTGTCA/G/JCAAGACCAACAAGGAGATGCCACTGCTGCTCTTTCCTTGTCTACTTCT
siSG1020 9b	75 AG ---	---	---	TCCTTTCTCTTTTCACTCTCAGTCACCATGATTCAAATAAACTAATTCCTCCTTAAGATCCCACCTTATTTTAA/GJCTCCAATAAATGTAATTATCAGCTGCTGAATT
siSG1020 9a	34 CT ---	---	---	TCCTTTCTCTTTTCACTCTCAGTCACCATGATTC/JAATAAACTAATTCCTCCTTAAGATCCCACCTTTAATTTTAACTCCAATAAATGTAATTATCAGCTGCTGAATT
siSG1021 8	29 TC ---	---	---	TACTAGACATGCAAAATGAGAAGATTACA/JCTGTAATATTTAAAGAAGTTATATTGTTTGACATAAATATGCATTGTACCCGGGCATAATAAAGTTAAAGCCAGTTATCTGA
siSG1025 2	108 AC ---	---	---	ATAGGTTTCAGGAACAAAATCATTAAATGAAAAATGAGAAGAAATTCCTTTATTTTGGACCAATTTTAGGCACCTTAAGAGATTTCTTCTCCTTCCCTTGATCA/JCJAGTGAAGATATGATAGGGAATTCAGAAATTTCTCTCTG
EST10915 0	123 AC ---	---	---	CTGTATTAAATTAAGAAGGCACTATTAAATGAGGGACGGAATAATCTACCTGTACACAAAATCTGTACTTTAAACAGCATCTTCAAAATAAACCTTTAAAGGATAATGGTTTACGATCATTTTAAAG/JCJATTTTAA GAACTGAGTTATTTGGAC
EST11023 1	166 TA ---	---	---	TTTTTGTAAACCAACCCCTGAAAGTTTCCACATGTGAATATAGATACAACAGTGAACAAAATATGTGGCTCCCATGTACATTTGGTTACCTATGTACAAGTATCCTATACACAGTAAACAGCAGGGCAATTAGTCAATTAATAAAATAGTACATGTAT/JAGTGAATAAAATTTAAATTTACAAAAGGCTTT TCCACTCGTGGATTGATTCCTTTTGGAGGGGAGTAATCCIGG
EST14096 8	71 GC ---	---	---	GGGATGTATATTACAGATAACACAACCTCAAAATATACCATCAGACATTTGAAAACCTAAGGCCATTCGTGA/JCJTTATTTTAAACCTGGTGTTTGCACATAATGATCTTAAAAAAAATGAATACCAAAACCAAGATTCTCTTCTAAATGAAAAATTTAATGCAGGTACAGGATAACTTTAGGGCTATATCTAATCTGAAG
EST22113 6c	125 CA ---	---	---	TGCAAAATTTGAGAAGGCAGCAGGGGCCAACCCCTGGGACCTCATCTCTGTCTAGAAATGTGAGGTGTCAGGGATGCTTAAGTCTCTCTCTGGCAGAGACCCCGAGGTGCAGAGATGATTCCTCA/JCJCCCTTC TCTCAGGGTCGTGGAG
EST22555 7	60 GA ---	---	---	TCAAGCATGTGTAAAGGCACTGCCCCGCCAGACCCCTTCTAACITCTGCACACTGGAAGGT/JAJAAACCTGGGAGAGAGAGACACTCCCTCCTCTAGCTTCTACCTGGGCCCCCTCCAAAGATGAGCATTCATCTTGGAGACCAAAATAAAAAAGGACAAAAGACCAGGGGCTCAGAG

EST22917 6	74 C T ---				GTAAACCTTGAACGCCATGCTAAATGGAAGCCTGACTGACCAGGGGCTCTGGGCTCTCAATGCA ATAGAAAC/C/TTGACATGGGGCCAAAAGACTTCCAGACAAAGCAGCGAAGGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST36458 6	65 A G ---				CAAGTTAGAACCATGCATCAGCTTTTCATCCATGGTGTAACTTAACCTCAGGCTGTCTACTCA/A GTTGGGTTTGCTAGCCTCACTCGCACACAGGAAGCTTGAATTTGGAGGCTCCAAGTCACTCTCCA
EST36745 3	56 A G ---				GAGGGGAACCTTCAAAGAGGATTCCAACAGTGAAGCAGAAATCATGGGGCAAAAGTC/A/GTATGG GGCCAGACTGAGGTTGGACCACACAGCACTCCAAGCTGGGCCAATCCAAACCGCTGGTGAAGCGCG ACAGCACGGAGTAGCCAT
STS- R37410c	201 A T ---				TGTGACCATACCAAACCTATGCAATAAAAGAAAGAAAAAATCCTCACTTAAAAAAACAAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAAGTTTCATAGCATTTTGGGA ATTTATGGTTTGAATAAAATACAAAATGTGTATCTCTGAGACACATTTATAACATTCTGGTATG T/A/TJTTTGTGAGTGGTCTCTAGTGGCCAAT
STS- R37410b	139 G T ---				TGTGACCATACCAAACCTATGCAATAAAAGAAAGAAAAAATCCTCACTTAAAAAAACAAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAAGTTTCATAGCATTTTGGGA ATTTAT/G/TJTTTGAATAAAATACAAAATGTGTATCTCTGAGACACATTTATAACATTCTGGT ATGTATATTGTGAGTGGTCTCTAGTGGCCAAT
STS- R37410a	48 C T ---				TGTGACCATACCAAACCTATGCAATAAAAGAAAGAAAAAATCCTCA/C/TJTTAAAAAAACAA AAAAACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAAGTTTCATAGCATTTT GGAATTTATGGTTTGAATAAAATACAAAATGTGTATCTCTGAGACACATTTATAACATTCTGGT ATGTATATTGTGAGTGGTCTCTAGTGGCCAAT
STS- R42778	74 C T ---				TATCGTGGGAAGTTCCAACTCATACTTATGCTGCTTTTCTACTTGTCTAATATTGGATGCTCTTGCCA GGCTC/C/TJTTAAATTGTGTAACTGGAAGAAACCTTCTACTCTCCACAAACCTGAA
UTR- 04350	125 C G ---				CAATCTGAAGAGATGCATAGCGGATTGGTGGCTTTAGCAGCTGTGGGAGGTGGGACTGAGGAGCG ACTGCTAATCAGTATGGGTTTCTCCCGGATGGTGAATAATGTTCCGGACCTAGATA/C/GTGAACGA AGGTAGCACGACACTGTGAGTGCACTAA
siSG1026 6	55 T C ---				GAAATAAACTAAACTGCAAGCAAAATCACTGTTAATAAGAAATTGTTCTTCTGTTT/C/GACAGTTG AAGTGGGTGTGAGATGGGCATAGCAATGAACAGTGGAGCCAAATGAGTCTCAGAAATGCGGGCAAA CTCCTCTGTGAAAATGTAT
siSG1028 2	70 T G ---				GTATAATTGAGCATAAGCCAAAGCCCTTTTAAATAACCAATACTATCATTTTATGAAATCTTTACA AGAT/GJAAGCAGAGTAGTACAATATTTAAGCATCTCAAGTCTCCATTTAAGAGTTGACTATC
siSG1031 0	128 C A ---				CACCTTAGATATGAGGAAAATGGTTTAAATGGACACAAAGGAGTCAGCCACGTTGGAAACCAACATAG TTTCATACCACGTTGAAACCATGTGTTTGTATGCAAAATACAGCAAAATATTTTTCACCT/C/AJTTG TCAATGCCAATGCATTGAAAGGCCAGAAAATGAGAAAAGGATACAAAACCTTTTGTATAAAAAGGTA AGAATTCTGTGTG

siSG1033	116 T C ---			TTTAAAGCTACATGTCTGAAAGAATGATGCTGCTGATTGAAATAAAGGAAGAAAGGATGCATTTCCGG
1b				GCTCCAACCTGTCTCTAGGAAGGCCTAGACCTCAAACACCAACACCTCCA/T/C/GCATTTTCTCTTTGG
				CTACTATGTCTTTTCCCTGACTTCTGCCTCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTTCATCTGA
				CTTAGGACCTCC
siSG1033	107 A T ---			TTTAAAGCTACATGTCTGAAAGAATGATGCTGCTGATTGAAATAAAGGAAGAAAGGATGCATTTCCGG
1a				GCTCCAACCTGTCTCTAGGAAGGCCTAGACCTCAAACACCAAT/CACCTCCAGTCATTTCTCTTTGG
				CTACTATGTCTTTTCCCTGACTTCTGCCTCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTTCATCTGA
				CTTAGGACCTCC
siSG1243	225 G A ---			ATTGGCAATGGGAAAATGACACCAATCATTTGATTACAGAAAATGGTTTTATAATCTCTCTCTTG
b				AAATTATGTTACGGCCAGCATGGTAGCTTATGCCTGCAATCCACGACCTTCGGGAGGCCAAGAGA
				AGGATCGCTTGAGCCCGAGGTTGACACACGCTCGGCAACATAGTAAGACCCCATCTCTGTTTTT
				TTTAAAAAAGAAATTCGTGTC[G/A]/AAGTATTTTCAGACCAAAAGGAGGT
siSG1345	60 G A ---			AACTGACGTATCACAGGGGCAAGTATCTGTGCATAAATTTGAAGTAGTTGCTTCTTAC[G/A]CGCT
b				TCACATTTTAGCATGGGCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA
siSG1345	54 T G ---			AACTGACGTATCACAGGGGCAAGTATCTGTGCATAAATTTGAAGTAGTTGCTTCTTACGGCT
a				TCACATTTTAGCATGGGCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA
siSG1385	117 T G ---			TTAATGTCATCCAGGGGGCCAGGGATGGAGGGAGGGTTGAGGAGCGAGAGGAGTTATT
b				TGGTGGGATTCACACATTTTCCCATGAAGAGGGGAGACTTGGTATTTTGT/GTTCATCATTAAGAA
				GACAAAAGGGTTGTGAACCTGACCTCGGGGGGATAGACATGGGTATGGCCTCTAAAAACATGGCC
				CCAGCAGCTTCAGTCCCTTTCTGCTCG
siSG139	69 T C ---			TCGTCTCTTTCCAGTGTCTTCCAGAAAGCATCCCATGATGTTGTACCGCACAGCACATTTGTGTCT
				TT/C/GCTTTGAGCACTTGCCACTCTGGCTGTGCTGCTGCCACTGATTTGTGACTGTCTTGCTGCC
				GATCTGGTTCCAGACAAGGCTGATTCAGAGACTCCACGTGGTCAAGGCTCTGTTGTTGTCAATCCCT
				TGGCTCTCCACTTCCAGTTGGCTTCTGTCTCTCA/T/CJAGTCTCTCCATGTGGCAACAAGATGGC
				TACTGGTGTCCAGGTTACGCTCTCAGCTTGAAATCCAGCAGCAAGAAGATGTCTCACTCCCA
siSG1427	103 T C ---			AAGTCCATAACTCAATCTTGGGAAG
				CCCTGGAGTTTCTGAACATAGGAAGAGAATGCAAGTCATGTGTTAGGTCC/AGTCTCCCTTGCATGA
				AATGTGGGAGAGGAAATAAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTACC
siSG1471	50 A G ---			GCA
				CAAAACCAAAATCTTCCACGATATATTACTATTTAGTCTAAGT/CJTTTAATTCAAAGTTGAGA
siSG1483	44 T C ---			ATGACGAATTCAGAAATTCITTCATACATAAATGCTTTCCTTAGTTCTGCAGATGGGTA
				CACACCCACAAGTTTCATGCTAATGCCAAGTATCAACTCTTGAGGACAAAGGCCAAACCCAGTGTGCA
				[C/G]AATGTGGAGGATGTCTGTTGCAGCTGTAGTTACTAATGCAGGAAACCCCAATGCAAAAGAGGAA
siSG1696	67 C G ---			AATGCCCTGA

siSG1847 b	95 GA ---			TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACACAATGCTACCCCTAAAAATGAAGAATTT AGAGGTTAAATAAACAAAGTGAGAGACC[G/A]TTTACTTACATCAGTTCCGGTTTATAGACATTTGAA TCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAAATTAATAAATAACTTGATCACTGTGCT TCAACACAACACTG
siSG1847 a	49 CA ---			TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACACAATGCTACC[C/A]CTAAATGAAGA ATTTAGAGGTTAAATAAACAAAGTGAGAGACCCTTACTTACATCAGTTCCGGTTTATAGACATTTGA ATCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAAATTAATAAATAACTTGATCACTGTGC TTCAACACAACACTG
siSG1897 a	83 AG ---			CTTAATGCCCCCTTCTCTCTCTGACAGGAGACACAGATGGGTAAACATAGAGGCATGGGAAGTGG AGGAGGACACAGGACT[A/G]GCCACCACCTTCTCTCCCGGTCTCCCAAGATGACT
siSG2022 a	86 TC ---			TGCTTTGAGGTTTCAAACTGAGATATCTATGGCAAGTTTATAAAAAGTACATTTGATCAAGGTACAA TTTTAACATTAAATATACAT[C/A]TTCCATAATCTCATCTATTTAACATTAAACACAGGCCTTTGTTGT TGTTATTTTTTCTCCCTACAATATTTCTGACTCTGTAGGGACAGTGGCCTCAGTTGGGGGTTGAC T
siSG2076	104 CG ---			AAACGTTGTCCCAAAATTTGTTCAGTTTCAAAAGTATAAAATAAGACTTCTGAAAAAAAGTTTACA ATTAGTTATAAACAACTTAAGAATATATTTTGACATT[C/G]ACATCACAGTGGGGCATTTT
siSG2108 c	71 AG ---			TTGAGCAACAATGATTCGCGAATTTGGCAGCTCCAAACCAAAAAATGATTGAGGGGCTCCACAGAGA GAGC[W/G]TAAGGGGAAGACTTTTATAGGACAACCTGTAGAACTAAAGCAAAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTTATTTGGTCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGTCTGA
siSG2108 a	49 TC ---			TTGAGCAACAATGATTCGCGAATTTGGCAGCTCCAAACCAAAAAATGATT[C/G]GAGGGGCTCCACAG AGAGAGCATAAAGGGGAAGACTTTTATAGGACAACCTGTAGAACTAAAGCAAAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTTATTTGGTCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGTCTGA
siSG2141 b	173 AG ---			TTATCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTATTTTAAACAAATGACTGCGTGTAC TGAATCTGACTGTGTGAAATAATCTCAGAAATGGCAGCACCCTGCGATGGCGATGGTGCAGGTGGT GCAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAG[A/G]AAGTTCCCTATTATTATTTAAGGC AGTTTTCAGAGCACTGGCATTCTTGTGTCTCTG
siSG2141 a	113 CT ---			TTATCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTATTTTAAACAAATGACTGCGTGTAC TGAATCTGACTGTGTGAAATAATCTCAGAAATGGCAGCACCCTGCG[C/T]ATGGCGATGGTGCAGGTG GGTGCAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAGAAAGTCCCTATTATTATTAAAGGC AGTTTTCAGAGCACTGGCATTCTTGTGTCTCTG



siSG2148	50	A G	---			TGGAAACAACCGGCTATAGTCTGAGTCATATTTTAGACGGTGATTTC/GJAAAGAAACAATAA ATGTGGATTAGAAAGGAACATCCATTACTGTATTTTCGATACCTTTGATGTTCCACAGACGAGCTC ATCAC
siSG2175	68	C T	---			CTCAATGAGGACTCCATAGCCAAAGCGTTTATATGGCAGATGAGCTGCTACAAATCTGTTGTGCT [C/T]GCCGCTGACTCAGCTAATGCTACCGGGTTGGAGCGACACCGAGCCAGCCACCTTTTCCAT ACCTGGGCAGAGGGAAGGGAGTGAAGGACCA
siSG2189	41	C T	---			CAAGTGGTGAAGCTGGGATTGAGCCTGATATTACACACTA/C/TCTACATTCCTCCAGTATAATA GGAACCTCATCGCTAACTTTGAGCACTTAGTGTTCTGAGTACTTCGTATAGTTATCTCAATCCTACTC CAGCTTTGCGAAC
siSG2200	49	T C	---			TGTTGATGACCATAGAGGATGCAAGCTCCGGGCTGGTCTGTATGATG/T/CJTATATTTATGTAT AATGTCTTACCTGATGATACCCCAACATATTACTAGCCTTATAGATGAGGATGGAGCTTGGCTG GTCAAT
siSG2243	85	G T	---			CATTTCTGCCCTCTGCTTCCCAGTACTACCCCGTCCAGCAACTGCCCTCTGTATAAATAAGTATCAA GATGGTCAGTAGAAAG/G/TAGAGCATCTCTCAGCCCTGGAAGACAGTGTGGAGCTTCAGCT
siSG2257	65	A C	---			TCAGTGATTGAGGAGCTGGCTAAGTCACTGTCTAACTCTGTGAGGAGGCTATCAGAAGGGCAG/A C/TGTCAGGAACCTCGCCCAAGCACTGGGCTGCTCTCAGGCAGAAATTCCTCCT
siSG2306	67	A G	---			GTCATACGCTAGAGGTCACTGGTATAAACAACAGTAGCTATATGATATTTGGAACTATTTTACA [A/G]TATGCTCCCATTTGGGTTTCCAAACTGATACAACCATGAGGTGAACACTTTTCACTGTTTCACAG TTCCTCCAGAGA
siSG2334	70	T G	---			GAAAACTACCCACAGCATCATGTTAAAGAAGAGAGATGAAAGAAAAATCCCGCAAAAAACA AAAAA/T/GTGCAGTGGAGGGGCTGTGGAGGGGTGAATG
siSG2339	63	T C	---			AGAGCAGAATGGTGAATCAACAAGACCTCAAATTGCTTGACTGCAGAAGTAAGTGTGTCAC/T/CJ GTTCTCAGAGTCACCATACGGTACTGTGCTATTTCTGGCTGTCTTCTTATTCATCA
siSG2465	76	C T	---			CAAGACTAAGAAGCCGACCGAGTGGTCCCACTCAAAAAAGAGATTTCTGATTCTACCTCAAAATG CAGAAACCA/C/TJACAGATTAAAGAGAAACACACACACACTTTGAGAAACTCGCCCTTCCCTC ATCTTCAAAAGTGTGGGTATGCA
siSG2549	140	T C	---			TTGCAGGCTTGTTATCCACAAATAACAAGTCATGTATAGAGAAATGTGAAATGATACTTGAAACCAA GATATATAAAATATTGAAGTCAATTTATGCCCTTTTGTGACTGGTTAAATATGCAAGCAGCTAAAG GAATAT/T/CJACACACCCACCCCTTTTAACT
siSG2577						AATTGCCAAATGGAAATTTCCAGAGGATTTTAGACCACACTTTGCCCTGTGCTATCCAGTTTGGT CCCAATATAGGCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAGCA/T/GJGAACAATC CCGGCCAGATTAAATTAT
b	123	T G	---			

siSG2577 a	121	CT	---			AATTGCCAAATGGAAAATCCCAGAGGATTTTAGACCAACTTTGCCCTGTGCGATTCGCCAGTTGGT CCCAATATAGGCTTCTGCAAGAAGAGATCAATGCCGAACCGAAGCTGTGAAG[C/T]ATGAACAATC CGGCCAGATTAAATAT
siSG2700	58	GA	---			ATCTCTCGACTGCTTAGTGGGAAAGGAATCAATATTTATGAACGTGTCGGCCCC[G/A]AGTCAC TCAGCGTTTGGGAAATAAACCACTGGTCCAGAGCAGAGGAGGCTACTTGAGCCGGACACCA
siSG2724 b	101	TG	---			AAACAAGCTTTGTCAATTTCCACTACATTTTGTGTGCTTTTATATTAATATTTGCAATGCTATAAT TTAATACTTATATCCAAATGCTTGCAATATCAAT[G/T]TTTTTAACTCTGGGTGTGAAGAAC
siSG2776 a	65	GA	---			GTGCCGATCTTACTTTCCAGAAAAGCGGTAAATAAAACCTGTAGAAAGTCTCGAATATGC[G/ A]TATTGGCCCTTTGGAGTTAGGCCAGGAACCTCAACAAGGGACACTGCTGGCCCAACCAAAAA ATATCCACTAATCCCGAATATAGTAACCTGCTGTCGCCGAATG
siSG2791 b	109	GT	---			AAGGAAAGGTGGAGGGAAGGGAAGAAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTTC TATTATCTTCTGAACGGTAAACTAGCAATTTTAATAATATTT[G/T]GGGCCACTTAAATCTATTA AAGCAGAAAGTGTAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
siSG2791 a	100	AG	---			AAGGAAAGGTGGAGGGAAGGGAAGAAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTTC TATTATCTTCTGAACGGTAAACTAGCAATTTTAATAATATTT[G/T]GGGCCACTTAAATCTATTA AAGCAGAAAGTGTAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
siSG2826	85	CT	---			CCGCAATTTCAACACACATCTATGAAAACTAAGGGTGGATCATGTACAAACACAAAAACAAGC TCCCTCCCTCCAAAAACAAC[C/T]GAACAAAAATAAGAAAGAAACCCATGAATGCCAGGTTTA ATTTTTTTC
siSG2850	88	GA	---			ATGGGTGCATTGTAAGGCAATTAATACATTTTTCAGGCAGGGGCTGGCAAAATTTAATGAGCTGA TGTGTCCTCAAGGAGACGGCC[G/A]GGCTCACACATCCCATCAATACTCCTCCCAT
siSG3031	71	TC	---			ATATCACGGGGGCTGAAGGCAATGTGAAGAGTGACTGCAAGTCCTGGCATTTTCTGTGGTGCAGC AAAT[C/G]CCCCCTTTATTTAATGATCCAGACATCTGGGCAGCATAGCT
siSG3058	81	GA	---			GTCCCAACTCTCTCTCTTAGAGAAAAAACTGTGATTACCTCAACTTGAATATGAAAGTGTGATTG AAAAAGTCAAAAC[G/A]TGAAGAGCATCAAGCCAAAAAGGCAAAACTGGCTGAGGC
siSG3092	94	TG	---			CAGCATCTCCAGAACATTCCTAGAACTGAACCATTCCTGTCACTATTGAAAAACAAGCCCAAGTTC CAATCCAAAAATAATAATGAACGTGCT[G/G]GATAAACATTCCTCTATGTTCCAGCCCCCTACTTT AGTT
siSG3230	95	AG	---			AAGAAGTACTTTGGTAGCTATTTAAATAAGAGGGGGTGGGAATGAATGTCGAGATACGAGCACCTG CATCTTTTAGTCAATTGTCAGTGGAGT[G/G]GTGGGGTCTAAGTGTCTGAAGTGAAGTAG
siSG3245	160	GC	---			ACATCTACATACCCAGTAAGATGCAAGAAAGGAATATCTGAGAGCAAGAGCCCTGCTCCAGGGGCC CAGGTATGTGAGAGGCCAGTGGGGTGGCCACTTGGTGTCTTACCAACCCCTGCCATCCAGTCTG GCCCCAGTACCTACCTGGGAGGT[G/G]CTGTACTTGGCTTAAGTACTTCAIGCTTTAT

siSG3255	42	T C	---			AGGTGAATGAGTTACTAAATGTAGCATTATTATTAAGGAATTC/GCATTGGAATAGTTTCTCAG TTTTTATTATGGAAGATGATGATTTCAGCCACATTCAGTGATGTTTCTTAATAACACAAATCGAC AGGACTGTCTGTTCAGTACAATGGAGACAGCTTTTCAGGGCAATGGGATTTCTTGATAATGCTAA ATCTGTCTTGTCAGCTGAATTTCTGGGCTTATGTGGCAGTGTGGTAAAA
siSG3269 b	141	C T	---			TGTACTTACTGTGTCATCCTATCCATCCCTCCCTGAGCCTGGACTGCTTCCAAAGGGAGACTAGG AGTGAAGGGAGGAGTCTCCCAAAGTTACCTTTAAGCTTGATAATAGCTCCATAGCCATGCTAAA GCATGA[C/T]GTAGATCCCAAGTCCCTGACACATTTTCTTAAGAACT
siSG3269 a	24	A G	---			TGTACTTACTGTGTCATCCTATCC[C/A/G]TCCCTTCCCTGAGCCTGGACTGCTTCCAAAGGGAGACT AGGAGTGAAGGGAGGAGTCTCCCAAAGTTACCTTTAAGCTTGATAATAGCTCCATAGCCATGCT AAAGCATGACTGTAGATCCCAAGTCCCTGACACATTTTCTTAAGAACT
siSG3284	130	C T	---			TTAACTCAAGAACTTTCAGTTACAGGAAGATTATCTAAATTTAAATGACTAAATACAAAAAGC ATAAAATGTTGAAGCCATTTTAAAGTTGTTTGAATCCATATTAGCACTCAGACTTCCCCA[C/T] TCCCTAACTTTTGTTAATGCTGTATGGGACATTTGTTGTTGATACCC
siSG3292	99	A T	---			GTCTCAAGTGAATCTGTAATACATTTTAAAGTCTGACTTCAAAATCGGTACATGAGGCTTAGACATA CACATCATTGGACAAGTGACTTAAATATCTAA[A/T]TACAAATCAAAATAGCATTTTCTAACTTCAA TAAATGTCATATCTTGTCTCTCACT[C/A]CCAGTGATCCATTTTCCCGAGCGGTAGAGCTTTTCTG TTTCTGTAGATTGGCTGTCTGGACATTTGATATAATGAGTGCTGTATCATGTTGACATCTCTC ACCTAGCATGATGTTTCAAGACACATCCATGCTGTAGCATGCTGCTTCATCTCTTTAA
siSG3323	26	C A	---			GATCCCCAGTATTATTTCTAAATGAACTTGTGTTGGAATAAAAATCTGAGGACCACCTCAGAG GG[C/T]ATAAGGGAACCTCTTTGTCTTAGTTCAATAGGACTTTCT
siSG3369	69	C T	---			CAAGACTGTAAAGACGTAGGCCCTTGTGAGAGTGAAGGAAGGATGCTCGAACTTGCCAGGACTCAGG CTTCAGCTTCACAATCCCGAGGAAGGAATGACATTTCCAACTGTACCTTTGTAGC[G/T]CTGGGT CAAAGTCTAAAGAGGACAAATAATAGAGACT
siSG3398	125	G T	---			TCTTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATCAG[G/C]TCACTGTAGCCTGGACCTCC TGGGTTCAAGTGATCCTTCCACCTCAGCCAACTGAGTAGTGCTGGCCTGCAGGACAAGTCACCATGCTA CCTAAGTTTTGTAGAGACAG
siSG3416 a	43	A G	---			GTAAGACAAAGTTTGTCTATGTTGACCAGGCTGGTCTTGAACCTCCTTGGCTTCAAGCGACCGTACCA CCTTGGCCTCCAAAGTTGCTGATATACAGGTGTGAGCCACTGCCCGCGGACTTTTAACTGAAT GTTGAAAATCATCTGCTCTTGTGCTGGTAAACACTGA[T/A]CAAGTTGCTTAACCTTTGTGAAACCCAC TTTCTTATCTGTAAACAAATGGACAACAGAACTTTTCTTTCCTCTC
siSG3424	173	T A	---			GTTTATGTTAAAGATTAGGAAGCTGTGGATGTGAGGGGTGAGGTGATGATGGAGGCTTCACAGA ATGAGTGGCAGAGAGGGCCCC[T/A]GAAATAGCTTACTCTGTTTTCCTATC
siSG3436	88	T A	---			

siSG3463	103	C T	---			GATACAGAAGATAGTGGTATGGATAGTATGAAGGACAAATAATACAAATATATTTATG AAATAACACAAAAATGCATACACAGCTCAATGGGTCA[C/T]TGGAAACAACTTGCTTGACTATATTA CTGA
siSG3491	71	G A	---			CAAGATACITTCATTGCTCTAAGTAGTGCAGTGGCAATAATTTCTCAGCAACAGGACGATTG AAGA[G/A]GTGGAATTAAGTGTGCAAGGAGTACTTTACCTCCAAATAGCTGCAATTTAGCAGTCTGA ACAACTTCTAATCTTTACTGGCACCTGTGGATTCTTATAAAGTCAATTTACTATTTCTGTGATG ACAGAAAAATAAGTTAAG
siSG3523	33	C T	---			TAGCCATCTTACTCTAGTCTTTTGGGTTT[A/C]TGCATATATGTGTACAAACACACACACACC CCTAATTCCTCAAAATGCTCTTGGCATAAGTTTATCTCTTACTGGTCTC
siSG3536	213	A G	---			AGTACAAACACAGATTTAAAGAGCTCAGCAGTATTGACACGCTGGAAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCCTACCTACACAGCTGTACAAACCCAAATACAGAATGGCTTC TGTGATCTGGCCTTGTGAAACGCACTCTCAGTCACTTCTTATTTGTTTAAATGAGCTTG TGCACCATTAG[A/G]TCCCTGCTGGGTGTTCTCAGTCCCTGGCCATGAAGTATG
siSG3583	112	G A	---			GAAAAAGCTTAACATACGATCCATGTGCAACCCCAACAGGATCTACGAACTCTGGCATGATCCA CATCGCTACACATACCATGCTGGAAGTGCACATCCACACAGGCAC[G/A]TAACATACACAGTACTGT CTAGTTATCAACACCTAG
siSG3586	60	G C	---			CCTAGTAACATAGTGAGACCTCGTCTCTACTAAAAATTTAAAAATCAGGTGGTGGT[G/C]ACG CCTGTAGTCCCTACTTGGAGGCTGAAGTAGGAGGACTGCTTGAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGCGCCATTGCCTCCAGCTTGAGACTGTTTCAAAA
siSG3589	101	T C	---			ATATAGTGGTGGTAGCATTATAAACTCCTTTAAAAAGCAATCTGGCCATATCAAAGGCAAAAAAGT GTATATACCAACCCCTGGCACAAAAACCCCAATGAT[C/C]CTATTCCAAAGATGTATCCAGATGAAA GTATCCAAACAAAAAGCTATATACAC
siSG3590	70	A T	---			GAGAGATGAGCTATTATTCTTTTACTTAATGAAGATGTAAGAAATGATCTTCTGTTCTAAAAAAA AAA[A/T]TTTCTCTGATGTCTCTTGACCCCTGTAGGAAACACATTCAGTTTCTACACT
siSG3619	78	A C	---			CAGTGAGACTTCTCAATTTATAGCAAAATACATTTTGGCAGCTTAAATTTCTTGAATTCATATACGCT TCTGTCAATTT[A/C]AACAACTCCAGAGAAAACTGGGCTCTATATATTTAAG
siSG3644	40	T C	---			ACATATGTAAGTGGCATTAGTAGCCATATTAGGATGAGAT[C/G]GATTGAGAGGCGATGAACCAAGG ATGCGTAATAATCATTATGAATAATAAGTTATCTGGGGAACGGCCATTTGTCCAACATTTACTAA GTGCCTACTA
siSG3646	70	G A	---			CTCATAATTAGATTGAGATTGTCATTTTGGCAAGAAATATATGATGATAACAATAATATGCTTACT GGT[G/A]ATATTAACTTTGATACCTTGGTTAAGATGGTGTCTGCTAAATTTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA

siSG3646 b	55 A G ---			CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAAATATATGATGATAACAATA[A/G]TATGTCTT ACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTGCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
siSG3646 a	43 A T ---			CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAAATATATG[A/T]TGATAACAATAATATGTCTT ACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTGCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
siSG3693 b	85 A C ---			ATTGTTCCCTGAACATTCCCGTGGTCTCCCTCTGAAAGCCGATGACCATCCAACCTGGACTCACCT GAAATATCCTACGAGGC[A/C]TCGCCCTCCGAGACTGACGATTATTAAACCACCCACACGGAAGG
siSG3693 a	30 C T ---			ATTGTTCCCTGAACATTCCCGTGGTCTCC[C/T]CTGAAAGCCGATGACCATCCAACCTGGACTCA CCTGAAATATCCTACGAGGCATCGCCCTCCGAGACTGACGATTATTAAACCACCCACACGGAAGG
siSG3698 b	145 G A ---			TCTTGCCCTTTGTTACCCCTAGAGAGATGSCACCCCAATCCCCAGGGTTGCTCTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGAGGAGCTCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTAAGTCT TTATTGGG[G/A]AGAATACCCACCCACCTTCCTCACTGCAGA
siSG3698 a	51 C G ---			TCTTGCCCTTTGTTACCCCTAGAGAGATGGCACCAATCCCCAGGGTTG[C/G]TCTCTGACTTCCA CCATTCACTGACTTTTATTGCCAGAGGAGCTCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTA AGTCTTTATTGGGGAGATAACCCACCCACCTTCCTCACTGCAGA
siSG3724	107 C T ---			ACCAGCCTCATGTGCAGAGGGTCTCCTGCTGGATCCCACTGGAGCCATCCCTGGGCCTAGACTTCT GTCTCCCTCACITTTAAATGAGTGCTCAGTGATGTGAAG[C/T]ACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTGCT
siSG3725	104 G A ---			GCCAAACAAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTTAA ATCAATATATTATTACAGCAACAGCAACAGACGCC[C/G/A]AGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAATAACGGCACATTTA
siSG3751	128 G A ---			CGGAAGAAAGAAACACAAATCCACAGGAACAATCTATGGTTTCATACCTTTTAGAAGAGATGATTTTG AGGGCTTCAGTATTAAAGGGGAAAGCAGGCTGGAGGGGAAAGAGAGAGATATGGTCCC[G/A]TT GCTGACTCCATGTGTTGCAAGAG
siSG3787	49 T A ---			TTCTGTGCAAAAGAATCCACATCATTTGTTGGTAGCAGAGGATCTCTTAT/AJAAAGTTCCCTAAGA CACTGAGGGCATAAAACCAACAAATAAAATAAGGAGTGATAGGCTAAAGCAGTATCTTCCCT
siSG3880 b	115 G C ---			GACAAGGGAAGAGATCGCCAGAGACAGGGCTGGGGAGCTGGGGGTCCCTGAGTCCAGGGCGC CACCACAGTCTGTGGTCAAGGGCCCTCTCTGAGGAGCAGGTCTA[G/C]GGCAGGAGGATGCAG GGCTGGGAGGGACCCACCTCGGGGACCCAAAGGAGTCCATTTCTGCCCT

siSG3880 a	36	G C ---				GACAAGAGGGAAGAGATGGCCAGAGACACAGGGCTG/CJGGCAGCTGGGGTCCCTGAGTGCCAGG CGCCACCACAGTCTGTGGGTCAAGGCCCTCTCTGGGAGCAGGTCTAGGGCAGGAGGATGCAG GGCTGGGAGGGGACCCACCTCGGGGACCCAAAGGAGTCCATTCTGCCCT
siSG3895	44	A G ---			---	AATCAGCCATTGTACACATTGCAGCTATGTATTGTAGTTG/CJGJTCTTTTCCATTAACTAA TACATGCCCTCATAGATATTCOAATTAGTGTATCACCATGGGAACAAGATGCTGATTCGTCAACTG AAAAAT
siSG3902	104	T C ---			---	TCTGTTGAGACTGGAGACAGGTACCAAGCACGACTCTGTGGGAACCTGGCTTCCTGATAACA TCATCTATTTCACTAAATGTGAACCTGCTTTCTTTCTG/CJTCAGCTCAATAGCTTAACATCTAATTC ATGTTGCTCCCTTTGCTGGACAAT
siSG3935	50	G A ---			---	GGGTGCTGACGGACAGGCACACCCAGCAGTTTCAACAAGCAATTTGTCCG/CJCTAGTGTGCAGGC TCCTCCCGAGTTCCACAGGCTGAGTACTATGGGTCAACAACCTTCCTGGACGT
siSG40	25	A G ---			---	GAGGAAGAGGTTGAAGAAGTGTG/CJGJAATATATTTAAGATTTCTTGGGAGAAATCTCGTGC CCAAACCTGGTGATGGATCCCTTACTATTTAGAAATAGGAACAATAAACCCCTTGTGTATGTATCA CCCA
siSG4009	32	A G ---			---	GTGTGGGCTGTCTGATGATGAATGGCGGCTC/CJGJACTCTTTACGGTCTTACACTTTTATGCTCCT ATGAATCTCTGATGGCTTTAAGGGCTGAACCAATATCTGAAGTTTCCACACTGCTTACA
siSG4033	123	T C ---			---	AGAAGCCTTGGGACAATGGCAGTGCCCTTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT TGAACCTACAGTGCAGTAACCAAGAACCTAATGTTTTCAAGCATAAAGGTACTTTT/CJGTGAAC AGGTGGGCAACAC
siSG4038 a	29	G A ---			---	GCTGAGAGCACGTGTACAGCCACGCTGTG/CJGGCAGGCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCTCAGTCAGGAGGTTCAAGGCTCCCGGAGAGCACCTGAGGGTTCCATCACT
siSG406	53	T C ---			---	ACTGTGTTCAACAGTATTGCGTTGTCAGACTAGGAAAGCTAAACGAACAAAT/CJGGTTTTAGTT TTGCTGAAGACTGGCCTTATTAAATGGACAGCTTCTCAACAAGAGATTATTAACTTTATCAGGTGTT AACATCTGTTTCAGGAACATGGCA
siSG4095 b	55	G T ---			---	ATCTGGGCTGAATTAGTCAAGCAGGTCAGATACTATTGTCTGCTAGATGTATTAG/CJTATAAAAA GTTTGCTTCTGTAATAGCTTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAAATCAAG CCTTTGGACTAACCCAGGGCATTGCCCTTCATCCCTGG
siSG4095 a	27	A C ---			---	ATCTGGGCTGAATTAGTCAAGCAGGTC/CJGATACTATTGTCTGCTAGATGTATTAGGATAAAAA GTTTGCTTCTGTAATAGCTTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAAATCAAG CCTTTGGACTAACCCAGGGCATTGCCCTTCATCCCTGG
siSG4120	65	G A ---			---	TGCATGTTCCACATCTTTTCAACAGCAAAATGTATAATAAACTTACGTACTTATGGATAATCAC/G/ A/CTTTTCCCTCAGAGAGCCACAGTTAAACACGTTCCAGCACACCACTTAATCCACCCGAGCT

siSG4128	54 A G ---	---	CTTGGCAGATAAGGGACTGTTTGCAGATATGACTTTCCTTTGGTACATTTCTTGGTATATTTT TACTTCTTGAAAATGCCACATAATTTGCAATAATGATTCACTCTTAGCTCCAAAGCAAGTCC TTTATCAAAATGCAAATGTTCCAGAGGG
siSG4209 b	128 G A ---	---	CACGAAACAGATGCAGCCTACACAGTGTGTAGGACCGAGGCTCACAACATCCACATGGCACAAGC AGGGCCGGCCACTCCAGGCAACGAAGCCACCCCGAACCTTGCAGAGCGGCACTCCCTG/GA/GC AGGGGACCACGGAGCGACAGGTCTTTGATGCCTCCGAAGAGCTGAGCTCCATTCCA
siSG4209 a	65 G A ---	---	CACGAAACAGATGCAGCCTACACAGTGTGTAGGACCGAGGCTCACAACATCCACATGGCACA/G /A/CAGGGCCGGCCACTCCAGGCAACGAAGCCACCCCGAACCTTGCAGAGCGGCACTCCCTCGGC AGGGGACCACGGAGCGACAGGTCTTTGATGCCTCCGAAGAGCTGAGCTCCATTCCA
siSG4254 b	31 G A ---	---	CATTACCCAGAACGCCATGGAGGACACAGAGC/GA/CACGGCCGGGACTCCCGCGATGGCTGGGGG GCTATGGCTCTGACAAGAGGATGAGCGAGGGCCGGGGCTGCTCTCCCCCAGGGCGAGACGTGAC TGGGGGACCATGGCCGAAGAGAGGATGACCGGTCA/G
siSG4301	81 T G ---	---	TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAAGAGAGGGTAGTGGCTCCACACTTTCCAT TTAAGCAAAATAAA/T/G/AGCTTCTGAGTAGTGTTCACAGTTTCAACCAACATTTTG
siSG4331 b	71 T G ---	---	CTCACAAGGGCCACACAGAAAAAGATACAAATACATTCACAGCTAATATTTAGTTTATGACAG AGAG/T/G/TTTCAAAAGTTAAGTGTCACCTGAAGAGCATGTTAAAAAGTTTAAAGTTATCACTT GGAGAGCAGATTCTTGGCCCTCGCCTTGTGATCTGTTTGAGGGGTGTGC
siSG4340	76 G A ---	---	TTTTGCAACAACATGGATGGACCTGGAGGCCATTAAAGTGAAGTAATGATACAGAAAGTCAAAAACC ACATGTTCTC/G/A/TAAGTGGAGATAAACAAATGTGTACACCTGGACGTGGAGAGCAGAA
siSG4361 b	109 A C ---	---	TTCCCAACCATTTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGGCAC AAGTCTTGGAATTTCCATAAGGGATAACTGCATCTTTTGC/C/C/CTTCACAACTAGAAAACGACTC AGCGACTTTTCTGTGAGCAAAATGTCGAGG
siSG4361 a	24 T C ---	---	TTCCCAACCATTTGAGTGACAGAGC/T/C/AGTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGG CACAAGTCTTGGAATTTCCATAAGGGATAACTGCATCTTTTGCACCTTCACAACTAGAAAACGACTC AGCGACTTTTCTGTGAGCAAAATGTCGAGG
siSG4376	73 A G ---	---	TTTCACTGCTACTGGTTTCGGTGTCTGAGTCTCAAACTCTGCTTTGCAAGTGTCTTCCAAAGGGGAG AACAG/A/G/CTGGAACCTGCGGCTCTGCAAGAAAGCCATCTTTCCAAAGCCATTTCTTCTCAGCTGC
siSG4381	50 T C ---	---	GAAGGCCACAACACTCCATAGCCAGAGAAATGACAACATACGATTTTCTTT/C/TCAGTCTTTGTAGT ATCCACAGTAGTGTCTGTCCATGTACAAGTGTCTGTCCAGAACACCCCAATTAATTTCCATGCC
siSG4410	79 A G ---	---	ACCAATGGTTCTGCTATGTGCATCCGATATTTTTGGCCGATCTGAAATCTGCAAGGGCTTAACCAT TCAAAACACCGC/G/ITGACAACGAACCCAGTGGACTGTGAAACTCAGGCTGCAGGAGGGTGGCTTGT CAGCTGGGT

siSG443	65	C T	---			AGCAGATCAGTCAGCCCACTTGCTCTCTCTTTAGGGAGAGGCTAGGCAGTGAACACATCA/C/
siSG4430					---	TGTATGCAATGAGAAATACCAACTGTAGGATGGGGAGGGGAGGCGAGGCAATAGGCAC
a	54	A G	---		---	AAATGGAATCTATCTGCTGCTCTCTCAGGTC
siSG4448	99	G A	---		---	ATGCACATTAAATGAATGGCCTACTACTGGAACTTTAGTAGTCTATAAGGTJAGJATTAAACATA
					---	GGTAGGATCCAGTTCCTATGACAGGCTGCTGAAGGAACAGATATGAGGCATCAAGAGGCCAATTT
					---	CCTCCCTCCCTTCCCTTCCCTTCCAGTCTTTCCATACTGTTCCCTCCCTCCGCCCCACCCAGGCTCT
					---	CGCTAGCCCTGCCCTCTGGGTCACTGCGJGJATGGGTAGGCCCCCAAAAA
siSG4449	92	T C	---		---	ATTAGCAATTCATCTTGCAACAATTGCTTTACTGTAACTAAGAGTACTGTACTGATGATGTTTACAAT
					---	TAACTTTGGACAACCTTAAACCTTA/TJTAGTGACATTGCTGTCTAATAATCAATACATTCATCATA
					---	GGCTGAACATAATTATTAAAGAGCAAGTTACCCCTCCC
siSG4467	42	C A	---		---	CAGACATGAGGGATGGCCCTGCTCTCTGGGACAGAGCCCTCA/CJAGATGATGTCCATGTTTGTGT
					---	GAATGAAACTCAAACTCTTCACTTTTAGAGTCAATTTCTGGTATCGAGCGCACACCCGAGGAG
					---	CACACCCTGCTTCCAAAGGCTGCTGCCCTCTGCACACAGT
siSG4475	21	A C	---		---	ACATGTCATTTCCTGACCAGGJACJATTAAATAGTTTATTAGAAGAAATGAGTTGAAGTGAGCGA
					---	TTAAGAGACACAACCTGGACTTTGTTTCTTTACTGTAGCACCCAGGTTTCATG
					---	GTAACATCTGGGGTGGGGTGAGACAACA/CJATGAACCAATAATTAAATACAATTATACATT
					---	TCAAGGAGACTTTAATCTAGTTAATGTGAACGCGACCATCAATGGTTTGTGAGGAAAAGGGAGA
siSG4477	32	A G	---		---	TGAAGTCTGCTCTGGGGCAACGTTTGGCTCATTCAGTCAGACTTGGC
					---	TGAATCAGAGCTGGTGGGAGCTGCAGGCGAGGGAGGCTGGGGGCCAGATGAGCCGCCGGGA
siSG4531	79	C T	---		---	CAGCAGGCGTGGTGGCAGCTCCTGGCGTTGGTAGAAGAGGACATAGGCTGCCCTGGACTCGATCT
siSG4550	86	G A	---		---	GATTCATTGACAGGGGAGACGCTGTGTCATCAA
b					---	TGCATTAAAGGAATGATACGGCATAATTTGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT
					---	AAAAGAGACAGTGGGCACGJGJCAATTGGAGGGGAAGGGCGGCGAGGGTTTATAGAGAAC
siSG4550	85	C G	---		---	TGCATTAAAGGAATGATACGGCATAATTTGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT
a					---	AAAAGAGACAGTGGGCACJGJGCAATTGGAGGGGAAGGGCGGCGAGGGTTTATAGAGAAC
siSG4590	47	A G	---		---	AATCAGGCACAAGCTCGGGAGAGAGCCAAACAAAAGCTCTCTGCACJAGJATGGGAGGGAGACAC
					---	CATTGAAAAGGCATGCTTCTTCTATGCAAGCGAGGCTGCCCTCCACAGGCATGGTCTCCTTG
					---	AATCTGTATCACCCAGCGTGGT/CJCAATGTACTAGTACTTCCACAGGGATTTTATACTATTC
siSG4623	22	T C	---		---	CTATAAGGTTTATCATGAATAAAAAGCTCACAACCTCTTTTCAGCCATTGCAGATTACATTATCT
					---	TAATATCTGTCAAGATGCTCTGGAG
					---	TAAAAAAAACAACCCCCCAAAAAACACCCAGAGTTTTTGTAGTTTTATGTTTTTGTAGTTTTAAAG
siSG4843	102	A C	---		---	GTAATTTCTTTCTAGCTTCTAAATTTTGTAGTCATJACATCAGAAAGCTTCCCTACTCCAAAGGTGA
					---	GAAAGGA



siSG4850 a	38 C T ---	---	---	GGAACTAACTGGGAATGCCGAGGAGGAAGGGGCTC/TGTCACATTGCAGGCCACGTCAGGAG AGCCAGCGGTGCTGCGGGAGGTTTCCAAGGTGCTCCGTGAAGAGCATGGCAAGTTGTCTGACAC TTGGTGGATTCTTGGGTCCC
siSG4879	86 A G ---	---	---	AACCTTCC AACTCTGAAGGGGTGACCTCAACCCAGCCCTTGTCTGTGAGGTCCTGCTTTTGCAGAATGGCCTG CCCCTGGGACTGGAGCAG/GJCTTGGTGAGCTAGGTGGAGGGTGGGGGCGCATAGAAAT
siSG4885	104 G A ---	---	---	AACTGACTGGCTGCTTGTGAGCCGGCTGAGCGGGTGGGACTGGGCTGACCACTCGCTCTTCAG AGACTGCCCCCGGTGACCACGACTACGCTCTGCG/GA/GTGGGAAAGCAGAAAGCAGGACC
siSG4896	112 C T ---	---	---	AAACAAATCAAAACCAATCCCCAGCAGTCTATGTACAGGGCCACTCCCTGCTCTGCCATAGAGA GGTTGGGGCAGCTGAGGAGTGGTGGGGCTGGGCACTTTTC/TGAGCCACAGGCCCTGAGG AATTAATTGACTG
siSG4932	22 G A ---	---	---	ACAGTGCCGATGGTTACACAAT/GA/JTTGTAATGTATTTAATCCCACTTACGAATGATTAATAATGA TAAATCTTATGTTTATTTTCATCACTACCAAAAGGCTGTGGGTGCAAGGGTGTGTTTCTGTGCT
siSG4950	24 A G ---	---	---	TCATGACTCCCAGGAAAGGTCTT/GJCTTAGCTTCCTCTCCCTACTTTCTCTACATGGTCAGC ACTGTAATGTAGCTAAGATATAGTAAGGCAITTGCTCCCTACCCCTACACTTCAAGG
siSG4957	136 G A ---	---	---	AGATACGGCAAAACACTGGGATGGCTTCTGACAACCTTAAGAGGTCTCCGAGTTATATTCTGGGTT GGGAACACTGACCCAGCCCTTATTCCTTCAAGGACTAGTCATTGGCAAGGAGGATTCATGAGCC CC/GA/GTGACACAGATGGGGCCCTGCTCTATATCAAC
siSG4961	91 C T ---	---	---	GAAGTGCTCTGAGGAGGTGTGACTCTCCCTGGCTGACAGGGGAAGGCTTAGCAGAGCTTTGCTTAG AGGAGTAGATGAAAGGAAAGTA/C/TJAGAGAGGGCATTGAGGCCAAGTCAGCAACACAGACAA
siSG4967	72 A G ---	---	---	ACTGTGCTCTCAGCAGATTCAGGGGTGTCGAGGGTGTGTCAGGGCTGTTACCAAACTCAGTAGGAGTGCAA GGGCT/GJTAGCCCCGGAGCTAGACAGCCCTGGGTTTGAATCTCAACTCTCCCTTTTCTTGCTGTGC AACCTTG
siSG4997	22 T C ---	---	---	CAAAGGAGAGTAGGAGCCCCAA/T/CJTTTTAAATGGTTTCTCTCCCTCATGCTATTGTATCCAAAA CTATATACAAATTTGTAGCAGTCTCTGTATAGTTATTACACATGTTTAGAAGGGAGGAGGCAAGAA GGGATAGGGAGAATGGTGATCCAAAAT
siSG6312	37 C T ---	---	---	ACAGGTTCTCACACTTTGAGCCTTTAGTGCAAAAACA/C/TJATGCGCATGCGGGAATATAAATGCTT ATCCAGTGGAGCGCTCCCTGATGCATTGAAATATTAGGACTCAAGCAGAAGAC
siSG6345 a	107 G A ---	---	---	GGCTGTGTCAGCAAAATCTCCAGGACAGAGCAACAAAGGACAGTAAACACACATGTATGACCCCTTA CAAGTGCTTTAAGATTTTAAAAATGTGATGTTTTGTCCAC/GA/JATAGTTTCAAGGCAATTAAGAATAT GCAACCCAGAGAAATTTCTGTGAAAAACATTTTGTCTTTGGCCTGGGTGGACAGAAAGGGTGGCCAA ATGGATTGAGTGATGAGCAGCATG

siSG6362	88 G C ---	---	TGTGAATGTACACTCAGGTCTAACAAATACCTATTATTCTCTGTTAAGAAGGTTTAGCAGGAGCCTCCAATGAGCACTGTATGTA[G/C]AGAAAGGGAAGGAGCAGGAGGAGGAACAGATCTGCACAGAT
siSG8010	62 G T ---	---	CACATCTGTGTTCTGGAGCAAGGGAACCCACAGAAAGCCAGGAGTTGGGTGTGCACTGG[G/T]GTCTTCAACTGGGTGGAACCAACTGAGTCCTTGAAGTCGCTCCTGAGGCTGCAGAAAGATAGA
siSG8022	53 G A ---	---	AGTCTCTGACTCCTCTTCAGTGACGTCATGTTGTAGCCTGAAATGGACCAC[G/A]GTGGGAGTTATTACACCATGGAACTGGAAACTCTACAAATCAATGCGTTATTCTTTATTTTCAGAGGGCAGGTTATCAGCACACGCTGTATCTCC
siSG8032	67 G C ---	---	TGATTGTTAGGATAAGTGGGCATTGTGTTTACAAATTACTTCCAAAGAAATTCAGAAATTTGTGTGTTG/CJTGGGAGCAGGTAGCAAGATAAAAGAGGGAGGACAGCTGGGTTGGTAAAA
siSG8064 b	46 C A ---	---	AGCTGGCTCTTCTCTGTGCGTGTTCGGGAGGCTTACGTCCTCG[C/A]CGGTGGTCCCTGGGTGGCC
siSG8064 a	23 G C ---	---	TGCAGGACCAGGGGTGGGAACAATGCCAGGGAGAAATCCTGTACATCAACACAGGGAACA
siSG8072	59 A G ---	---	AGCTGGCTCTTCTCTGTGCGT[G/C]TTCCGGAGGCTTACGTCCTCGCCCGTGGTCCCTGGGTGGCC
siSG8100	40 A G ---	---	TGCAGGACCAGGGGTGGGAACAATGCCAGGGAGAAATCCTGTACATCAACACAGGGAACA
siSG8102	138 T C ---	---	CACCATCATCATCGAGTAGGCTGAGGAGCAGGAGGGGTGGTCTTCTGTCTTAGGG[G/G]TGGCAGAGGAGAAGGAAGTCCGAGTATTAGTGGCCGATCGAGTCAAGCCTGTGCTGTTCAAAA
siSG8105	110 A G ---	---	ATACACCCACACACCCACTCAACCTTGTATCAAAATCC[A/G]AAGTGAACATAAGTATAAGAAATATCATGACTAGTTAAAGATAGCAAAATACCAATAAGGTACAAGTTCAAGTATTAGTATAACAAGTATCTGAGTAACAATGTCTTGGAAATGGG
siSG8130 b	96 T C ---	---	AAGGCTCCTTTGAAAGCATGGTTATTGTTCCATTAACTGTTCTCAGCTATACTGAAGTATGATTGACAAATAAACTTGCATATATTGAGATGTACAGTGTGATGATACATGTATGATACAAATGTGAAA
siSG8130 a	36 C G ---	---	TGAT/CJGTGCATAATCATATAATCAATAATTGGTATATTGGTTTAGGAATGTGATGGT
siSG8145 b	124 T A ---	---	CAGTGGTTCTCAAACTCCAGCGTACACGAGGATGGTCTTGCTTGTAAATACACAGATGACTAGGCCCACCTGGGGAGTTCCTGTGGAGTCTAGGCCCTGAGAAATTC[A/G]TTTCTAACAAAGTCCCAGGTGACCCCTGAGGCTCTTGACTGGGGAACATGCTTTGAG
		---	GTGTGTACATCATTTGGGAATGGAGGAAATAAATGACTGGATGGTGGTCTGCTTTTAAGTTTCAAAATTGACATTCCAGACAAGCGGTGCCTGAGCCCT[C/GTGGCTGTCTTCAGATCTTCACAGCACAGTTCC
		---	GTGTGTACATCATTTGGGAATGGAGGAAATAAATGA[C/G]TGGATGGTGGTCTTTTAAGTTTCAAAATTGACATTCCAGACAAGCGGTGCCTGAGCCCTGTGCTTCAGATCTTCACAGCACAGTTCC
		---	TTGGGAGCTTCAAAATTCCTTCTTCAGATTTTAAATGACATTATGATGATACATATTTTAAATTTAGACACATTTTAGAGAACACAAATGTGAACACAAATCTAAGAAATGAATGAGATGTT[A/J]CTGAAA
		---	TCTGATTCAAAAGACTTATCTTAAAGTACTGACTTCTGTCAATCCTCTCTGCTGTGAAGG

siSG8145 a	97	C T	---	---	TTGTGGACITTCAAATTCITTCCTTCAGATTTTAAATGACATTATGCATGTACATATTTTAAATTT AGACACATTTTAGAGAACACAAATGTGAACCTGACAAATCTAAGAAATGAATGAGATGTTCTGAAA TCTGATCAACACACTTATCTAACTGACTCTGTCATCTCTGCTGTGAAGG
siSG8150	36	A G	---	---	ATTGTTCTTGCAATTGCTTGGATTTTTCAGAAATAGTGA/JATAAATAAATACGGGAATCCTAGGCAT TCGTGTTTTCTATGTTTTTAAACAGGATTTTCTCTAATGTTTCTGCTATTAAATACCATGCAGGAAAT GGGAAAT
siSG8340	30	C T	---	---	AGAGGATTATGGAGAGAGCTGGGAGGATCCTTCAACATTATGACCCCTGAACCTCCAGAACTGGAT TCACTAGAAAGAGAGAGAGAAAACGCTCATCAAAA
siSG8466	111	G A	---	---	TGTGATTGGGTGACTGTAGCCTAAGGATAAATGAAATAATGACAGCAATGTTTAAAGCAGTGGGA GGAGTGAACCTGGGAATACTTGGTTACAAGGTATTTGCACTACCT[G/A]TGAAGCAGCACAGCAATTAT TTGAAAG
ESTD-ACE	--	--	---	---	GATCAAGCAGTGCACACGGGTACGATGGACCAAGCTCTCCACAGTGCACCATGAGATGGGCCATATA CAGTACTACCTGCAGTACAGGATCTGCCCGTCTCCCTGCGTGGGGGCCAACCCCGGCTTCCATGA GGCATTGGGGACGTCTGGCGCTCTGGGTCTCCACTCTGACATCTGCACAAAATCGGCTGC
ESTD-ADA	--	--	---	---	ACCATCTTATCTATGGCAGGTAAAGTCCATACAGAGGCCCTCTCTCCCTGGGATTTGAGTGGGTC CCAGCTCCACCCAGAGGCCCTGGGAAATCCAGGGCTACTTCTCTGCTGCTGCTGCTGGGAAT CAAGCCAGCTCCAGGCCAGAGTGGGACTGTGAGGACATGGAGGCCCTCGGCACTGAGCTGCAGACCC GCAGACCAACTCCTGAGCTTCTTGGGCCCTGAGTCTGTCCTC
ESTD-AK- 168	--	--	---	---	GGGAGTGACAGCTAGAGCACCAAGGGGGGCTCTACAGCTGTGTTCTCATGGAGGACAGGCTTCTGCTC ATTCTGG
ESTD-ALB	--	--	---	---	AATCCAGCACTTTAGGAGGCTGAGGCAGGCATATCACAGAGGTCAGGAGTTTGAGACCACTGA CCAACATGTTGAAACCCCATCTCTACTAAATAACAAAATTAGCCAGGCATGGTGTGCATGCCGTG AATCCAGGAGGCTGAGCAGGAGAAATCGCTTGAACCTGGGAGGCGAAGGTTGTGTGAGCCGAGAT GGCACCATTCACCTCAGCCTGGGCAACAAGAGTAAACTGCTCTTC
ESTD- ANT1	--	--	---	---	TCTCCTGTCAATTCCTACTCCATTAGTTCAAGGTCAAGTGAAGAACTGGGGCAATTAACCAAGTAATCA TGGACTGCCCAACTCGAAACAAGAGGGCGCAGTGGAGCAGGAGTATTATGCTACGGCGTTACCTT TTTTATGGAGGACCGAACTGAGGCTGAGCTCAGATGATCCTGT
ESTD- APOA2	--	--	---	---	CCAGGTGTTGTGGCACGTGCCCTGTAAATCCAGCTACTCGGGGAGACTGAGGCATGAGAACTTTTGAAC CGGGAGGCGGAGGTTGCAGTGAGCTGACATCGGCCCACTGCACTCCAGCCTAGGTGACAGAGCAAG ACTCC
ESTD- AFSB	--	--	---	---	GGAAGAAATGGAGCCTGTGGGAAGGAGCGTCCGAGGGGTGGCTTTGTGGCAAGGCCCTTGTCTGA AGCAGAAGGGGTGAAGAACCGGGAGCTCATCCATCTCTGACTGGCTGGCCAACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGAATGGCTTGCAGCTGTGGAAACCACATCAGTGAA GGAAGCCCATCCCCCAGAAATGAGCTGCTGCATAATATTGACCCCAAC

ESTD- AT3a	--	--	--	---	---	AGACCTCAGTTTCTCTTCTGTAAAAGGGAAGTTTGTCTTGATCTCCATGGGCCAGCCAGCACTG GTCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGACCCAGGTGGAGAGAAATTTGAAAGGGCAATTG GAATTCAGAGCAAAAGAGACAGATATTAAAGAGCTGGGAAATGTGG
ESTD- B3AR	--	--	--	---	---	GGCTCCAGGGGTTCTGTGGGAGGCGCCCTAGCCGGGGCCCTCTCTGGGCTGGGGTCTGGCCACC GTGGAGGCAACCTGCTGTGTCATCGTGCCATCGCCGGACTCCGAGACTCCAGACCATGACCAACGT GTTCTGACTTCGTGGCCGCGAGCCGACCTGGTGATGGGACTCTGTGTGGCCGCGGGGCCACCTTT GGCGC
ESTD- BA511	--	--	--	---	---	GGCAACATAGTGAACCCCATCTCTACAAAAAATACAAAAATTAGCCAGGTGTGGTAGCAAGTGC CTGTAGTCCAGCTACTTGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGAGGTGGAGGTGCAG TGAGCCAAAGATGGTGCCACTGCA
ESTD- BCL2	--	--	--	---	---	AGCTGGATTATACTCCTCTCTTCTGGGGCCCGTGGGGTGGAGCTGGGGCGAGAGGTGCCGTT GGCCCCGTTGCTTTTCTCTGGGAAGGATGGCGCACGCTGGGAGAACAGGGTACGACAAACCGGGAG ATAGTGATGAAGTACATCCATTATAAGCTGTGCGCAGAGGGGCTACGAGTGGGATGCGGGAGATGTGG GGCGCGCCCGCGGGGGCCCGCCCGCCGACCCGGGCACTCTCTCTCTCCCA
ESTD-BCR	--	--	--	---	---	CAGTGGCTGAGTGGACGATGACATTCAGAAACCCATAGAGCCCGGAGACTCATCATCTGCGCAAGA GACCAAGAGGTCAGCTTCTGTTTCCCGGGAAGGGAGGCGAGGTGACAACTACTCTGCTTCAAA ATCAACCATCCGGTGGACACTGTGGCTGCCATCTGCTCTGGCACA
ESTD- BRCA1a	--	--	--	---	---	AAGAAGAGAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGCCCAAGATCTCATGTTAA GTGGAGAAAGGGTTTGCACACTGAAAGATCTGTAGAGAGTAGCAGTATTTCACTGTACCTGTGAC TGATTATGGCACTCAGGAAAGTATCTGTTACTTGGAAAGTTAGCACTCTAGGGAAAGGCAAAACAGAA CCAAATAAAT
ESTD- BRCA1b	--	--	--	---	---	ACTAAATGTAAGAAAAATCTGCTAGAGGAAAACTTTGAGGAACATTCAATGTCACTGAAAGAGAA ATGGGAAATGAGAACATCCCAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAAAATGTT TTTAAAGAAAGCCAGCTCAAGCAATATTAAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTA TTAATGAAA
ESTD- BRCA1c	--	--	--	---	---	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGGAAGATAC TAGTTTGTGTAATAATGACATTAAAGGAAAGTTCTGCTGTTTTAGCAAAAGCGTCCAGAAAGGAGAG CTTAGCAGGAGTCTAGCCCTTACCCCATACACATTGGCTAGGGTTACCGAAGAGGGGCCCAAGA AATTAGAGTCTCTCAGAAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
ESTD-C1R	--	--	--	---	---	ACACAGGTGCTGGCACTGGGGCTGGGGATCCTCTCCCTTAATTGCTCCGGGAAGCACATTCATCAA CCAGTCAAGTTGGGGACAGCCATGCAGTGAAGCTCTGTGTAGGCTTTCAACCATGCAATTCATCTAA GCTCTGCAAAAT
ESTD-C6	--	--	--	---	---	

ESTD-C7	--	--	--	--	---	---	ATATCGTGGCCTTAGTTACGTAGAGCTGGACAATCCTGCTGGA
ESTD-CB22	--	--	--	---	---	---	GGCAAGTTTTATTGATAGAGAGGAATCAAATAATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGCAGTGGCCAAACCATAGGGCGGATACAAAAGAC AGGCAAGGAAGGGGTAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAAGCAAGGAGGACCTAG TAACATAATTGCTCTCATTATGCTCTTCCCGGCTTCTCTCTCACACAC
ESTD-CB23	--	--	--	---	---	---	TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCAATTATGGTCTTCCCGGCTTCTCTCACACATACAGAGCCCCCTACCGAGGACGACAGCT CTCAGAGCAACCCCTAGCCCCATTACCTCTTCCCTTTCAGAGGACCTGAAAAACGTTTCCACCCGA GGTGGCTGTGTTGAGCCATCAGAACGAGAGATCTCCACACACCAAAA
ESTD-CB24	--	--	--	---	---	---	ACCAGGACAGACAGCTCTCAGAGCAACCCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAA AAACGTGTTCCACCCGAGGTCGCTGTGTTGAGCCATCAGAGCAGAGATCTCCACACACCAAAAG GCCACACTGGTATGCTGGCCACAGGCTTCTACCCGACCAACGTGGAGCTGAGCTGGTGGTGAATGG GAAGGAGGTGCACAGTGGGGTCAGCACAGACCCCGCAGCCCCCTCAAGGAG
ESTD-CB25	--	--	--	---	---	---	GTITTTCTTCAGACTGGCTTACCTCCGGTAAGTGAGTCTCTCTTTTCTCTCTATCTTTCGCCGTC TCTGCTCTGAACAGGGCATGAGAAATCCACGGACACAGGGCGTGAGGAGGCCAGAGCCACCTG TGCACAGGTACCTACATGCTCTGTTCTTGTAACAGAGTCTTACCAGCAAGGGGTCCTGTCTGCCAOC ATCCTCTATGAGATCTTGCTAGGGAAGGCCACCTTGATGCCGTG
ESTD-CB27	--	--	--	---	---	---	TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTGTGTTGGGCTGGTTGCATTCAGGAGTGTCTGTGGAGTCTGCTCATCTGACCTATCTTCTGA TTTAGGGAAGCAGCATTCCTTTGGACATCTGAAGTGACAGCCCTCTTTCTCTCCACCCCAATGCTGCT TTCTCCTGTTCATCTGATGGAAGTCTCTCAACACCATTTCCATACC
ESTD-COL2A1c	--	--	--	---	---	---	AGAAATGATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGTTGACATACGTTGCTATTATGCTCTCTTTCCTGTCACTTTCAGGGTGTTCAGGGTGGAAAAAGT GAACAGGGTCCCGCTGGTCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACAATACTGCGCTTG GTCAGCCTATTGAGCTGTAATACCATACCGTACCT
ESTD-COL2A1d	--	--	--	---	---	---	TGAGAGAACACCTAGTCTCCATCTTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTGCTGGGACCTGGAACACTGGACTCTTCTACTGCAGCAGACAAGACTTACCC AAGAGAGATTATGGCAAGATATACAATAACAATTTTATTTGACCAAAACACTATCATGGAACAGC ATT
ESTD-CPT2	--	--	--	---	---	---	GCCGCAATGCCCGGAGTTTCTCCAATGTGTGGAGAGGCCCTTAGAAGACATGTTTGATGCGCTTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGCAGATGAAAAGCTACCATCACTTCTCATCATGAAAAAC TGGAGGCGCGGCATAGTGTCTGCTGATGCCGTGTAATCCAGCATTTTGAGAGGCTGAGCGGGTGGATCAC TTGAGGTGAGGAGTTTGAGACCAACCTGGCCCAACAT

ESTD- CTLA-4	--	--	--	---	---	---	ATGGCTGGCTTGGAATTCAGGGACAAAGGCTCAGCTGAACCTGGCTACCGAGACCTGGCCCTGCAC TCTCTGTTTTTCTCTCTCATCCCTGTCTCTGCAAGCAATGCACGTGGGCCAGCCTGCTGTGGT ACTGGCCAGCAGCGAGGCATCGCCAGCTTTGTGTGAGTATGCATCTCCAGGCAAGCCAC
ESTD- CYP2D6	--	--	--	---	---	---	CAGGCCAGGTGGTCGAGGTGGTCAACATCCCGGCAGAGAACAGGTGACGCCACCACTATGCACAGGT TCTCATCATTTGAAGCTGCTCTCAGGGTTCCCTTTGGCTTGAGCAGGGCCGAGAGCATACTCGG
ESTD- D11S1873	--	--	--	---	---	---	AAAAACAATTTAACACCTTTTCAATCATATACACCATAAATTTCCATTTTTCACATAAGTCAGTT TGAGCTGAGTTTTCCAATTACTTGCAATCTAAATGTCATAACTGATTAATGCAAGTTCAACAGACA ACTTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATATGCCCATAT CTGCATGTC
ESTD- D17S33	--	--	--	---	---	---	CATCCCAAGCCATCCTTAGCAGCTGGCATTTTGGCGCTCTGACAGATACACTCAGGGCCGT CATGCTGCACATCCAGGGGGCCCTACCTTTGTAGTCCATGGGAAGGCTCTCTGGGGCGGTG GGGTGTGGCTATGTGGTGTCTTGTGTAGACGGGGCTTTGGTTTCAGTTGCACATTTGCGTTATT GCAGATTGCTTTGTCTTCCACCTGAGCGAGCCTC
ESTD- D18S8	--	--	--	---	---	---	TTTGAGACCACCTGGCCAAACATGGCGAATCACAATCTCTACCAAAATTAACAAAATTAGCTGGGTG GGTGTACATGCCATCGTAATCCAGCTACATCGGGAGGCTGAGGCAGGAGAAATGCTTGAACCCA GGAGGCAGAGCTTGAGTGAGCCAAAGATCACCCACTGCACCTTACAGCCTGGTGACACAGTGGAGA CTCTGTCTCAA
ESTD- D3S11	--	--	--	---	---	---	AACTGATTAGAACCCTGAAAATACATATTTATCTGAAAAAAGTGGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAATAAATCCAAATAAGTACACTGTAAATAAGAAATTAACAGAAATATCATTTGT TTATTCAAACTATTTATCACATTTATTTATTGGTAAGCCATACTAAATTTCTAAAGCATGTTTCTGAAAG TTTTA
ESTD- D3S12	--	--	--	---	---	---	AGGTTCCACATTATTGCTGATGTTTGTGATGTTTCCAGGAGCCTTGATGTCATTCTGTATCTCCTCAG GTATCCACCTTGAGACGTACTTTTCAAAAACCTCTCTACAGCCGTTGTTGTTATTAAATCAAGGTTGA ACATAAAGTA
ESTD- D3S2	--	--	--	---	---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAAACTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGATTTCCC AGAAGTGAACACATACTGCTCTAGAACCCAGAGTCATACTGGATGTTCTGTTCGGTCTTCACGATGG CAGGTATGAATATAATAATCTGTCTCTTTATTGGAAGGATGCGCGGTATGT
ESTD- D4S338	--	--	--	---	---	---	TTTTCTGTTTACCTGTTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATGAAATGTATTT CTTAACAATAAATCTGAAAGTCCAAAATTTACCTTTGATCCATGGACTGCAGAAATAAATGTTATTT TAGCTGTCAGAAAAACAATACTAATCTTGTCATATGTTTCATCAGAGCCCTTTGGGTGACCCAGGTGTTT GCCAATAAGCAGTAATAATTTTGGAGGGAATCTTGTTTTCATGCAAGTAG
ESTD- D4S95	--	--	--	---	---	---	CTTTTCATGCAGGATAGGCTTCTCTACTAATACAGAAATTTTGAGAAGAGCAAAACAACCTTTCAAGG ATAATGGGCAATCACTTCTTCTTCTTCTTTAGAGTCTACCGG

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ESTD- D7S399	--	--	--	---	---	TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCCTACATCATCTTTTCAAAAATTTTCATCCATGGACTCCATACTAG AATATTTGAAGAAACAAACATGACAAAATTTTC
ESTD-DM	--	--	--	---	---	GTGGGGACACGAGGGCTCCAGGCTGGCGCTTGACAGTGTGGCTCAAGCAGCTGCTCGGCCTCCACT TCCATGGGTGTGGGCTGGGACCTCACTGTCCCTGGGGAGAGGAGGGAGTGGGAGGGGAGACA GAATGCTGATTATCTGGTGGAGAACCAAGAACTTCTGGCTGTGGCTAGGGCAGCTGCTTCCAAAGACC TCCTGATTTGAGGAAGGGAGCAGCAGAGCGAAGAGACAGAT
ESTD- DRD1	--	--	--	---	---	TCCCAGCCCTATCGGTATATTGGACTATGACACTGACGTCTCTCTGGAGAAAGATCCAAACCATCAC ACAAAACGGTCAGCACCCCAACCTGAACCTGCAGATGAATCTCTGCCACACATGCTCATCCCAAAGCT AGAGGAGATTGCTCTGGGCTGCTATTAAAGAACTAAGGTAC
ESTD- DRD2	--	--	--	---	---	TCTGCCCTTGGTCAGGAGGCTGCCCGCGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGGACCCGGTACAGCCCATCCACCCAGCACCAAGCTGACTCTCCCGACCCCG TCCCACACGGTCTCCAGAGCACTCCCGACAGCCCGCCCAACCCAGAGAAATGGGCATGCCAAAG ACCAACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	--	--	--	---	---	AAGACGATGGCCAGGATGAGCGCGCAGTAGGAGGGCATAGTAGGCATGTGGCGGGCTGGCTGG CACTGTGGAGTTCTGCCCCACAGGTGTAGTTCAAGTGGCCACTCAGCTGGCTCAGAGATGCCATA GCCAGAGGGAGGTGGTGTATGCCAAGGGCTTCTCTGTGAGGAGA
ESTD- ERB82	--	--	--	---	---	TCTTTCAAGGATCCGATCTGGCCCTGTTGGGCATCGCTCCGCTAGGTGTACGGCTCCACCCAGCTGG GGTGAGGGGGTGGTGGTCAAGTCCGGGGGCGGGTGCAGACCCACCGGGCTGGGAGGACTTCACCC CGCCTCACCTCCGTTTCTCGCAGCAGTCTCCGCTCGTACT
ESTD- ETS2	--	--	--	---	---	ACTCACAGTGCCTTTAAGTGAATGGTCGAGAAAGAGGACCCAGGAAGCCGCTCCTGGCGCCTGGCA GTCCGTGGGACGGGATGGTTCTGGCTGTTGAGATTCTCAAAGGAGCGGATGTGTGGACACACAC AGACTATTTTAGATTTCTTTTGCCTTTTGCACACGAGGACGCAATGCAAAAATCTTTTGAGAGG GTAGGAGGGTGGGAAGGAAACCAACCATGTCATTTTCAGAAAGTTAGTTG
ESTD-F2	--	--	--	---	---	GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCTAGTAGCCCAACTGTGCATGCACGCTTAACCTCT GCACAAATGGCTCCAAAGGCCCGTAGGGGAACCTGGGGGATCTAGGGGATGGGTGAGGAATGGCCC AGCCAGTCCGGCCGGTGGTGGTCCCAACAGAGGAGGCGCTGGAGGAGGAGACAGGAGATGGGC TGGATGAG
ESTD-F9	--	--	--	---	---	AGATCCTGATGATTTTTCCTATTTTCTAAATGTTTACAGTTTGAAGTTTAGATTTATGCCCA TGCTCCATTTTGAGTTAATTTGTGTAAGATGATGTTTAAAGTCAAACTTCATTTTTTTTCCATA GGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACAAAAAC

ESTD- GCH	--	--	--	---	---	---	CGCAGACCGTGAGTGGGGTCGGAGTGTGGAGGGAAGGAGGAGGAACTGGGGTTTAGGGACT TTCCGGGTGACTTTCCCGTTCTGTGCTTGCAGAGAAGCGGGAGAACACAGAGCCAACTGGCTAA GTGTAAGGACCTCTGGTGCACCGTGTGTCTGCTGCCCTGTTACGCTGTCTGTCTGCGCGAGTCGA CTCTGTCCCGGAAATCCGAGAGCT
ESTD-GCK	--	--	--	---	---	---	GTTTATGTCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCTCTGGTCACCATGAC AACACAGGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGATCCCCACCCACACCTGGCTGG AGCAGGAAATGCCGAGCGCGCTGAGCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTCACC TGCAGCCTAATTACTCAAAGCTGTCCCGAGGTACAG
ESTD- GNAT2	--	--	--	---	---	---	GACCTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACACAGGCATCATTG AAACCAAGTTTCCGTCAAAGACTTGAATTCAGGTAAGTGCATGGTTCCCTAGG
ESTD- GPPK2L	--	--	--	---	---	---	AGTCTCATCTGCGGTGTCAGGTAGATCCCTTTACCCGCCGAGAACTGCTCGATATC
ESTD- HRAS	--	--	--	---	---	---	CTGGCTCGCCCGCAGCAGCTGCTGGCACTGGACGGCGCGCCAGGCTCACTCTATAGTGGGTGG TATTGCTCCACAAATGCATCTGGATCAGCT
ESTD- HSD3B1	--	--	--	---	---	---	TTGAAAGTTCTCCACTGTTAACCCAGTCTATGTTGGCAATGTGGCCTGGGCCCCACATTTCTGGCCTTG AGGGCCCTGCAGGACCCCAAGAAAGGCCCAAGCATCCGAGGACAGTTCTACTATATCTCAGATGACA CGCCTACCAAAGCTATGATAACCTTAATTACACCTGAGCAAGAGTTGCGCCTCCGGCTTGATTCC AGATGGAGCTTCCCTTATCCCTGATGATTTGGATTGGCTTCTCTGCTG
ESTD-HT2	--	--	--	---	---	---	GGGCTAAATTTCCGAGCACTTTGCATAGACTGTTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGAGAGGAAAGATGTGTACAGTTTGTACAGAGAATAAAAGGATAACCTGGGGTTTCTGTGC TTTGCTTCTACATCCCTGGGGAGTTAATAGCTGCAATTTTCAAAGAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTCAAAGACACACCTT
ESTD-HT4	--	--	--	---	---	---	ACCAACGAGCGCGATACAGACACTCTTAAGTTTTCCTAAGGCTCATTCAAATCATTAGGCATTTT CTGATAAACTAGGTTCTTGGGTGCTTCTATCGGCAAGATGCGTACTATTTGAATAGTAGAGGTAA ACCACAGCCCCCAAGAGTCACTGAGACTGGCAGGCTTCTGACGAGGCGTGAACCCCGTAGCCTAAA TGACAGCGGAAGAGGCGCGAAGACATGCAGATGTGC
ESTD-HT5	--	--	--	---	---	---	AACACAAAGCCCCAGCGAGAAATTGAACCTCGCGACCCCTGGTTTACAGACCAGTGTCTTAACCCCT GAGCTATGGAGCCCTCGTCTGCTGTTGGTTTCTCTCTTCACTCTATAGATTGATGTTATGCTCCTA GCATTCCGGCTACCGAATAGGATGTTAGCTTGAGTAAATTCAGGATATTCCTACAAAATGAAA ACATTTCTGTGCTCTGTAATCCCTCGAAAAGTTCT
ESTD- IGFBP1	--	--	--	---	---	---	ACCCAGTGGAGCCCGCTCATTTGCACGGTCTTGGCAGGAGGTGCCCTGGGAGAAGAGGAGATGTTTC CAGGGCACACATAGCTTAGTGGAGACTC





ESTD-NFKB1	--	--	--	---	---	AACATGGACTTGATATTGTACAAAAAAGTTTTTCTAAAAAGAAAAAGAAAGAA
ESTD-NPPA	--	--	--	---	---	AAATTTAAAGGGGTACTATATCCACACTGCACCTGCTAGCCCAAAACGCTCTATTGTGGTAGG
ESTD-NRAMP	--	--	--	---	---	ATCAGCCCTCATTTTGTGCTTTGTGAACCTTTGTAGGGAGAGAAAGATCATTTGAAATTTCTGAG
ESTD-NRAS	--	--	--	---	---	AAAATCTCTTTTAAACCTCACCTTTGTGGGGTTTTTGGAGAAAGGTTATCA
ESTD-OTC	--	--	--	---	---	TGTCCCTAGGCCAGCCCTGCTTGCTCCCTGGCTGTTATCTTCAGTACTGCAAAAGAGAACACAGAC
ESTD-PAL1	--	--	--	---	---	AT
ESTD-PAR	--	--	--	---	---	GGAGGAGGAGTGGGGAGGGGTCTGTCTCCAGGTCACAGACAGAGAGGCGCCTCAGTG
ESTD-PBDA	--	--	--	---	---	TATCCCCACCCCCAATGTGGCGCTGGGAGATGAAGAGGAGTTGATGSCAGGT
ESTD-PS-1	--	--	--	---	---	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATAATCTTTCTGCAGGCATATAGAATTTGGT
ESTD-PXMP1	--	--	--	---	---	GGTTTTCTTTATGTAGGTGATATTGGATACCTTTTGTGTGATTATATATTAGCAATTTGAGGG
ESTD-PerIRDS	--	--	--	---	---	ACAAACCAGATAGGCAGAAATGGGCTTGAATAGTTAGATGCTTATTAAACCTTGGCAATAGCATTGC
	--	--	--	---	---	ATTCCCTGTGGTTTTTAATAAAAAAT
	--	--	--	---	---	GTGACCTTCTCACTTTAAAAAACCTTTACCGGAGAGAAATTTAAATATATGCTATGGCTATCAGCAGA
	--	--	--	---	---	TCTGAAATTTAGGATAAAACAGAAAGGAGAGGTATGTAACA
	--	--	--	---	---	GCCACCACCCACCCACCCAGCACACCTCCAACCTCAGCCAGACAAGGTTGTACACACAAGAGAGCCC
	--	--	--	---	---	TCAGGGGCACAGAGAGTCTGGACACGTGGGAGTCAGCGTGTATCATCTCGAGGCGCGCGGCAC
	--	--	--	---	---	ATGCGAGGGATGAGGAAAGACCAAGAGTCTCTGTTGGGCCCAAGTCTTAGACAGACAGACAAAACCTAG
	--	--	--	---	---	ACAATCACGTGGCTGGCT
	--	--	--	---	---	CTCTTCAGGAACCCAGCTCTCTTACCACACGACTTATTTGCTGTCCGAGAGGTACAACCCGTAGA
	--	--	--	---	---	ACTTCTCCTAACTGTAATTTAGTTAAAGGAATCGAACTGGCTCTGAAGACATGGAGATACTGCCT
	--	--	--	---	---	AATGACTGGCTTTCATTAGCTCTGTGAGTGTTTTCTTTCACATTTCTGTGTTCTAGAACGTTTTCTAG
	--	--	--	---	---	GACTGGCAGTTTAAGCTTTCATTAGGCTTCTGTATACCCATGCC
	--	--	--	---	---	CCTTCTCATGCCAGATGAAATTCACGTCCCTTCAGGATCTGCCATACCTGTGACAGTCTAAAGAGT
	--	--	--	---	---	CTGAGCGTGGCTGGGAAGGCGAGGACTAATCCAAATCTCTACCGCAGCTTGCTCGCATACAGACG
	--	--	--	---	---	GACAGTGTGGTGGCAACATTGAAAGCCTCGTACC
	--	--	--	---	---	GGGGAGTAAACCTTGGATTGGGAGATTTCATTTTCTACAGTTCCTGGTTGGTAAAGCCTCAGCAACA
	--	--	--	---	---	GCCAGTGGAGACTGGAACACACCACTAGCCCTATTTCTAGGCCATAATAATGGTTTGTGCCCTTACAT
	--	--	--	---	---	ATTACTCCTTGGCATTTTCAAGAAAGCATTGCCAGCTCTTCCAAATCTCCATCCACCTTTGGGCTTGTTT
	--	--	--	---	---	CTACTTTGCCACAGATTATCTTGTA
	--	--	--	---	---	ATGAAACATGGTCTTTAAATTTATGATATGTTTATAGTACTCTTAAAGGGGCTCTTTTTTTTA
	--	--	--	---	---	ATGCAGAAAGAGGGGAAAAAGAGCGAGCTGTGGTGACAAGGTGTTTTCTCAAGGCTCATACAGA
	--	--	--	---	---	TTCTGAAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAAGTCTTATGAAATTATAATCTT
	--	--	--	---	---	ACCTACAGACGTGCTGGATGGTGTGCCAACCCCGAGGAATCTGAGAGCGAGAGAGGGCTGGCTG
	--	--	--	---	---	CTGGAGAAAGAGCGTCCGGAGACCTGGAAGGCCCT

ESTD-FDS	--	--	--	--	CCGAGGAATCTGAGAGCGAGAGCGAGGGCTGGCTGCTGGAGAAAGAGCGTGCCGGAGACCTGGAAGG CCTTCTGGAGAGTGTGAAGAGCTGGGCAAGGGAACAGAGTGGAAGCCGAGGGCGGAGAGCGAGG CCAGGCCAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCGAACTAGTGCACCT CCAGAAACGTGGATCTCCCCCTCATCCAACTCCGAAAGTCTGAA
ESTD- RYR1	--	--	--	--	CTTCGTGACGGGAGGTACGCTCCGCTCTTTCATGGACATATGGATGAGTGTCTGACCATTTCCC CTGCTGACAGTGTATGACACGCGCAGACTTGTCTACTATGAGAGGGGAGCTGTGTGCACTCATGCGCGC TCCCTCTGGAGCTGGAGCAGTGAATCAGCTGAGTGGAGTGGAGCCACCTGCGCTGGGGCCAGCCACT CCGAGTCCGGCATGTCTACTACCGGCGAGTACCTAGCGCTACCCGAGG
ESTD- SPTB	--	--	--	--	TGAAACACCCCTGTGGTCCGGAGCCAGGTTGTGTTCTCCTCGGAGCCTGAGGAGTTTGTCTGTGTG CAGTCCCCCGCCACCTGCTGGTTGAGCTGGACATACACCTTCACCTCTTGGCCCGGAGAGAC ATTTACCCACTGGCCATGTCCCTGGCCTGTTGTGCACACCCCTCTGTGAAGACCCCAACCCCTGCCTCC CCACCCCAAGCCAGTTTCTCTAGCAAGGCGCAGGAC
ESTD- SSA1	--	--	--	--	TTCACTTTGTGGATTGTTCTTTGCTGTGCAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAG TTTGCCTTGGCTGCCTGTGCTGTGGGATATTTGAAGAGATCTTTGCCAGTCCCAATGTCTAGAGAG TTTCCCAATGTTTCTTGTATAGTTTCATAGTTTGAGGCCCTTAGATTTAAGTCTTTAATCCATTTTG ATTGTATTCTGTGA
ESTD-TAT	--	--	--	--	AAATGGTCAGGACCCCTGATCCACAAGAGTGGTACCATTTCATCAGGGCCCATCAGTTCATTGAGCTC CCATGACTGGGATGCTAAGTCAAGCACTGAGTTCAATTCATCTTAAATGACTTGTGGGACAGGATCA ATTTCTCTCACCTAGAACGTTTGTTTACAACTTTCTCCAGTATGGATGGGATTTATGATGGGGG GAGAAGCAAATTTTAAATAGGACCCATGAGACATCA
ESTD- THR8	--	--	--	--	TGCGGCCTTTCCTCCGGCAGGGTAGACTTCTTACTTGGCTGTGATTTCAGAGAAAGAGTCCCAAG CACACGAAACAGAGTTGCAGATCCCATGAGGCCAGTCTCAAATCACACAGGATCACTTCATCCA CACTGGATTGGCCCAACAAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG
ESTD- TNFA	--	--	--	--	TTCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACCCAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGGCATGAGGACGGGTTTCAAGCTCCAGGGTCTACACACAAATCAGTCAGTG GCCAGAAAGACCCCTCAGAAATCGGAGCAGGAGGATGGGAGTGTGAGGGGTATCCTTTGATGCTT GTGTGCCCAACTTTCCAAATCCCCGCCGCCGCGATGG
ESTD-TYR	--	--	--	--	TAGTGAAGTTTTTCATCTCCTGTGAGCTCTGAGTTCTTGTTCACCCGCAACAAGAGAGTCTATGC CAAGGCAGAAAGCTGGTCTTCATGGGCAAAATCAATGTCTCCAGATTTCCAGATCCCCCAAGCA GTGCATCCATTGACACATAATATGATCCAGACAAAGAGGTCAATAATTTGATGTGCTTAAACAT GGGTGTTGATCCATTTCATTTGGCCATAGGTCCTATGGGGATGACA

ESTD-TYRP1	--	--	--	---	---	---	AGTAGTGGATGAAGCTAACAGCCTCTCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAAATCCTAATCAGTCTGTGGCTAACAAATGCCCTACTCTCTTATGCAATTAGTATCACA AACCACCTGGTTGAATATAATAGATTGAGTTATTAAGTGTATTTCTTTTCACCTTTATTACCTTCTCTCT AATACAAGCATATGTTAGAAITTAAGTTCTAGGCATACTT
ESTD-VB12	--	--	--	---	---	---	TTCCCAAGGCCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTGTTTCTATTACAA GGACACATGGATGCTGGAAATCACCCAGAGCCCAAGACACAAGGTACAGAGACAGGAACACACAGTG ACTCTGAGATGTCACCCAGACTGAGAACCCACCGTTATATGTACTGGTATCGAACAAGACCCGGGGCATG GGCTGAGGCTGATCCATTACTCATAT
ESTD-VWF	--	--	--	---	---	---	AGGTAGGAAAAGCAAAGAGTTGATTAGTGAAGGAGAGAAATGGACCTACCTTCCACACTGTCCTTTGG TCCCTAGAGTCTG
ESTD-WT1	--	--	--	---	---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCCTCCCTTCCTCTTACTCTCTGCCTGCAGGATGTG CGACGTGTCCCTGGAGTAGCCCCGACTCTGTACGGTGGCATCTGAGACCAGTGAGAAAACGCCCTT CATGTGTGCTTACCCAGGCTGCAA
ESTD-s14544	--	--	--	---	---	---	TTGGGAAGTTAGAGCCTATATTAAATTACGGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAAATGTCTCAGTTCGCTGTGTGGTTAGATGCAGGATTTATATGATCCCGTTAAC TCT
EST71770 6	--	--	--	---	---	---	AGCACACCTCTCACGTCAAGCCTCAGCACACAGATGCTGTTCTATAAGGATGACGTGCTGTTTACAA CATCTCCTCCATGAAGAGCACAGAGATTATTTATCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTACTGTGATTGTGAACAACAAGAGAAAAACCCTGCAGAGTACCAGCTGTGTGGTGAAGG AGTGCCAGTCCACAGGGTGACACTGGACAAGAAAGAGGCCATCCAAAGG
EST52418 6	--	--	--	---	---	---	CAAATTACAGSGTCAACTGCTATGATGTGTTTGGAGCCAGTCAACCTTTGGTGGCTACAAGATGTGG GGGAGTGGCCGGGAGTTGGCGAGTACGGGCTGCAGGCATACACTAAAGTGAAGAACTGTGAGTGTGG
EST13586 3	--	--	--	---	---	---	CCCCTCTATTTGCCAGCCCCAGGACAGAGCTGATCCTTTGAACCTCTTAAGTTCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCCAGGGCTGGCTTATCAGCCTCCACGCCACAGACCCCTGGCTGCAGCAT AAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGTGCCTGCTGCCTGCCCTGCCCGG GTCACTC
EST51976 7	--	--	--	---	---	---	AGGCAGAAACTGGGCCCCCATGTCGGGGGACGTGGAAGGCACTTGAAGCTTCTCTCTGGAGAAGGACCTGA GGGACAAGGTCAACTCCTCTCTTCAGCACTTCAAGGAGAAAGAGAGCCAGGACAAGACTCTCTCCCT CCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGCAGGACGACGAGGAGGAGTGCAGATGCTGGCC CCCTTGGAGAGCTGAGCTGCCCTGGTGG

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EST11458 6	--	--	---	---	---	CCACTTGGTAGTCCAGTGTGACTCATCCACAATGATTTCTCCAGTGCCTCATCTTGTCTCGAGTTT CTCGCCATGTTGCTATTGCAGGACGGACCTGTCCAAAGCCAGATGATTTACCATTTTCCACAGTGGT CCATTAAACAATTCTATGAGCCAGGAGAGATACGTATCTCTGCAAGCCGGCTATGTGTCC CGAGGAGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC
EST39852 8	--	--	---	---	---	CGGTCTTCTTCCAGGTATTGTGAGAAGGCCGAGATGACCTCTATGTCTCAGATGCATCCATAAG GCATTCTTGAGGTGAGTACACCTTCCCACTCTTACGGTACAGAAAGAGATGCATGAACAGCA GGAACACGTGGAAGGCCCTGTTCCAGTGTTAAGGCATGCAAAAGGCCCTCCACAGGCTGCTATAAT ACAGGCCCT
EST62448 0	--	--	---	---	---	ACCTGGTGTGCTGTGGGTGAACCTGGTCTCTTGGCAITTCGCCGCCCTCTGGGGCCCGTGG TCTCTCTGGTGTGGGTAGTCTGGAGTCAACGGTCTCTCTAGTGAAGCTGGTGTGATGGCAACC CTGGGAACGATGGTCCGCCAGGTGCGATGGTCAACCCGACACAAAGGAGCGCGGTACCCCTGG CAATAT
EST36027 2	--	--	---	---	---	AGTGACTTCCAAGGAAATGGCTACCCAACTTGCCCTTCATGCGCCTGCTGGCCAACTATGCCTCTCAGA ACATCACCTACCACTGCAAGAACAGCATTGCATACATGGATGAGGAGACTGGAAACCTGAAACAGG CTGTCAATCTACAGGGCTCTAATGATGTTGAACCTGTTGCTGAGGGCAACAGAGTTTACACT GTCTTGTAGATGGTCTCTAAAAGACAAATGAATGGGGAAAGACAA
EST12274 0	--	--	---	---	---	CCCCAGTTGACAGCCACTGCTTAGACTAAGTTTCTTGCTTCCAAATAGAGCCCTTACCAAAGTGTAT TACATAAAGAAAGTCAAGTGGTTTACTCTCATGACCAAATATTTCTTCCCTCTTAGGATGAGGTGA TAGTAAATGACCGATGGGGTCAGAACTGTTCTGTCCACCATGGAGGATACTATAACTGTGAAGATAA ATTCAAGCCACAGAGCTTGCCAGATC
EST76807 EST44438 7	--	--	---	---	---	ATGCTAAGGGGATCGACATGAAAGGACCCCTGTGAGCCGATTGTCTATCTCCAGCGGCCCTGTCTATC CAGCTCACTCATCAATGGGGCCAGTCAGGCCAGGCACTGGGCTCCGGAGGACTCACCACTGCCCCCT GCTGCCATGTGACTGGTGAAGTTGAGGACTTCTTG GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATCGGGACCTCAAGCTCGACTTCAAGGAGCTCT GCTCCGACCTAAGCGGAGAGCCCTCAAGAGCCGAGCGGTGGG
EST12839 3	--	--	---	---	---	TGCAAAACACACAAAATCTTCTCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAGATCAAGTCCAAGG CCATTGGCTATCTCAACACTGGTGAAGTATTACTTGAAGGAAACCTTGAATGTTATTCAACTGG ATTCCAGTAGGTTTCACTTACTTGAATATTATGATACTTAGCTTAG
EST54419 8	--	--	---	---	---	CTTCTGCCTAATTTGAATGATATTGTTGCTGTGGGACCTGAGCACCTTTATGGCACAAATGATCACTA TTTTCTTGACCCCTACTTACAATCTCGGAGATGATTGGGTTTAGCGTGGTGTGCTATGTTGCTACTA TAGTCCAAGTGAA

EST10398 2	---	---	---	---	---	TGCCTGGGGTGGCAAGGCTGCAACAAGGAGGCAACCCAGGAGGCTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGTATGATGTTTACATTTGGGCTTGACCTTCCACACGGAGAAG CATTGTTTCTCGGGCCAAAGGATCTACCAATAGTGTCTATTAGGCATTGG
EST36751 7	---	---	---	---	---	CCAAAGTCGTTCAATTTTAGCTTTCAGGTTTAACTCGAATGCTTTTCTATTCAAATCTCTGTAAAA TTGAAATATGAACCTAGTTTCTGATCTATGGTTTCAAGTTAAACAG
EST40562	---	---	---	---	---	CACGTGAAAGGAGCTATTTTGGAGGCTTAAAGATAAGAACTGTCTCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAATTTCACTGGATGCTTAATAACAAATATTTACCTTTTGAAAAATAAATG AAGGATTTGACCTGCTCGCTCTGAAAGAGTATCCGTACCGTCTGACGTTTGAACAATACAGAT GCCTTCCCTTGTAGCAGTTTTCAGGCTCTCTACCCCTA
EST18288 3	---	---	---	---	---	GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGTAGAA GATTGACAGGTTTCAGAGGCTGTACAGGATGGAAGACTGGCTGCTCCTGACGGAGCCAGTGTGG ACAGCACCTGGCTTCAACACCTAGTCCACTTCCAAGGTAAGGCAACCTCTCTGCTGGCTCTGGC CCTAGGACTTAGTATCC
EST70523 3	---	---	---	---	---	TTCCGCCAGCCCCCATCTTGGCACCTTGGTCCCTCAGGGGCAACCCCGGSCACTCACCGCTCT CGCTCTGGGTAACTCCGGCCGGCGCGCTCTTGAGCACATAGCCTGGACCGTTTCCGTATAGGAGG ACCGTGTAGGCTTCTGTCCGGGCTTGCCAGGGCCAGCCCTGCAGAGAGAGGGTCCCTGTGGT TGAGCTGAACACAGCTGTGGAGTGTCTCCACGTTG
EST58707 7	---	---	---	---	---	CAGTGTATCTGGAAGCCTACAGGACACCAATAACCTTAACTCAATGTTTACAGGAGGCTTT AAGTTGAGCATCTTTGGCTCACATGAAGGCCAAATTCGAGAGACCTAGAGATACACGAGACCGA ATGATCAAATGGACATTCAGCAGGAACCTTCAACGATACCTGTCTGGTAGGCCAGGTTTATAGCA CACTTGCACCTACATTTCTGATTGGTGGACTCTTGTCTGCTAAGAACCCTT
EST74167 6	---	---	---	---	---	AGACCATGAAGGAGTTGAAGGCTTCAAAATCGAACTGGAACTGGAGGAACAACGTACCCCGTGGCGGAGG AGACGGGACACGGCTGTCCAGGAGCTGCAGGGCGGCGAGCCCGGCTGGCGCGGACATGGAGGA CGTGGCGGCGGCTGTGTGCACTACCGGGCGAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGC TGCGGGTGGGCTCGCTCCACCTCGCAAGCTGGCTAAGCGGCTCCTC
EST43211 8	---	---	---	---	---	CGCCTGGTGCAGTACCGCGGAGGTGCAGGCCATGCTGGCCAGACGCCAGGAGCTGGGGTGGG CCTCGCTCCACCTGCGCAAGCTGCGTAAGCGGCTCTCCGGATGCCGATGACCTGCAGAGAGCGCC TGGCAGTGTACAGGCGGCGGCGGAGGGCGGCGGAGCGGCGCTCAGCGCCATCCCGGAGGCGCTG GGGCGCTGTGTGAACAGGGCGGCTGGCGGCGGCGGCTG
EST36770 4	---	---	---	---	---	TGTAGCCAAAGTCACCTGCATCATCTTGGCTGTGGCAGGCTTGGCCAGTTTGCAGCTATAATCC ATCGAAATGTATTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTCCATTATGATCCCAAAAT TCAACCCCTCCGATAGGCTGGGCTGACCAAAATATACCTGGTTTCTGTTTCTCTGATCAT TCTTACAAGTTATCTCTTATTGGAAAGGCCCTAAAGAAAGGCTTATG

EST26021 1	..	..	..	..	..	TAATGTAAGCTCATCCACCAGAAGCCTGCACCATGTTTGGAGTTGAGTGACATGTTTCGAAACCTGT CCATAAAGTAATTTGTGAAGAAGGAGCAAGAGCAATCTCTGCAGCATTCTACTACCAAAATGA GCATTAGCTACTTTTCAGAAATTGAAGGAGAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTCTTTCTTTTGAACAAGCAAAAGCC
EST51212 0	..	..	..	..	..	ATCCTGAGCTCGCCAATAGCTTCTTGTTCTACTTCTCTCCACAAGCCCCAATTTCACTTTCTCA GAGGAATCCCAAGCTTAGGAGCCCTGGAGCCCTTTGTGCTCCCACTCAATACAAAAGGCCCTCTCT ACATCT
EST20118 2	..	..	..	..	..	GTCCGAATCCCTCCTCTGAAAGTGCCCGGGTTTAACTGCTCATGACGCTGCGGCTGTGTCCAGCT GAGGTGAGGGCCCTTGAAGCTGGAGTGGGTTTAGGACGCGGTCTCTGCGCATCCTAAGCTCT GAGAGCAACCTCCCTTGAAGCTGGGAGTGGGGTTTAGGACGCGGGTCTCTGCGTGCATCCTAAGCT CTGAGA
EST53018 6	..	..	..	..	..	ACAATCCAGGTACACATTCCAGAAGAGGAGGGGTGGTCAGTGAGCCTGGGTAGGTCCAGTAATCCA AGGATTGAGGAAGGAGGCCACGAGGATCGAAGTAGTGAAGTC
EST68787 5	..	..	..	..	..	CTTCTATGGGATTGACITTTATTTCTCCATTGCTTACCTTTTACAGGTGTTAATATAGTGAAAAG GAAGCTTGAGCTCATGACAAATTTGAAGCTGACAAATTACAGAAGGAAATAAATTCACAGTCAA AGAATCAAGCACITTTTCGAAACATTGAAGTTGTTTTGAACCTTGGTGACCTTTAATACAACCTAG CAGACGGAAGTGAAGTCAAGGTTAAGAAAT
EST34088 2	..	..	..	..	..	GTGGGGCAACAGTGGGAGAGAAGGGGCCAGGGTATAAAGGGGCCCCACAAGAGACCGGCTCAAGG ATCCAAAGGCCCAACTCCCGAACCACCTCAGGGTCTCTGTGACAGCTCACCTAGCTGCAATGGCTACA GGTAAG
EST37382 5	..	..	..	..	..	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCCACCCCCCTCTTCTCTTCTCCCTTGA CTTTGAGTCAAAATGGCCTGGACTTGAGTCCCTGAACCAAGCAAGAGAAAGAGAGGCCAGCAAAAT CACAGGTGGGCACGTGCGTCTACCGCCATCTCCCTTCTCACGGGAAATTTTCAGGGTAACT
EST74082 0	..	..	..	..	..	TCCAGGGTGGCTGGACCCCAAGGCCCCAGCTCTGCAGCAGGAGGAGCGTGGCTGGGCTCGTGAAGCATG TGGGGTGAGCCCAAGGGCCCCAAGGCAGGGCACTGGCTTACGCTGCCCTCAGCCCTGCTGCTGCTC CCAGATCACTGTCTCTTCTGCCATGCCCTGTGGATGGGCTCTCTGCCCTGCTGGGCTGCTGGCCCTC TGGGGAACCTGACCCAGCCGCGAGCCTTTGTGAACCAACACCTGTGCG
EST45311 0	..	..	..	..	..	GCCTCCTCTCTTCCAAATCTGTCCCTATAGTTTTCTCTATTAAAGTGAACATGACATGCTTTTAGT GGATAGATGCACACAAACACAGAGCCATTATGGGGAAGGATCCACGTGTGGCCATATTGTAACA CATTTTCTGCAAAATCACCTCTTTCATTTAACAGCCCTTATTCAATGGCCCTTTTCTTTTTCAGTAGTA CATACACATCTGTGTCATTGTGAAT

EST65258 8	--	--	---	---	---	TGCCCCATACGGCGGCCGAGACATGGCTTGCCACAGCTCTGAGGATGTACCAATTAACCAGAAAT CCAGTTATTTCCACCCTCAAAATGACAGCATGGCCGCGGGTCTTCTGGGGCTCGTCGGGGGG ACAGCTCCACTCTGACTGGCACAGTCTTTGCATGGAGACTTGAGGAGGGAGGGCTTGAGGTTGGTGAG GTTAGGTGCGTGTCTTCTGTGCAAGTCAGGACATCAGTCTGATTAAA
EST38216 3	--	--	---	---	---	ATGCAGGATGAAGGTGGACAGGGAGAGAGGGCCCAACCTGTCTATCCAGGGCCTGCAGATGTCGCTG GACTATGGGTTTGTACCCCACTGACCTCCATGAGCATCAGGG
EST62782 --	--	--	---	---	---	ATACTAGTACAAGTGGTAAATTTTGTACATTACACTAAATTAATAGCATTTGTTTAGCATTACCTAA TTTTTTCCTGCTCCATGCAGACTGTAGCTTTTACCTTAATGCTTATTTTAAATGACAGTGAAG TTTTTTTTCTCGAAGTGCCAGTATCCAGAGTTTGGTTTTGAACTAGCAATGCCTGTGAAAAA GAACTGAATACCTAAGATTCTGTCTGGGGTTTTGGTGCATGCA
EST35879 9	--	--	---	---	---	GAGATCGGTGTGAGTATTAGGCATGGTACCTGTGATTCGCCAATCTTGTGCGTTCACACCGATG GAACTGCCGGCAATCCTGACAGCTGTGCACCCAGGCTGTACCCAAATAGGTGAACATGGCTTCGAG AGAGTTGAACAGATTCTGGAAGACAGCAGCGGGATGGGGCAGGAGAGCTGCCCTGGATGAA
EST68308 5	--	--	---	---	---	GGAAAGAGATTTAAGAAGCTTGAATTTGGACAATTCGTGTTCTTTGAGTGTGGAAGAGTTTCATGTCTCT GCCTGAGTTACAACAGAAATCCTTTAGTACAGCGAGTAAATAGATATATTCGACACAGATGGGAATGGA GAAGTAGACTTTAAGGTAAAGAAAGTAGTATTTTTTA
EST54045 6	--	--	---	---	---	GGAATATTAATAATTTTAAATACCTCCATTTTGCCTTATCTCTTTAGTGAAGATGATACCTGCAA AAGACATGGCTAAAGTTATGATTGTCATGTTGGCAATTTGTTTCTTACAAAATCGGATGGGAATCT GTTAAGTAAGTACTGTTTGGCTTGGAAATGGATTTTAAATGTTGACTTTATCAT
EST52908 0	--	--	---	---	---	ATCACAGGTCTCTGGTCTCTGGCCATCATTTCTCTGGGAGAGATGGATGGTCTGCAAGCCCTTTGG CAATGTGAGATTGTATG
EST19590 --	--	--	---	---	---	AGGAGAAGCTGAGGAGGGGAAGAGAGACAAGATGACATTGATGAGTGAAGATGTGGGCTCAGGAT GCCGGAATAATGAC
EST76136 --	--	--	---	---	---	TGAAGCTTCTGCCAGCTTGCTGTCATTGTTTCTAGGAGAACCCGCTCATACCTTTATCTATAGCCTTCCCC TAGGTCCT
EST58607 0	--	--	---	---	---	CTCTGGATGGGTTACAGGTGGCAGGCACAAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCTCACTGGAGAACAAAGACAGCCACATGGCGGGGATGGCGGGGAGTTCTGGT TGCGGCCACGGCTGTGGCTCTGTTGTAACGGTAGCCTTTGCGGTTGCGATGCCCTAAACCTTTGTTCT TGGCCAAGGAGGGGGGTGCCATGCTGAGATGATAGTCGGCC
Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer 6=SNP Reverse Primer 7=Sequence						



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## EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that

5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the

10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

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## CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,  
or a portion thereof which includes a polymorphic site,  
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is  
biallelic.
8. The segment of claim 1, wherein the polymorphic form  
occupying the polymorphic site is the reference base  
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form  
occupying the polymorphic site is an alternative form  
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a  
20 segment of a fragment shown in the Table, column 7 or  
its complement.
11. The allele-specific oligonucleotide of claim 10 that is  
a probe.

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12. The allele-specific oligonucleotide of claim 10,  
wherein a central position of the probe aligns with the  
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is  
5 a primer.
14. The allele-specific oligonucleotide of claim 13,  
wherein the 3' end of the primer aligns with the  
polymorphic site of the fragment.
15. The allele-specific oligonucleotide of Claim 10, which  
10 is selected from the group consisting of the nucleotide  
sequences of the Table, column 5..
- 16..The allele-specific oligonucleotide of Claim 10, which  
is selected from the group consisting of the nucleotide  
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the  
Table, column 7 or the complement thereof, wherein the  
polymorphic site within the sequence or complement is  
occupied by a base other than the reference base shown  
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising  
obtaining the nucleic acid from an individual; and  
determining a base occupying any one of the polymorphic  
sites shown in the Table.
19. The method of claim 18, wherein the determining  
25 comprises determining a set of bases occupying a set of  
the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method  
5 further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.

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